Genes	Correspo	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	
	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
4992	0.015924	tissue factor pathway inhibitor (lipoprotein-		Hs.170279	NP_006278
1		associated coagulation inhibitor) (TFPI),		*	-
		mRNA /cds=(1,915) /gb=NM_006287		•	"
	·	/gi=6715569 /ug=Hs.170279 /len=915		· ·	1. 1
4993	0.023148	likely ortholog of mouse hepatoma-	NM_016073	Hs.127842	NP_057157
		derived growth factor, related protein 3			_
	•	(HDGFRP3), mRNA /cds=(156,767)	*	-	1
		/gb=NM_016073 /gi=21359902			
		/ug=Hs.127842 /len=1973	Ŷ		
5004	0.00527	cytochrome P450, family 1, subfamily B,	NM_000104	Hs.154654	NP_000095
		polypeptide 1 (CYP1B1), mRNA			
	e '	/cds=(373,2004) /gb=NM_000104	-X-,		
		/gi=13325059 /ug=Hs.154654 /len=5128		<u> </u>	
5006	0.041254	cDNA FLJ33181 fis, clone	AK090500	Hs.379218	
- 1		ADRGL2003684, highly similar to HLA	*		
].		CLASS I HISTOCOMPATIBILITY			· 0
×		ANTIGEN, ALPHA CHAIN H			
ľ	7	PRECURSOR./gb=AK090500	9		
<u></u>	<u></u>	/gi=21748675 /ug=Hs.379218 /len=2290			
5009	0.011469	basic transcription factor 3 (BTF3), mRNA	NM_001207	Hs.101025	NP_001198
*	ï	/cds=(240,728) /gb=NM_001207			
-27.		/gi=20070129 /ug=Hs.101025 /len=952			
5016	5.96E-04	ribosomal protein L17 (RPL17), mRNA	NM_000985	Hs.82202	NP_000976
	·	/cds=(287,841) /gb=NM_000985			]
5000	0.004507	/gi=14591906 /ug=Hs.82202 /len=898	100000	11. 07.4004	NE OLIOSO
5022	0.024587	ORM1-like 3 (S. cerevisiae) (ORMDL3),	NM_139280	Hs.374824	NP_644809
		mRNA /cds=(141,602) /gb=NM_139280			
5000	0.040000	/gi=27544926 /ug=Hs.374824 /len=2109	NINA 020004	11- 204000	ND 445500
5023	0.012262	ASC-1 complex subunit P100	NM_032204	Hs.334686	NP_115580
· .		(FLJ21588), mRNA /cds=(115,2388)			
1		/gb=NM_032204 /gi=20270252 /ug=Hs 334686 /len=2808	0		
5027	0.027601	nucleobindin 1 (NUCB1), mRNA	NM_006184	Hs.172609	NP_006175
3021	0.027091	/cds=(27,1412) /gb=NM_006184	14W_000104	IDS. 172009	INP_000175
		/gi=20070227 /ug=Hs.172609 /len=2311			
5032	0.024587	hypothetical protein FLJ90811	NM_153339	Hs.400659	NP_699170
1 0002	0.02.4007	(FLJ90811), mRNA /cds=(31,942)	14111_100000	113.400000	_033170
		/gb=NM_153339 /gi=23503258			
	÷	/ug=Hs.400659 /len=1262		٠.	- ( -
5036	0.004536	peptidylprolyl isomerase B (cyclophilin B)	NM 000942	Hs.394389	NP 000933
	3.55 ,556	(PPIB), mRNA /cds=(150,800)		1.10.004000	[
	1	/gb=NM_000942 /gi=20149505		1	<u>†</u>
,	,	/ug=Hs.394389 /len=1028			
5037	0.024587	MAP kinase-interacting serine/threonine	NM_017572	Hs.261828	NP_060042
		kinase 2 (MKNK2), mRNA /cds=(23,1267)		1	_5555 ;2
o-		/gb=NM_017572 /gi=9994196			0.2
1		/ug=Hs.261828 /len=1549	]		
7 70				<del></del>	<del></del>

		nding To Differentially Expressed Genes  Description	Gene	Unigene	Protein
Spor	p-value.	Description	Accession	Accession	Accession
5042	0.004202	laminin receptor 1 (ribosomal protein SA,	No. NM 002295	<b>No.</b> Hs.181357	<b>No.</b> NP_002286
5042	0.004203		14141_002295	MS. 101357	JNP_002200
		67kDa) (LAMR1), mRNA /cds=(86,973)		* :	
i		/gb=NM_002295 /gi=9845501			
5011	0.000400	/ug=Hs.181357 /len=1039	NNA 000004	0.050	ND 000407
5044	0.008133	S100 calcium binding protein A4 (calcium	NM_002961	Hs.81256	NP_062427
		protein, calvasculin, metastasin, murine			10.00
		placental (S100A4), transcript variant 1,			
	8	mRNA /cds=(70,375) /gb=NM_002961			
		/gi=9845514 /ug=Hs.81256 /len=512			
5046		topoisomerase II alpha-4 (AF285159)	AAG13405		
5047	0.01925	hypothetical protein DJ328E19.C1.1	NM_015383	Hs.218329	NP_056198
		(DJ328E19.C1.1), mRNA /cds=(18,2783)			
		/gb=NM_015383 /gi=7657016 ,			10.
		/ug=Hs.218329 /len=3689			
5049	0.008133	mRNA for KIAA0592 protein; partial cds.	AB011164	Hs.439367	
	- *	/cds=(1,4062) /gb=AB011164			
		/gi=3043707 /ug=Hs.439367 /len=4623		140	
5053	0.031117	tubulin-specific chaperone d (TBCD),	NM_005993	Hs.12570	NP_005984
	] .	mRNA /cds=(110,3688) /gb=NM_005993			
		/gi=8400735 /ug=Hs.12570 /len=3927.			
1				· .	
5058	0.029363	U6 snRNA-associated Sm-like protein	NM_012321	Hs.76719	NP_036453
	ł .	(LSM4), mRNA /cds=(49,468)			=
	,	/gb=NM_012321 /gi=6912485			
		/ug=Hs.76719 /len=1033			V
5062	0.0261	KIAA1208 protein, partial cds	AB033034	Hs.7041	NP_077288
		/cds=UNKNOWN /gb=AB033034			
	Ł	/gi=6382021 /ug=Hs.7041 /len=6447			
5064	0.03489	nipsnap 1 (C. elegans) (NIPSNAP1),	NM_003634	Hs.173878	NP_003625
	`	mRNA /cds=(255,1109) /gb=NM_003634		ļ	
		/gi=4505398 /ug=Hs.173878 /len=2233			
5068	0.008133	KIAA1115 protein (KIAA1115), mRNA	NM_014931	Hs.72172	NP_055746
	} -	/cds=(769,3033) /gb=NM_014931			
		/gi=7662489 /ug=Hs.72172 /len=3781	, ,		
5069	0.003332	hsp70-interacting protein (HSPBP1),	NM_012267	Hs.53066	NP_036399
	-	mRNA /cds=(312,1400) /gb=NM_012267			
	1	/gi=21361406 /ug=Hs.53066 /len=1795			, ,
	, .				
5070	9.44E-04	cDNA FLJ12776 fis, clone	AK022838	Hs.372558	
		NT2RP2001678. /gb=AK022838		-00-	*
		/gi=10434465 /ug=Hs.372558 /len=2629			*
5087	0.018081	mRNA; cDNA DKFZp451M092 (from	AL713650	Hs.336425	-:
		clone DKFZp451M092) /gb=AL713650			4
		/gi=19584326 /ug=Hs.336425 /len=3645	1		I.

		nding To Differentially Expressed Genes			
Spot	p-value		G ne	Unigene	Protein
			Accession	Accession	Accession
5004	0.000400		No.	No.	No.
5094	0.006106	sterol regulatory element binding	NM_004599	Hs 108689	NP_004590
	-	transcription factor 2 (SREBF2), mRNA		ĺ .	
•		/cds=(170,3595) /gb=NM_004599			<i>U</i> ,
•		/gi=27477112 /ug=Hs.108689 /len=4325			
5095	0.00489	nucleoporin 62kDa (NUP62), transcript	NM_153719	Hs.9877	NP_71494
		variant 1, mRNA /cds=(408,1976)		*.	
		/gb=NM_153719 /gi=24497608	0.0		
* '		/ug=Hs.9877 /len=3403			
5096	0.043576	ribosomal protein S27a (RPS27A), mRNA	NM_002954	Hs.311640	NP_00294
		/cds=(39,509) /gb=NM_002954			*
•	<u> </u>	/gi=27436941 /ug=Hs.311640 /len=541			
5102	0.003332	cofilin 1 (non-muscle) (CFL1), mRNA	NM_005507	Hs.180370	NP_00549
		/cds=(52,552) /gb=NM_005507	Y.		
		/gi=5031634 /ug=Hs.180370 /len=1059			*
5103	0.016974	signal transducer and activator of	AF417842	3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
		transcription 6, interleukin-4 induced	,		
:		(STAT6) gene, complete cds			<u> </u>
5104	0.003893	T-cell activation leucine repeat-rich	NM_015350	Hs.199243	NP_05616
•		protein (TA-LRRP), mRNA	-		· _
		/cds=(565,2976) /gb=NM_015350			
		/gi=21245133 /ug=Hs.199243 /len=3588	-	-	
5105	0.012262	hypothetical protein FLJ20312	NM_017761	Hs.7862	NP_06023
		(FLJ20312), mRNA /cds=(384,803)	<del>-</del>	0	
	· .	/gb=NM_017761 /gi=20127576			
		/ug=Hs.7862 /len=2382	* *	·	
5106	0.03489	c-myc binding protein (MYCBP), mRNA	NM 012333	Hs.78221	NP_03646
0		/cds=(39,350) /gb=NM_012333			_
		/gi=8850230 /ug=Hs.78221 /len=2070			*
5108	0.046005	calponin 2 (CNN2), mRNA /cds=(28,957)	NM 004368	Hs.169718	NP_00435
		/gb=NM 004368 /gi=4758017			
		/ug=Hs.169718 /len=2122	P		
5110	5 42F-04	mRNA for KIAA0472 protein, partial cds.	AB007941	Hs.6874	
01.0	0 0.	/cds=(1,1100) /gb=AB007941		, 10.007	
		/gi=3413905 /ug=Hs.6874 /len=5494	•		
5111	0.008133	chromosome 14 open reading frame 94	NM 017815	Hs.8886	NP 06028
3111	0.000133	(C14orf94), mRNA /cds=(211,1302)	11111_017010	113.0000	_00020
:*	]	/gb=NM_017815 /gi=8923395			ļ
		/ug=Hs.8886 /len=1618	a	*	
5113	0.008722	likely ortholog of Xenopus dullard	NM 015343	Hs.84359	NP 05615
3113	0.000722	(HSA011916), mRNA /cds=(31,765)	11111_013343	113.04355	_05015
	}	//gb=NM 015343 /gi=7661721		l	}
		10 -			
5107	0.020262	/ug=Hs.84359 /len=1356	AK001489	Hs.372616	<del>                                     </del>
5127	0.029303	cDNA FLJ10627 fis, clone	ANUU 1489	HS.3/2010	
	*	NT2RP2005555. /gb=AK001489			
F 4 2 2	0.0000	/gi=7022777 /ug=Hs.372616 /len=1626	D 400 10	11- 70400	
5144	0.029363	KIAA0084 mRNA, partial cds	D42043	Hs.79123	. *
		/cds=(1,1947) /gb=D42043 /gi=577298		~	
ė	L	/ug=Hs.79123 /len=2918	<u> </u>	I	<u> </u>

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
	· .		Accession	Acc ssion	Acc ssion
_	· ′		No.	No.	No.
5151	0.018081	602271085F1 NIH MGC_84 cDNA clone	BF968646	Hs.380945	
		IMAGE:4359261 5', mRNA sequence	*		
		/clone=IMAGE:4359261 /clone end=5'	4	-	,
		/gb=BF968646 /gi=12335861	**		
	٠,	<u> </u>		,	
F400	0.007570	/ug=Hs.380945 /len=1098	AE460042	Hs.351379	-,
5160	0.007578	hepatocellular carcinoma-associated	AF469043	⊓S.301379	*
		antigen HCA25a mRNA, complete cds	12		
		/cds=(1935,2396) /gb=AF469043			
		/gi=21311562 /ug=Hs.351379 /len=2878		7	
5161	0.046005	basic transcription factor 3 (BTF3), mRNA	NM_001207	Hs.101025	NP_001198
		/cds=(240,728) /gb=NM_001207	• .		. <del>.</del> .
		/gi=20070129 /ug=Hs.101025 /len=952			
5170	0.029363		NM_001483	Hs.152707	NP_001474
		mRNA /cds=(9,869) /gb=NM_001483	· · · · · · · · · · · · · · · · · · ·		
		/gi=4503936 /ug=Hs.152707 /len=1975			
•					
5176	0.021781	mRNA for KIAA0379 protein, partial cds.	AB002377	Hs.32556	
		/cds=(1,3181) /gb=AB002377			
_ (6		/gi=6634024 /ug=Hs.32556 /len=4408			
5183	0.010015	basic transCRiption factor 2 p44 (btf2p44)	1180017		-
3103	0.010013	gene, partial cds, neuronal apoptosis	000017		
		inhibitory protein (naip) and survival motor		1	
	- ×				
E404	0.004405	neuron protein (smn)	M24732		
5191		lamin-like protein (low match)		115 42000	NP 057289
5198	0.008133	platelet derived growth factor C (PDGFC),	NM_016205	Hs.43080	NP_05/269
		mRNA /cds=(492,1529) /gb=NM_016205			0.
		/gi=9994186 /ug=Hs.43080 /len=3007	1 .		
			7		·
5219		ataxia telangiectasia(ATM) gene	U82828		
5220	3.35E-05	calcium-independent alpha-latrotoxin	AF063102		
	· · ·	receptor homolog 2 (CIRL-2) mRNA,			1
**	`	complete cds		<u> </u>	
5224	0.007056	ubiquitously-expressed transcript (UXT),	NM_153477	Hs.172791	NP_705582
		transcript variant 1, mRNA			
		/cds=(155,664) /gb=NM_153477			1
		/gi=24041017 /ug=Hs.172791 /len=734			
5231	0.016974	KIAA0066 mRNA, partial cds	D31886	Hs.227881	
	-	/cds=(1,2948) /gb=D31886 /gi=505099			
	·	/ug=Hs.227881 /len=3635			
5238	0.046005	NRAS-related gene (D1S155E), mRNA	NM_007158	Hs.69855	NP_009089
0200	0.0.000	/cds=(428,2824) /gb=NM_007158			
		/gi=20070240 /ug=Hs.69855 /len=4076			
5243	0.031117	chromosome 14 open reading frame 2	NM 004894	Hs.109052	NP_004885
0243	0.031117		14141_004094	113.103032	111 _004000
		(C14orf2), mRNA /cds=(61,237)		,	÷
		/gb=NM_004894 /gi=4758939			
*****		/ug=Hs.109052 /len=627		11 000151	lun saiss
5252	0.00489	stromal cell protein (LOC55974), mRNA	NM_018845	Hs.292154	NP_061333
	7	/cds=(61,726) /gb=NM_018845	1	-2-	, -
	1	/gi=10047123 /ug=Hs.292154 /len=1316			1 .

Genes	Correspoi	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	* *
		D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
5269	0.032959	hypothetical protein FLJ20707	NM_032560	Hs.334657	NP 115949
		(FLJ20707), mRNA /cds=(83,2173)			· . <del>-</del>
	1 7,1	/gb=NM_032560 /gi=19923643	•	٠.	
		/ug=Hs.334657 /len=2794		*	
5276	0.013102	myosin light chain 2 (HUMMLC2B),	NM 013292	Hs.50889	NP_037424
		mRNA /cds=(60,569) /gb=NM_013292	<del>-</del>		
		/gi=28372498 /ug=Hs 50889 /len=687			
5293	0.007578	chromosome 6 open reading frame 48	NM_016947	Hs.109798	NP 058643
٠.	*	(C6orf48), mRNA /cds=(42,422)			_
		/gb=NM_016947 /gi=8393383			
	·	/ug=Hs.109798 /len=711			
5307	0.013991	mitochondrial ribosomal protein S33	NM_016071	Hs.83006	NP_444263
		(MRPS33), nuclear gene encoding	<del>-</del>		. –
		mitochondrial protein, transcript variant 1,			
		mRNA /cds=(139,459) /gb=NM_016071	* 3		
	· · ·	/gi=16950595 /ug=Hs.83006 /len=727	* *		
5312	0.018081	testis specific, 14 (TSGA14), mRNA	NM_018718	Hs.27027	NP 061188
		/cds=(48,1169) /gb=NM_018718			
•		/gi=16306478 /ug=Hs.27027 /len=3526			
5315	0.005674	splicing factor, arginine/serine-rich 5	NM_006925	Hs.166975	NP 008856
00.0	0.00007	(SFRS5), mRNA /cds=(219,542)	1000020		
•	1): 4	/gb=NM 006925 /gi=5902077		,	
	1	/ug=Hs.166975 /len=1865			
5325	0.043576	eukaryotic translation elongation factor 2	NM_001961	Hs.75309	NP 001952
17		(EEF2), mRNA /cds=(69,2645)			
		/gb=NM_001961 /gi=25453476	- 00		
		/ug=Hs.75309 /len=3148	1.0	5	
5327	0.001737	zinc finger, DHHC domain containing 14	NM_024630	Hs.38270	NP 714968
	-	(ZDHHC14), mRNA /cds=(498,1964)			
	٠	/gb=NM_024630 /gi=24371240			*
		/ug=Hs.38270 /len=2821			
5328	0.041254	CDC20 cell division cycle 20 (S.	NM 001255	Hs.82906	NP_001246
	0.011201	cerevisiae) (CDC20), mRNA		,,0.02,000	
		/cds=(111,1610) /gb=NM_001255	ļ	. · ·	· ·
		/gi=4557436 /ug=Hs.82906 /len=1686	·		•
5329	0.021781	dolichyl-diphosphooligosaccharide-protein	NM 005216	Hs.34789	NP 005207
0020	0.021701	glycosyltransferase (DDOST), mRNA	1.4140002.10	110.011.00	1.1000201
		/cds=(60,1430) /gb=NM_005216			
		/gi=20070196 /ug=Hs.34789 /len=2045			
5330	0.023148	discs, large 7 (Drosophila) (DLG7),	NM 014750	Hs.77695	NP_055565
2220	0.020140	mRNA /cds=(218,2758) /gb=NM_014750	1.1111_014700	1.13.7.7333	
		/gi=21361644 /ug=Hs.77695 /len=2979			1
•		//gi-2 130 1044 /ug-115,/ / 033 /left-23/3			
5338	0.027604	thursid harmona recentor interactor 2	NM_004773	Hs.2210	NP_004764
აააბ	1.0.027091	thyroid hormone receptor interactor 3	INIVI_UU4773	F15.22 TU	INF_004/64
		(TRIP3), mRNA /cds=(39,506)	1		
	*	/gb=NM_004773 /gi=22094078		*	**
	<u> </u>	/ug=Hs.2210 /len=950		<u> </u>	T

		nding To Diff rentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
5341	0.020482	hypothetical protein FLJ20203	NM_017710	Hs.20594	NP_115668
		(FLJ20203), mRNA /cds=(6,2099)	. —		
		/gb=NM_017710 /gi=8923193			
		/ug=Hs.20594 /len=2994	*	•	=0
5348	0.006566	KIAA0066 mRNA, partial cds	D31886	Hs.227881	
		/cds=(1,2948) /gb=D31886 /gi=505099		÷	
	9 9	/ug=Hs.227881 /len=3635			<
5364	7.18E-04	hypothetical protein DKFZp547I224	NP 064606		- "
	0	(RefSeq aa 9e-31)	_		
5365	0.020482	cDNA FLJ31667 fis, clone	AK056229	Hs.48692	
		NT2RI2004840. /gb=AK056229			
	-	/gi=16551572 /ug=Hs.48692 /len=2052			
5373	0.012262	mRNA for KIAA1609 protein, partial cds.	AB046829	Hs.14449	
		/cds=(1,1423) /gb=AB046829			
		/gi=15425661 /ug=Hs.14449 /len=4683	a	·	
5381	0.00242	mRNA; cDNA DKFZp686K192 (from	AL832209	Hs.259347	
	0.002,12	clone DKFZp686K192) /gb=AL832209	, 12302200	11.0.2000 11	
	α	/gi=21732754 /ug=Hs.259347 /len=6707			:
5388	0.002625	peroxiredoxin 1 (PRDX1), mRNA	NM 002574	Hs.180909	NP 002565
ÇÇOO	0.002020	/cds=(61,660) /gb=NM_002574	002374	113.100303	141002505
		/gi=4505590 /ug=Hs.180909 /len=937			1-8
5390	0.008133	golgi apparatus protein 1 (GLG1), mRNA	NM_012201	Hs.78979	NP 036333
0000	0.000100	/cds=(27,3560) /gb=NM_012201	14101_0 (2201	113.70373	_000000
		/gi=6912389 /ug=Hs.78979 /len=3909			
5392	0.008722	clone IMAGE:5398100, mRNA	BC035584	Hs.407477	
0002	0.0007.22	/gb=BC035584 /gi=23273438	D0033304	113.407477	
		/ug=Hs.407477 /len=1570			
5402	0.027601	brain cDNA, clone:QnpA-21421	AB050422		
5405		retinoic acid induced 16 (RAI16), mRNA	NM_022749	Hs.299148	NP 073586
5405	0.03409	/cds=(382,783) /gb=NM_022749	14141_022749	115.233140	NF_07,3300
		/gi=21359938 /ug=Hs 299148 /len=2259		:	
5410	0.003803	hypothetical protein FLJ21016	NM 025160	Hs.289069	NP 079436
3410	0.003033	(FLJ21016), mRNA /cds=(33,1136)	NIVI_023100	115.209009	1117_079430
		/gb=NM_025160 /gi=24432014			
	,	/ug=Hs.289069 /len=3165			
5411	0.000340	DKFZp566J2446 (from clone	AL050082		NP 008944
5411	0.009349		ALU30062		INP_000944
5412	0.027601	DKFZp566J2446) mRNA for hypothetical protein (ORF1)	A 1207702	Hs.11114	
5413	0.027691		AJ297792	Ins.11114	
•		/cds=(327,989) /gb=AJ297792			
5423	0.015024	/gi=27526568 /ug=Hs.11114 /len=4110 ribosomal protein S29 (RPS29), mRNA	NIM 004030	Uo 520	NP_001023
5423	0.015924	· · · · · · · · · · · · · · · · · · ·	NM_001032	Hs.539	NP_001023
		/cds=(31,201) /gb=NM_001032			4
E 420	0.000400	/gi=13904868 /ug=Hs.539 /len=346	AK004000		ND 005000
5436	v.uu8133	Hypothetical protein(cDNA FLJ10768 fis,	AK001630	1	NP_005229
- 4 4 4	7.007.6	clone NT2RP4000150)	100/5-0-		
5441		lipoyltransferase, complete cds	AB017567	11	
5446	0.027691	heme binding protein 2 (HEBP2), mRNA	NM_014320	Hs.111029	NP_055135
		/cds=(276,893) /gb=NM_014320			
	1	/gi=7657602 /ug=Hs.111029 /len=1137			i

Cnot	n value	nding T Diff r ntially Expressed G nes			Protein
Spot	p-value	Description	Gene	Unigene	
121	3		Accession	Accession	Accession
		<u>n</u>	No.	No.	No.
5447	0.001344	602344930F1 NIH_MGC_89 cDNA clone	BG166990	Hs.440568	1
•	1	IMAGE:4454934 5', mRNA sequence	• •		
:		/clone=IMAGE:4454934 /clone_end=5'			
		/gb=BG166990 /gi=12673693	•		:
* .		/ug=Hs.440568 /len=1137			
5448	1.81E-04	eukaryotic translation initiation factor 4A,	NM_001967	Hs.173912	NP_001958
		isoform 2 (EIF4A2), mRNA		8 .	
		/cds=(16,1239) /gb=NM_001967		_ 0	
		/gi=9945313 /ug=Hs.173912 /len=1864			-2-
5451	0.032959	tumor protein, translationally-controlled 1	NM_003295	Hs.401448	NP_003286
		(TPT1), mRNA /cds=(95,613)			-
		/gb=NM_003295 /gi=4507668			
		/ug=Hs.401448 /len=830			
5453	0.031117	nuclear factor (erythroid-derived 2)-like 2	NM 006164	Hs.155396	NP 00615
		(NFE2L2), mRNA /cds=(114,1931)			
		/gb=NM_006164 /gi=20149575			
		/ug=Hs.155396 /len=2439			
5455	0.039034	type I sigma receptor (SR-BP1), transcript	NM 147160	Hs.24447	NP 67151
		variant 5, mRNA /cds=(75,278)	<del>-</del>		
	1	/gb=NM_147160 /gi=22325389	e" .	ļ	
		/ug=Hs.24447 /len=1706	0,00	9	
5460	0.043576	ql63e03.x1 Soares_NhHMPu_S1 cDNA	AI275510	Hs.148055	
0.00		clone IMAGE:1877020 3', mRNA		3	·
		sequence /clone=IMAGE:1877020		1	
	1.5	/clone_end=3' /gb=Al275510 /gi=3897784	c		
•		/ug=Hs.148055 /len=303	*	*	
5464	0.046005	chloride intracellular channel 4 (CLIC4),	NM_013943	Hs.25035	NP 03923
	1 3.0 10000	mRNA /cds=(198,959) /gb=NM_013943	, , _ , , o o , o	1.10.2000	
•	*	/gi=7330334 /ug=Hs.25035 /len=4318			
5494	0.00489	proteasome (prosome, macropain) 26S	NM_153822	Hs.148495	NP 72254
0-10-1	0,00400	subunit, non-ATPase, 4 (PSMD4),	11111_100022	110.110100	111111111111111111111111111111111111111
		transcript variant 2, mRNA /cds=(63,869)		·,	
		/gb=NM_153822 /gi=25121957	*		,
•.	X	/ug=Hs.148495 /len=1508			·
5509	0.003603	brain protein 44-like (BRP44L), mRNA	NM 016098	Hs.108725	NP_05718
2203	0.003003	/cds=(123,452) /gb=NM_016098	14141_0 10030	113.100725	147 _057 10
	i	/gi=7706368 /ug=Hs.108725 /len=988		•	
5510	0.03480	eukaryotic translation initiation factor 3,	NM_003753	Hs.55682	NP_00374
. 5510	0.05469	subunit 7 zeta, 66/67kDa (EIF3S7),	14141_003733	115.55002	NF_00374
		mRNA /cds=(372,2018) /gb=NM_003753		٠	*
	]	, , , , , <del>,</del> , =			
	17.	/gi=23238220 /ug=Hs 55682 /len=2169			
5511	0.044034	cytochrome o cyldago cybunit IV icoform	NIM 001961	Hs.433419	NP_00185
9911	0.014931	cytochrome c oxidase subunit IV isoform	NM_001861	175.433418	INE_00 100
		1 (COX4I1), nuclear gene encoding			
•	*	mitochondrial protein, mRNA	}		
		/cds=(165,674) /gb=NM_001861			-
		/gi=17017985 /ug=Hs.433419 /len=802			

		nding To Differentially Expressed Genes	Gene	Unigene	Protein
Spot	p-value	Description	,		
-			Accession	Accession	Accession
E 5 4 4	0 004447	11 11 11 11 11 11 11 11 11 11 11 11 11	No.	No.	No.
5514	0.031117	ribosomal protein L4 (RPL4), mRNA	NM_000968	Hs.286	NP_000959
	-	/cds=(57,1340) /gb=NM_000968			
		/gi=16579884 /ug=Hs.286 /len=1449		<u> </u>	ļ.,,
5520	0.048543	transforming growth factor-beta type I	AF035669		
		receptor			
5529	0.027691	SWI/SNF related, matrix associated, actin	NM_003077	Hs.250581	NP_003068
		dependent regulator of chromatin,		}	**
		subfamily d, member 2 (SMARCD2),	lasi'		
		mRNA /cds=(423,1850) /gb=NM_003077		1.	
		/gi=21264350 /ug=Hs.250581 /len=2704	) ·		
EE24	0.004202	cDNA FLJ30089 fis, clone	AK054651	Hs.131887	· · · · · · · · · · · · · · · · · · ·
5531	0.004203		CQ4001	1115. 13 100/	
	* -	BNGH41000013. /gb=AK054651 /gi=16549236 /ug=Hs.131887 /len=2527			
EEAO	0.00480		BC029202	Hs.382189	
5548	0.00489	clone IMAGE:4704802, mRNA	BC028293	JUS:205109	. ]
		/gb=BC028293 /gi=22418059		1	
	2 245 04	/ug=Hs.382189 /len=2776	NINA 000004	Hs.323949	NP 002222
5577	3.34E-04	kangai 1 (suppression of tumorigenicity 6,	NM_002231	IDS.323949	NP_002222
	·	prostate; CD82 antigen (R2 leukocyte		0.0	
	ļ	antigen, antigen detected by monoclonal		ľ	,
•		and antibody IA4)) (KAI1), mRNA			***
	-	/cds=(182,985) /gb=NM_002231			
5500	0.044054	/gi=13259537 /ug=Hs.323949 /len=1623	NINA 000745	11- 00000	NP 006706
5593	0.041254	mannosidase, alpha, class 2C, member 1	NM_006715	Hs.26232	NP_006/06
. •		(MAN2C1), mRNA /cds=(57,3245)		'	
		/gb=NM_006715 /gi=6631092	()		
5004	0.000700	/ug=Hs.26232 /len=3300	NINA 004000	11- 470000	ND 070400
5601	0.008722	hypothetical protein FLJ12443	NM_024830	Hs.179882	NP_079106
	† ·	(FLJ12443), mRNA /cds=(475,1188)		-]	
		/gb=NM_024830 /gi=21314725			
5000	<u> </u>	/ug=Hs.179882 /len=3476	1114 000 405	11. 454744	ND 00000
5609	0.00223	peroxisomal proliferator-activated	NM_033405	Hs.151714	NP_208384
		receptor A interacting complex 285			
	ļ	(PRIC285), mRNA /cds=(425,6667)		.] *	
		/gb=NM_033405 /gi=21703357			
		/ug=Hs.151714 /len=7804			115 001050
5616	6.03E-05	solute carrier family 31 (copper	NM_001859	Hs.380728	NP_001850
	,	transporters), member 1 (SLC31A1),	1		*-
		mRNA /cds=(153,725) /gb=NM_001859			•
	2 2 2 2 2 1 1 1 1	/gi=4507014 /ug=Hs.380728 /len=1804		<del> </del>	
5625	0.007578	opioid growth factor receptor (OGFR),	NM_007346	Hs.67896	NP_031372
	,	mRNA /cds=(206,2062) /gb=NM_007346	:	1	
·	ŀ	/gi=6671492 /ug=Hs.67896 /len=2423			
					No delega
5638		mRNA for KIAA0244 gene, partial	D87685		NP_055968
5640	1 0.032959	nonhistone protein HMG1	M21683	1:	

G nes	Correspon	nding To Differentially Express d Genes	in Figure 12 -	Hypertension	
	p-value	Description	Gene	Unigene	Protein
		3	Accession	Accession	Accession
		· ·	No.	No.	No.
5643	0.005674	solute carrier family 26, member 4	NM_000441	Hs.159275	NP_000432
00.0	0.00007	(SLC26A4), mRNA /cds=(225,2567)		1,10.1002,0	
		/gb=NM 000441 /gi=4505696	. + '		
		/ug=Hs.159275 /len=4930			
5646	0.01025	hypothetical protein (KIAA0608)	AB011180	1	<del></del>
			U07802	+	<del></del>
5654	0.016974			110 493434	ND OOFTE
5657	0.021781	ATPase, H transporting, lysosomal	NM_005765	Hs.183434	NP_005756
		(vacuolar proton pump) membrane sector			
		associated protein M8-9 (ATP6M8-9),		·	
		mRNA /cds=(103,1155) /gb=NM_005765			
		/gi=15011917 /ug=Hs.183434 /len=2044			
	<u> </u>				
5664	0.01925	TEA domain family member 4 (TEAD4),	NM_003213	Hs.94865	NP_003204
,		mRNA /cds=(164,1468) /gb=NM_003213			
		/gi=4507426 /ug=Hs.94865 /len=1670			
•.					
5672	0.03489	clone IMAGE:5265581, mRNA	BC035165	Hs.400548	<del>   </del>
		/gb=BC035165 /gi=23272508			
	-8-	/ug=Hs.400548 /len=2237	*		′
5692	0.001232	mRNA for MEGF6 protein (KIAA0815),	AB011539	Hs.56186	+
3032	0.001202	partial cds. /cds=(153;3893)	AD011000	113.50100	
			• 40	•	•
		/gb=AB011539 /gi=20269128		*	1
==7.5		/ug=Hs.56186 /len=4501	0.1107700	100500	-
5710	0.002054	UI-H-DF0-bes-i-11-0-UI.s1	CA427703	Hs.428583	1
		NCI_CGAP_DF0 cDNA clone UI-H-DF0-			
		bes-i-11-0-UI 3', mRNA sequence			9
	]	/clone=UI-H-DF0-bes-i-11-0-UI			]
Leon		/clone_end=3' /gb=CA427703		_	
		/gi=24790429 /ug=Hs.428583 /len=1096			·
5717	0.004203	MLL septin-like fusion (MSF), mRNA	NM_006640	Hs.181002	NP_006631
		/cds=(258,1964) /gb=NM_006640		*	
		/gi=19923366 /ug=Hs.181002 /len=3929			
5744	0.036914	DNA segment on chromosome X (unique)	NM 004699	Hs.54277	NP_004690
	1	9928 expressed sequence (DXS9928E),	-		
		mRNA /cds=(76,1095) /gb=NM_004699		·	1
		/gi=4758219 /ug=Hs.54277 /len=1311			
			*		
5747	0.007056	chromosome 20 open reading frame 14	NM 012469	Hs.31334	NP_036601
5141	0.007050	(C20orf14), mRNA /cds=(100,2925)	14141 0 12408	1:13.0 133 <del>4</del>	14F _020001
_					
		/gb=NM_012469 /gi=6912731			
	0.0400-	/ug=Hs.31334 /len=3060	AIN 4 005000	11- 70400	ND 005005
5751	0.01925	serine/arginine repetitive matrix 1	ИМ_005839	Hs.18192	NP_005830
		(SRRM1), mRNA /cds=(6,2468)			
		/gb=NM_005839 /gi=5032118	·	1	
		/ug=Hs.18192 /len=3698			
5754	0.043576	KIAA1360	AB037781		NP_060458

		nding To Differentially Expressed Gen s			
Spot	p-value	Description	Gene	Unigene	Protein
		*	Accession	Accession	Accession
			No.	No.	No.
5788	0.020482	aryl hydrocarbon receptor nuclear	NM_001178	Hs.74515	NP_001169
		translocator-like (ARNTL), mRNA	· -		
		/cds=(370,2250) /gb=NM_001178	90	*.	
•	*	/gi=20127415 /ug=Hs.74515 /len=2776	,		
5795	1 32F-04	progestin induced protein (DD5), mRNA	NM_015902	Hs.278428	NP 056986
0,00	1.022 01	/cds=(34,8433) /gb=NM_015902	11111_010002	110,270120	
İ	, , ,	/gi=15147336 /ug=Hs.278428 /len=8838			
5798	1 015 05	myotubularin related protein 9 (MTMR9),	NM 015458	Hs.48802	NP 056273
3/90	1.61E-05		NIVI_015456	IDS.40002	INP_030273
		mRNA /cds=(83,1732) /gb=NM_015458			
		/gi=19923423 /ug=Hs.48802 /len=7081			1000000
5806	8.63E-04	5'-nucleotidase, cytosolic II (NT5C2),	NM_012229	Hs.138593	NP_036361
	*	mRNA /cds=(145,1830) /gb=NM_012229			'
ì	,	/gi=20149601 /ug=Hs.138593 /len=3364			
5807	0.046005	mRNA for KIAA2019 protein.	AB095939	Hs.57548	
		/cds=(15,8408) /gb=AB095939		-8	
"	1	/gi=24899201 /ug=Hs.57548 /len=9217		*	
5814	0.003603	ribosomal protein L36a-like (RPL36AL),	NM_001001	Hs.419465	NP 000992
<b>.</b>	1 5.50000	mRNA /cds=(95,415) /gb=NM_001001	5555	1.14	
		/gi=16306559 /ug=Hs.419465 /len=537			
5819	0.001232	nuclear factor of kappa light polypeptide	AF213884	<del> </del>	
3019	0.001232		AF213004		
	4.5	gene enhancer in B-cells 1(NFKB1) gene,			
5000	0.001417	complete cds	1114 004004	11 404000	NID 004000
5822	0.031117	enhancer of zeste 1 (Drosophila) (EZH1),	им_001991	Hs.194669	NP_001982
		mRNA /cds=(123,2366) /gb=NM_001991			
		/gi=19923201 /ug=Hs.194669 /len=4640			
				•	<u> </u>
5824	0.006566	activated RNA polymerase II transcription	NM_006713	Hs.349506	NP_006704
		cofactor 4 (PC4), mRNA /cds=(57,440)			,
		/gb=NM_006713 /gi=19923783			7 g .
	İ				
		1/uu=ns.349300 /len=1330			
5829	4 93E-04	/ug=Hs.349506 /len=1336	NM 152608	Hs 99210	NP 689821
5829	4.93E-04	hypothetical protein FLJ35382	NM_152608	Hs.99210	NP_689821
5829	4.93E-04	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235)	NM_152608	Hs.99210	NP_689821
5829	4.93E-04	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244	NM_152608	Hs.99210	NP_689821
•	/ / .	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349	*	Hs.99210	
5829 5830	/ / .	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-	NM_152608 D30036	Hs.99210	
5830	0.003332	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha)	D30036	Hs.99210	NP_006215
5830 5836	0.003332	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha) SNRPN mRNA, 3' UTR	D30036 U81001		NP_006215
5830	0.003332	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha) SNRPN mRNA, 3' UTR MYE4197a Myeloma (MYE) cDNA library	D30036	Hs.99210 Hs.332023	NP_006215
5830 5836	0.003332	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha) SNRPN mRNA, 3' UTR MYE4197a Myeloma (MYE) cDNA library cDNA, mRNA sequence /gb=BF174993	D30036 U81001		NP_006215
5830 5836	0.003332	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha) SNRPN mRNA, 3' UTR MYE4197a Myeloma (MYE) cDNA library	D30036 U81001		NP_006215
5830 5836	0.003332	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha) SNRPN mRNA, 3' UTR MYE4197a Myeloma (MYE) cDNA library cDNA, mRNA sequence /gb=BF174993	D30036 U81001 BF174993		NP_006215
5830 5836	0.003332 0.00223 0.046005	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha) SNRPN mRNA, 3' UTR MYE4197a Myeloma (MYE) cDNA library cDNA, mRNA sequence /gb=BF174993	D30036 U81001		NP_006215 NP_073715
5830 5836 5843	0.003332 0.00223 0.046005	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha) SNRPN mRNA, 3' UTR MYE4197a Myeloma (MYE) cDNA library cDNA, mRNA sequence /gb=BF174993 /gi=13441207 /ug=Hs.332023 /len=338	D30036 U81001 BF174993	Hs.332023	NP_006215 NP_073715
5830 5836 5843	0.003332 0.00223 0.046005	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha) SNRPN mRNA, 3' UTR MYE4197a Myeloma (MYE) cDNA library cDNA, mRNA sequence /gb=BF174993 /gi=13441207 /ug=Hs.332023 /len=338 ATP synthase, H transporting, mitochondrial F0 complex, subunit e	D30036 U81001 BF174993	Hs.332023	NP_006215 NP_073715
5830 5836 5843	0.003332 0.00223 0.046005	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349 Phosphatidylinositol transfer protein (PI-TPalpha) SNRPN mRNA, 3' UTR MYE4197a Myeloma (MYE) cDNA library cDNA, mRNA sequence /gb=BF174993 /gi=13441207 /ug=Hs.332023 /len=338 ATP synthase, H transporting,	D30036 U81001 BF174993	Hs.332023	NP_689821  NP_006215  NP_073715  NP_009031

SOM	p-value	Description	Gene	Unigene	Protein
Spor	p-value	peacubtion	Accession	Accession	Accession
ļ					
E0/17	0.012102	clone IMAGE:5286336, mRNA	No. BC043158	No. Hs.434381	No.
5847	0.013102	/gb=BC043158 /gi=27693197	BC043130	105.434301	
5007	0.040540	/ug=Hs.434381 /len=2786	NAO 40 40	<del></del>	
5867		keratin 18 (K18)	M24842	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	ND 000503
5868	0.036914	serine (or cysteine) proteinase inhibitor,	NM_000602	Hs.82085	NP, 000593
		clade E (nexin, plasminogen activator	_	*	
.		inhibitor type 1), member 1 (SERPINE1),			
	43.4	mRNA /cds=(76,1284) /gb=NM_000602			*
		/gi=10835158 /ug=Hs.82085 /len=2876			
5876	0.004203	COX15 cytochrome c oxidase assembly	NM_004376	Hs.226581	NP_510870
		protein (yeast) (COX15), nuclear gene	·	:	1
		encoding mitochondrial protein, transcript	ĺ		
		variant 2, mRNA /cds=(52,1218)			4
7		/gb=NM_004376 /gi=17921986			
		/ug=Hs.226581 /len=2841			
5884	.2.97E-05	polymerase (RNA) II (DNA directed)	NM_006232	Hs.432574	NP_006223
		polypeptide H (POLR2H), mRNA		*	
		/cds=(88,540) /gb=NM_006232			
		/gi=14589952 /ug=Hs.432574 /len=821			
5897	0.032959	destrin (actin depolymerizing factor)	NM_006870	Hs.408576	NP_006861
		(DSTN), mRNA /cds=(73,570)			
-		/gb=NM_006870 /gi=6466447	e * .		
•		/ug=Hs.408576 /len=1439		•	,
5901.	0.003893	lipin 1 (LPIN1), mRNA /cds=(68,2740)	NM_145693	Hs.81412	NP 66373
		/gb=NM_145693 /gi=22027647	_		_
		/ug=Hs.81412 /len=5363			
5906	0.007578	602034564F1 NCI CGAP Brn64 cDNA	BF337136	Hs.398001	
0,000	0.001070	clone IMAGE:4182759 5', mRNA	10. 00. 100	110.00000	
1	]	sequence /clone=IMAGE:4182759			
		I/clone end=5'/gb=BF337136			
		/gi=11283240 /ug=Hs.398001 /len=1223		. *	
5909	0.006566	LIM domain containing preferred	NM 005578	Hs.180398	NP_005569
2909	0.000000	translocation partner in lipoma (LPP),	14141_000070	113.100330	141 _005008
	]	mRNA /cds=(247,2085) /gb=NM_005578	j		]
		/qi=5031886 /uq=Hs.180398 /len=5656			
		/g =5031666/ug=rls.160396/lef1=5656			
E04.4	0.000004	ribaccimal protein COO (DDCOO) DNA	NIM OCACOO	Ha 0100	ND 00404
5914	0.039034	ribosomal protein S20 (RPS20), mRNA	NM_001023	Hs.8102	NP_001014
		/cds=(128,487) /gb=NM_001023			
F0.1=	0.00000	/gi=14591915 /ug=Hs.8102 /len=539	DO 1000		
5917	0.039034	RED CELL ACID PHOSPHATASE 1,	P24666		,
	}	ISOZYME F (ACP1) (LOW MOLECULAR	1		9
		WEIGHT PHOSPHOTYROSINE	·		
		PROTEIN PHOSPHATASE)	1		
	l	(ADIPOCYTE ACID PHOSPHATASE,		1	
	1	ISOZYME ALPHA) (62% aa)		I.	

	p-value	nding To Differentially Expr ssed Genes Description	Gene	Unigene	Protein
Spor	p-value	Description	Accession	Accession	Accession
	*	•			
E044	0.022140	ribosomal protein S6 (RPS6), mRNA	No. NM 001010	<b>No.</b> Hs.380843	<b>No.</b> NP_001001
5944	0.023146		NNI_001010	П5.300043	NP_001001
		/cds=(43,792) /gb=NM_001010 \		1	
5050	0.000076	/gi=17158043 /ug=Hs.380843 /len=829	1100001	7.	in
5959		germline T-cell receptor beta chain	U66061	10 == 226	ND 055570
5987	0.01072	DAZ associated protein 2 (DAZAP2),	NM_014764	Hs.75416	NP_055579
		mRNA /cds=(70,576) /gb=NM_014764	·		
		/gi=7661885 /ug=Hs.75416 /len=1897			<u> </u>
6003	0.020482	tumor protein, translationally-controlled 1	NM_003295	Hs.401448	NP_003286
		(TPT1), mRNA /cds=(95,613)	. *	<u>.</u>	9
		/gb=NM_003295 /gi=4507668	1		
		/ug=Hs.401448 /len=830			
6004	0.039034	UDP-glucose pyrophosphorylase 2	NM_006759	Hs.77837	NP_006750
	1	(UGP2), mRNA /cds=(85,1611)			
		/gb=NM_006759 /gi=13027637			, ; ,
		/ug=Hs.77837 /len=1832			
6005	0.008722	mitochondrial 16S rRNA	Z70759		
6018		bullous pemphigoid antigen 1	NM_015548	Hs.198689	NP_065121
		(230/240kD) (BPAG1), transcript variant	<del>.</del>		_
		1eA, mRNA /cds=(103,15618)			
	100	/gb=NM_015548 /gi=20357497	*		
	7	/ug=Hs.198689 /len=16384		,	
6020	0.006566	cDNA FLJ37774 fis, clone	AK095093	Hs.119533	
0020	1.0.00000	BRHIP2026021, highly similar to Mus	1,11,000000	110.110000	
	+:	musculus formin binding protein 30			]
	1	mRNA. /gb=AK095093 /gi=21754285	`		
		/ug=Hs.119533 /len=2767			1
6037	0.001506	splicing factor, arginine/serine-rich 2	NM 003016	Hs.73965	NP 003007
0037	0.001396	(SFRS2), mRNA /cds=(156,821)	NIVI_0030 10	IUS.12902	INF_003007
	ļ.		in		
		/gb=NM_003016 /gi=4506898			1.
00.40	0.00700	/ug=Hs.73965 /len=1879	NA 000000	11 100055	ND 00000
6042	0.008722	laminin, gamma 1 (formerly LAMB2)	NM_002293	Hs.432855	NP_002284
		(LAMC1), mRNA /cds=(300,5129)	* .	8	
		/gb=NM_002293 /gi=9845497		*	
		/ug=Hs 432855 /len=7923		, , , , , , , , , , , , , , , , , , , ,	
6046	0.018081	KIAA0092 gene product (KIAA0092),	NM_014679	Hs.151791	NP_055494
	1	mRNA /cds=(54,1478) /gb=NM_014679	- "		
		/gi=7661899 /ug=Hs.151791 /len=2913	<u> </u>	*	
6049	0.008722	chromobox 1 (HP1 beta Drosophila)	NM_006807	Hs.77254	NP_006798
		(CBX1), mRNA /cds=(292,849)			, +
	,	/gb=NM_006807 /gi=21359877			
		/ug=Hs.77254 /len=2242			
6052	0.046005	thioredoxin (TXN), mRNA /cds=(64,381)	NM_003329	Hs.432922	NP 003320
		/gb=NM_003329 /gi=4507744	_		
	1	/ug=Hs.432922 /len=501	Ī		1

Genes	Corresp	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	4-
	p-value	Description	Gene	Unigene	Prot in
•	• ,		Accession	Accession	Acc ssion
			No.	No.	No.
6061	0.005674	v-rel reticuloendotheliosis viral oncogene	NM_021975	Hs.75569	NP_068810
	,	A, nuclear factor of kappa light			
		polypeptide gene enhancer in B-cells 3,		•	*
		p65 (avian) (RELA), mRNA		- 1 -	
		/cds=(39,1652) /gb=NM_021975		į.	* `
•	*	/gi=11496238 /ug=Hs.75569 /len=2444		· ·	*
6064	0.005674	actin related protein 2/3 complex, subunit	NM_005719	Hs.293750	NP 005710
.000 .	0.00007	3, 21kDa (ARPC3), mRNA /cds=(94,630)	11111_000110	,,	
		/gb=NM_005719 /gi=23397667	<u> </u>		-
		/ug=Hs.293750 /len=912			
6065	0.043576	NADH dehydrogenase (ubiquinone) 1,	NM 004549	Hs.193313	NP_004540
0000	0.043370	subcomplex unknown, 2, 14.5kDa	14141-00-10-10	113.133313	141004040
		(NDUFC2), mRNA /cds=(151,510)		ļ. ,	
		/gb=NM 004549 /gi=19923255	177	1	
		/ug=Hs.193313 /len=2168	9 ,		
6066	0.020483	actin related protein 2/3 complex, subunit	NIM 152862	Hs.83583	NP_690601
0000	0.020402	2, 34kDa (ARPC2), transcript variant 1,		1 15.03303	1145_090001
la :		mRNA /cds=(113,1015) /gb=NM_ 152862			· c*
		, , , , , , , , , , , , , , , , , , , ,		2	i
		/gi=23238210 /ug=Hs.83583 /len=1462			
6068	0.405.05	mitachandrial ribacomal protoin L27	NINA 140574	Hs.7736	ND 692412
0000	0.40E-00	mitochondrial ribosomal protein L27	NM_148571	IDS.//30	NP_683412
		(MRPL27), nuclear gene encoding		,	
•		mitochondrial protein, transcript variant 2,	-		
*	, .	mRNA /cds=(32,316) /gb=NM_148571			
		/gi=22547130 /ug=Hs.7736 /len=2472		· .	
6060	C EEE OA	otropo poposiated and and ambomic reticulum	NINA O1444E	110 76609	ND 055060
6069	0.55E-04	stress-associated endoplasmic reticulum	NM_014445	Hs.76698	NP_055260
	T - EE	protein 1; ribosome associated	,		
		membrane protein 4 (SERP1), mRNA	(2) v (4)		
		/cds=(316,516) /gb=NM_014445		• .	100
		/gi=19923408 /ug=Hs 76698 /len=2488	ė	1	:
0000	0.555.04	h	D50040		NID COSO04
6092		hypothetical protein (KIAA0128)	D50918		NP_665801
6094		nidogen (=M27445;M30269) (low match)	X84837		
6106		EST (ym17h04.s1 clone 48282 3')	H11657	11 010000	ND 000540
6113	5.52E-06	low density lipoprotein receptor (familial	NM_000527	Hs.213289	NP_000518
		hypercholesterolemia) (LDLR), mRNA			
		/cds=(94,2676) /gb=NM_000527	1		}
0444	6.040074	/gi=8051613 /ug=Hs.213289 /len=5175	514005040	11 470040	
6141	0.0169/4	UI-E-CL1-aez-k-18-0-UI.r1 UI-E-CL1	BM695043	Hs.170843	
		cDNA clone UI-E-CL1-aez-k-18-0-UI 5',	] <sub>2</sub> ·	.*	
	1	mRNA sequence /clone=UI-E-CL1-aez-k-	1	1 .	1 .
		18-0-UI /clone_end=5' /gb=BM695043			1
		/gi=19008301 /ug=Hs.170843 /len=1245			
6145	0.00223	replication factor C (activator 1) 2, 40kDa	NM_002914	Hs.139226	NP_002905
		(RFC2), mRNA /cds=(208,1272)			
		/gb=NM_002914 /gi=4506486	1		1
		/ug=Hs.139226 /len=1709			1

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigen	Protein
			Accession	Accession	Accession
•			No.	No.	No.
6163	0.029363	ribosomal protein L36 (RPL36), transcript	NM_015414	Hs.433411	NP_378669
	*	variant 2, mRNA /cds=(153,470)			
1		/gb=NM_015414 /gi=16117793			
	* 1	/ug=Hs.433411 /len=545			
6166	0.004203	ribosomal protein L10 (RPL10), mRNA	NM_006013	Hs.412900	NP_006004
		/cds=(42,686) /gb=NM_006013	. *		
		/gi=15718685 /ug=Hs.412900 /len=2188	•		
6177	0.01925	DNA directed RNA polymerase II	NM_145325	Hs.375569	NP_663165
	120	polypeptide J-related gene (POLR2J2),			
	-	transcript variant 1, mRNA /cds=(47,523)		t.	
		/gb=NM 145325 /gi=21704273			
		/ug=Hs.375569 /len=793			
6195	0.039511	myoM [Dictyostelium	AB017910	11	
0100	0.000011	discoideum](38%ORF)	7.0017,010		
6231	0.010964	methylenetetrahydrofolate reductase	AF260233		
0231	0.010304	(MTHFR) gene, exon 11 and 3' UTR,	AT 200200		- 6
		alternatively spliced	·	•	
6020	0.010015	tb97a11.x1 NCI_CGAP_Co16 cDNA	Al343476	Hs.183850	
6238	0.010015	clone IMAGE:2062268 3' similar to	A1343470	IUS 102020	
				*	
		contains Alu repetitive element;, mRNA	• .		
	1.	sequence /clone=IMAGE:2062268		1	
•		/clone_end=3' /gb=Al343476 /gi=4080682			
		/ug=Hs.183850 /len=515			1.10 00005
6258	0.012262	deleted in liver cancer 1 (DLC1), mRNA	NM_006094	Hs.8700	NP_006085
		/cds=(296,3571) /gb=NM_006094			
		/gi=6633799 /ug=Hs.8700 /len=3821	· ·		
6262	0.007056	UDP-glucose ceramide	NM_020121	Hs.22983	NP_064506
	· ·	glucosyltransferase-like 2 (UGCGL2),			
		mRNA /cds=(72,4622) /gb=NM_020121	,		
		/gi=11386200 /ug=Hs.22983 /len=4848			
6264	0.048543	BNIP3H (BNIP3H) nuclear gene for	AF255051		
	*	mitochondrial product			
6266	0.014464	cosmid LL12NCO1-67C6, ETV6 gene,	U81831		
		intron 1A, partial sequence	-4	. `	
6268	1.58E-06	cDNA: FLJ22008 fis, clone HEP06934.	AK025661	Hs.193700	
	1	/gb=AK025661 /gi=10438250			-
		/ug=Hs.193700 /len=2207		0.0	
6272	7.18E-04	cDNA, 5' end /clone=IMAGE:4148900	BF342391	Hs.30469	NP_055313
		/clone_end=5' /gb=BF342391	,		_
		/gi=11289392 /ug=Hs.30469 /len=803	•	·	
6286	0.027691	ribosomal protein S13 (RPS13), mRNA	NM 001017	Hs.165590	NP_001008
<b>4_00</b>	5.52,551	/cds=(33,488) /gb=NM 001017			-33.330
		/gi=14591910 /ug=Hs.165590 /len=529			
6289	0.03480	BRCA1-associated RING domain protein	AF038042		<del>                                     </del>
0209	0.03469	(BARD1)	1,11,000042		
620F	0.205.06	Notch 2 (Drosophila) (NOTCH2), mRNA	NM 024408	Hs.8121	NP 077719
6295	0.295-00		14141_024400	115.0121	NF_0/// 18
		/cds=(257,7672) /gb=NM_024408	· .		
	1	/gi=24041034 /ug=Hs.8121 /len=11433	1		l .

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
6298	1.63E-04	homeodomain interacting protein kinase 2	NM_022740	Hs.236131	NP_073577
		(HIPK2), mRNA /cds=(109,3705)			
	<b>[</b>	/gb=NM_022740 /gi=13430859			-
		/ug=Hs.236131 /len=4000	4		• 8
6310	0.016974	eukaryotic translation initiation factor 2,	NM_004094	Hs.151777	NP_004085
:	e <sup>e</sup>	subunit 1 alpha, 35kDa (EIF2S1), mRNA	_		_
		/cds=(100,1047) /gb=NM 004094		l	*
		/gi=19923248 /ug=Hs.151777 /len=2992			ĺ
• 1		3			
6312	0.004203	bridging integrator protein-1 (BIN1) gene,	U84000		
	1	intron 1, partial sequence			
6340	0.043576	phospholipase D1, phophatidylcholine-	NM 002662	Hs.82587	NP 002653
		specific (PLD1), mRNA /cds=(96,3320)			
	l	/gb=NM 002662 /gi=4505872			
	*	/ug=Hs.82587 /len=3609			
6347	0.024587	mitochondrion, complete genome	NC 001807		
6360		heterogeneous nuclear ribonucleoprotein	NM 005463	Hs.372673	NP 112740
J J J J		D-like (HNRPDL), transcript variant 1,	-		
	-	mRNA /cds=(581,1843) /gb=NM 005463	1		
÷ , .	la ·	/gi=14110410 /ug=Hs.372673 /len=3514			
	•		-8-	100	
6365	0.01072	epidermal growth factor receptor	NM 005228	Hs.77432	NP_005219
		(erythroblastic leukemia viral (v-erb-b)	_		, . <del></del>
		oncogene avian) (EGFR), mRNA	æ	1	1
	·:	/cds=(187,3819) /gb=NM_005228		*	
		/gi=4885198 /ug=Hs.77432 /len=5532			
6383	0.029363	S100 calcium binding protein A6	NM 014624	Hs.275243	NP_055439
		(calcyclin) (S100A6), mRNA			
		/cds=(103,375) /gb=NM_014624			
*		/gi=9845517 /ug=Hs.275243 /len=470			
6395	0.00242	SOCS box-containing WD protein SWiP-	NM 134264	Hs. 187991	NP 599027
0000	0.00212	1 (WSB1), transcript variant 3, mRNA	14111_101201	1.10.707001	
		/cds=(317,1051) /gb=NM_134264	•		
		/gi=20143909 /ug=Hs.187991 /len=4243			
6408	5.42F-04	ir24c06.y1 HR85 islet cDNA clone	CA848700	Hs.389121	<del> </del>
0400	0.425,04	IMAGE:6546227 5', mRNA sequence	10710700	113.003121	,
	*	/clone=IMAGE:6546227 /clone_end=5'	* 8.		
	**	/gb=CA848700 /gi=26999906		,	
	1 .	/ug=Hs.389121 /len=616	}		
6416	0.002625	MAD, mothers against decapentaplegic 5	NM 005903	Hs.37501	NP 005894
0410	0.002023	(Drosophila) (MADH5), mRNA	14141_003903	115.57501	141-002034
		/cds=(193,1590) /gb=NM 005903	1		
			190		
6418	0.020024	/gi=20070216 /ug=Hs.37501 /len=2049	NIM 003600	Un 10574	ND 003694
0418	0.039034	protein kinase, interferon-inducible double	111111-003090	Hs.18571	NP_003681
		stranded RNA dependent activator			
		(PRKRA), mRNA /cds=(108,1049)			
		/gb=NM_003690 /gi=20149526			,
		/ug=Hs.18571 /len=1843			L

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
6422	0.009349	soc-2 suppressor of clear (C. elegans)	NM_007373	Hs.104315	NP_031399
		(SHOC2), mRNA /cds=(278,2026)			
•		/gb=NM_007373 /gi=6677944			]
		/ug=Hs.104315 /len=3872			4.4
6429	0.011469	ubiquitin A-52 residue ribosomal protein	NM_003333	Hs.5308	NP 003324
		fusion product 1 (UBA52), mRNA			1.5
		/cds=(39,425) /gb=NM 003333	·		14
		/gi=15451941 /ug=Hs.5308 /len=515	** :		
6432	0.016974	protein kinase, cAMP-dependent,	NM_002736	Hs.77439	NP_002727
		regulatory, type II, beta (PRKAR2B),	100		_
		mRNA /cds=(167,1423) /gb=NM_002736			•
		/gi=4506064 /ug=Hs.77439 /len=3259	**)		
	ļ :	791 4000004 749 118.77 400 71011 0200	- 32		
6444	0.027691	protein phosphatase 3 (formerly 2B),	NM_021132	Hs.151531	NP_066955
, <del>,,,,,</del>	0.027,031	catalytic subunit, beta isoform (calcineurin	14101_021102	113.131331	111 _000333
		A beta) (PPP3CB), mRNA			
	1	/cds=(117,1691) /gb=NM_021132	* *	×	
C4C4	0.000400	/gi=11036639 /ug=Hs.151531 /len=3079	NIA 044027		ND OFFCE
6464		KIAA0250 gene	NM_014837	14	NP_055652
6465		KIAA0761 protein, partial cds	AB018304		NP_055942
6468		reverse transcriptase related protein	1207289A		1207289A
6481		PRO1722	AAF69605		
6485	1.23E-05		NM_006642	Hs.300642	NP_006633
		8 (SDCCAG8), mRNA /cds=(1,2142)	·		1
		/gb=NM_006642 /gi=28269671			
		/ug=Hs.300642 /len=2142			
6493	1.46E-04	RNA binding motif protein 3 (RBM3),	NM_006743	Hs.301404	NP_006734
:		mRNA /cds=(277,750) /gb=NM_006743			8.
•	,	/gi=5803136 /ug=Hs.301404 /len=1556	*		
6496	0.041254	TATA element modulatory factor 1	NM_007114	Hs.267632	NP_009045
	+ .	(TMF1), mRNA /cds=(1,3282)			Y
		/gb=NM_007114 /gi=6005903	·		ļ
	•	/ug=Hs.267632 /len=3282			
6519	0.03489	eukaryotic translation initiation factor 2B,	NM_015636	Hs.169474	NP_056451
		subunit 4 delta, 67kDa (EIF2B4),	· ·	-	
		transcript variant 1, mRNA			
		/cds=(20,1588) /gb=NM_015636			
		/gi=26986531 /ug=Hs.169474 /len=1643	· ·	*	
6532	0.010015	LCN1b gene	Y10826		T
6535		Similar to cerebellar degeneration-related	BC017503	Hs.75124	
		2, clone MGC:23119 IMAGE:4873337,	- 00000		44
		mRNA, complete cds /cds=(324,1655)			L
		/gb=BC017503 /gi=17028382			· · ·
	·	/ug=Hs.75124 /len=2713			
6544	0.033050	matrix metalloproteinase 11 (stromelysin	NM_005940	Hs.155324	NP_005931
<b>ψυ44</b>	0.032838		14141_009940	115.100024	NE_009931
		3) (MMP11), mRNA /cds=(23,1489)		1	1
		/gb=NM_005940 /gi=13027795			
		/ug=Hs.155324 /len=2260	L ·		

Spot	p-value	Description	in Figure 12 - Gene	Unigene	Protein
opor	P value	Degenphoni	Accession	Accession	Accession
			No.	No.	No.
6548	0.041254	TANK-binding kinase 1 (TBK1), mRNA	NM 013254	Hs.21712	NP_037386
00.0	0.0,71201	/cds=(63,2252) /gb=NM_013254	. ((11,_0 : 0, 20 :		-00,00
		/gi=19743810 /ug=Hs.21712 /len=2982	•		
6570	0.01/031	VAMP (vesicle-associated membrane	NM_003574	Hs.9006	NP 00356
0370	0.014901	protein)-associated protein A, 33kDa	14141_000074	113.5000	111 _00000
٠		(VAPA), mRNA /cds=(25,753)		4	
		/gb=NM_003574 /gi=20070155	•		
		/ug=Hs.9006 /len=1390			
6577	0.026014	ornithine decarboxylase antizyme 1	NM 004152	Hs.281960	NP_00414
03//	0.030914		14141_004102	IDS.20 1900	NP_00414
		(OAZ1), mRNA /gb=NM_004152			
0500	0.00000	/gi=9845504 /ug=Hs.281960 /len=986	A D000400	11 450405	
6590	0.003332	mRNA for KIAA0981 protein, partial cds.	AB023198	Hs.158135	]
	ii.	/cds=(1,1738) /gb=AB023198	8	ľ	۲.
		/gi=4589605 /ug=Hs.158135 /len=5182			
6594	0.012262	lactate dehydrogenase A (LDHA), mRNA	NM_005566	Hs.2795	NP_00555
		/cds=(98,1096) /gb=NM_005566			
		/gi=5031856 /ug=Hs.2795 /len=1661			
6595	0.039034	H factor 1 (complement) (HF1), mRNA	NM_000186	Hs.250651	NP_00017
	.*	/cds=(74,3769) /gb=NM_000186			
		/gi=4504374 /ug=Hs.250651 /len=3926			
6598	0.001128	phosphomannomutase 2 (PMM2) gene	AF157794		1 3 2 3
		(5e-10 match)	•		. *
6599	0.021781	N-myc downstream regulated gene 1	NM 006096	Hs.75789	NP 00608
		(NDRG1), mRNA /cds=(111,1295)			_,
	Į.	/gb=NM_006096 /gi=5174656	,		
		/ug=Hs.75789 /len=3020	(	,	
6603	0.00489	tm68a09 x1 NCI CGAP Brn25 cDNA	Al498805	Hs.436349	
	. 0.00400	clone IMAGE:2163256 3', mRNA	7.11.750000	110.100010	·
	1	sequence /clone=IMAGE:2163256			
		/clone_end=3' /gb=Al498805 /gi=4390787	91		
		/ug=Hs 436349 /len=460			
6604	0.020492	splicing factor, arginine/serine-rich 1	NM 006924	Hs.73737	NP 00885
0004	0.020462	1 ' -	_	П5./3/3/	14P_00900
		(splicing factor 2, alternate splicing factor)	<u> </u>		
		(SFRS1), mRNA /cds=(36,782)			
		/gb=NM_006924 /gi=19923382	· · ·	[ · · · · · · · · · · · · · · · · · · ·	
		/ug=Hs.73737 /len=2708			
6607	0.011469	eukaryotic translation initiation factor 2,	NM_004094	Hs.151777	NP_00408
	j ·	subunit 1 alpha, 35kDa (EIF2S1), mRNA			,j
٠.		/cds=(100,1047) /gb=NM_004094			*
	-	/gi=19923248 /ug=Hs.151777 /len=2992			
	<u></u>	·			
6618	0.014931	eukaryotic translation elongation factor 1	NM_001404	Hs.256184	NP_00139
		gamma (EEF1G), mRNA /cds=(38,1351)		•	
		/gb=NM_001404 /gi=25453475	·		
		/ug=Hs.256184 /len=1429			
6622	0.036914	aquaporin 1 (channel-forming integral	NM 000385	Hs.76152	NP_00037
		protein, 28kDa) (AQP1), mRNA	_ :::::		
		/cds=(39,848) /gb=NM_000385			
	1	/gi=4755121 /ug=Hs.76152 /len=1662		1	i

Genes	Correspoi	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	Primary of the second
	p-value	Description	Gene	Unigene	Prot in
			Accession	Accession	Accession
			No.	No.	No.
6635	0.021781	mitochondrial ribosomal protein L19	NM_014763	Hs.75574	NP 055578
		(MRPL19), nuclear gene encoding			
	!	mitochondrial protein, mRNA	1		141
	[	/cds=(59,901) /gb=NM_014763	_		'
		/gi=21735600 /ug=Hs.75574 /len=1347			
6636	0.023148	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM_001358	Hs.5683	NP_001349
		polypeptide 15 (DDX15), mRNA		,	
f.		/cds=(162,2603) /gb=NM_001358	•	}	
		/gi=4557516 /ug=Hs.5683 /len=3028			
6642	0.0261	runt-related transcription factor 1 (acute	NM 001754	Hs.129914	NP 001745
		myeloid leukemia 1; aml1 oncogene)			
1		(RUNX1), mRNA /cds=(445,1887)			
		/gb=NM_001754 /gi=19923197		l	'
-		/ug=Hs.129914 /len=6212	Ŧ		
6643	0.00527	proteasome (prosome, macropain)	NM_002795	Hs.82793	NP_002786
		subunit, beta type, 3 (PSMB3), mRNA	- · · · · · · · · · · · · · · · · · · ·		
В		/cds=(79,696) /gb=NM_002795			
A		/gi=22538464 /ug=Hs.82793 /len=784		=	
6646	0.007056	protein phosphatase 1, regulatory	NM_002480	Hs.16533	NP 002471
		(inhibitor) subunit 12A (PPP1R12A),	:		
		mRNA /cds=(1,3093) /gb=NM_002480			
		/gi=4505316 /ug=Hs.16533 /len=4613	·	* * * * * * * * * * * * * * * * * * * *	
6650	0.004203	tetratricopeptide repeat domain 1 (TTC1),	NM_003314	Hs.7733	NP 003305
		mRNA /cds=(51,929) /gb=NM 003314	· <del>-</del>		_
ŀ		/gi=4507710 /ug=Hs.7733 /len=1407			
	di .				
6661	0.008722	stromal antigen 1 (STAG1), mRNA	NM_005862	Hs.286148	NP_005853
		/cds=(401,4177) /gb=NM_005862	_		
,		/gi=5032062 /ug=Hs.286148 /len=4337			
6677	0.001344	solute carrier family 25 (mitochondrial	NM_001152	Hs.79172	NP 001143
		carrier; adenine nucleotide translocator),	_		_
	383	member 5 (SLC25A5), nuclear gene			
·		encoding mitochondrial protein, mRNA	X-		-
	iei.	/cds=(69,965) /gb=NM_001152			ķ-
		/gi=4502098 /ug=Hs.79172 /len=1225			3
6678	0.006566	vesicle-associated membrane protein 8	NM_003761	Hs.172684	NP_003752
		(endobrevin) (VAMP8), mRNA	,	:	
- 44		/cds=(54,356) /gb=NM_003761		· .	
· `		/gi=14043025 /ug=Hs.172684 /len=702		, ,	
6679	0.018081	hypothetical protein PP1057 (PP1057),	NM_031285	Ĥs.108557	NP_112575
		mRNA /cds=(498,971) /gb=NM_031285			
	<u> </u>	/gi=13775195 /ug=Hs.108557 /len=2030	·		
6680	0.027691	KIAA1483 protein (KIAA1483), mRNA	NM_020861	Hs.24106	NP_065912
		/cds=(136,1680) /gb=NM_020861		1	
		/gi=24308240 /ug=Hs.24106 /len=3105			
6691	0.043576	runt-related transcription factor 3	NM_004350	Hs.170019	NP_004341
	,	(RUNX3), mRNA /cds=(10,1257)			
	1	1/ab-NIM 004250 /ai-4757047	I	1	
		/gb=NM_004350 /gi=4757917	*		

Spot	p-value	Description	G ne	Unigene	Protein
Opor	p value		Accession	Accession	Accession
	•	*	No.	No.	No.
6692	0.008722	mitochondrial ribosomal protein S18B	NM_014046	Hs.274417	NP_05476
, ,		(MRPS18B), nuclear gene encoding	0.1.0.10	7.10.27 4417	-00 1700
		mitochondrial protein, mRNA			
		/cds=(38,814) /gb=NM_014046			
	. +	/gi=16554601 /ug=Hs.274417 /len=1439		·	
6693	0.002054	PHD finger protein 1 (PHF1), transcript	NM_024165	Hs.166204	NP_077084
0000	0.002004	variant 2, mRNA /cds=(216,1919)	14111_02-100	113.100204	_07700
		/gb=NM_024165 /gi=13435396		[	.1
		/ug=Hs.166204 /len=2260		1	
6707	0.005674	NADH dehydrogenase (ubiquinone) 1	NM_002493	Hs.109646	NP 002484
0/0/	0.000014	beta subcomplex, 6, 17kDa (NDUFB6),	14141_002433	1113.103040	141 _00240
	- 33-	mRNA /cds=(104,490) /gb=NM_002493	× (	·	
		/gi=20149518 /ug=Hs.109646 /len=733			
6708	0.007578	erythroid differentiation-related factor 1	AF040247		+ :
6713		cDNA FLJ23648 fis, clone COL04718.	AK074228	Hs.375782	<del> </del>
0/ 13	0.00403	/gb=AK074228 /gi=18676772	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	113.373702	=
		/ug=Hs.375782 /len=2295		]	
6714	0.006106	chromosome 20 open reading frame 43	NM 016407	Hs.182281	NP_05749
07 14	0.000 100	(C20orf43), mRNA /cds=(71,991)	14141_010407	113.102201	1111 _037,43
•		/gb=NM_016407 /gi=7705482		,	
	* 1	/ug=Hs.182281 /len=1639			
6718	0.00480	nucleoporin 210 (NUP210), mRNA	NM 024923	Hs.270404	NP 07919
0710	0.00403	/cds=(84,5747) /gb=NM_024923	14141_024323	113.270404	_0/3/3
	ļ	/gi=27477133 /ug=Hs.270404 /len=7191		, ÷	
6728	0.043576	Kelch-like ECH-associated protein 1	NM_012289	Hs.57729	NP_03642
0120	0.043370	(KEAP1), mRNA /cds=(113,1987)	14141_012209	113.57725	141 _05042
		/gb=NM_012289 /gi=22027641			
	` :	/ug=Hs.57729 /len=2513			×
6734	0.006566	PAI-1 mRNA-binding protein (PAI-RBP1),	NM_015640	Hs.165998	NP_05645
0754	0.000000	mRNA /cds=(86,1249) /gb=NM_015640	14141_013040	113.100000	_00040
	-	/gi=7661625 /ug=Hs.165998 /len=2201			÷
6735	7 88F-04	DKFZp586J021 (from clone	AL110197	Hs.6441	NP 00324
0,00	1.002 01	DKFZp586J021) /cds=UNKNOWN	1,12110101		
	ļ	/gb=AL110197 /gi=5817115 /ug=Hs.6441	11.	<b>'</b>	
е.		/len=1896			
6744	0.031117	ribosomal protein, large, P0 (RPLP0),	NM_053275	Hs.406511	NP_44450
<b>.</b>	0.901111	transcript variant 2, mRNA			
	ľ	/cds=(111,1064) /gb=NM_053275			
		/gi=16933545 /ug=Hs.406511 /len=1148			· ·
6750	0.008722	ADP-ribosylation-like factor 6 interacting	NM 016638	Hs.103561	NP_06116
	5.53,5,22	protein 4 (ARL6IP4), mRNA		, , , , , , , , , , , , , , , , , , ,	
	*	/cds=(63,719) /gb=NM 016638			1
		/gi=7706183 /ug=Hs.103561 /len=952		-8	
6752	0.023148	tumor endothelial marker 6 (TEM6),	NM 022748	Hs.12210	NP_07358
0,02	0.023140	mRNA /cds=(93,3710) /gb=NM_022748	14141_022770	1.13.122.10	_0,000
		/gi=17511208 /ug=Hs.12210 /len=6702			I

	p-value	nding To Differentially Expressed Genes Description	Gene	Unigene	Protein
Spot	p-value	Description			
		, w	Accession	Accession	Accession
	72 3		No.	No.	No.
6755	0.024587	solute carrier family 25 (mitochondrial	NM_002635	Hs.78713	NP_005879
		carrier; phosphate carrier), member 3			-
		(SLC25A3), nuclear gene encoding		0,0	
	8	mitochondrial protein, transcript variant			
	* •	1b, mRNA /cds=(49,1134)		* .	
		/gb=NM_002635 /gi=4505774			
		/ug=Hs.78713 /len=1330			*
6758	0.039034	proteasome (prosome, macropain) 26S	NM_002803	Hs.61153	NP_002794
<u>~</u>		subunit, ATPase, 2 (PSMC2), mRNA	-		-
		/cds=(71,1372) /gb=NM_002803	5		
	·	/gi=24430152 /ug=Hs.61153 /len=1545		•	
6760	0.027691	2-hydroxyphytanoyl-CoA lyase (HPCL2),	NM_012260	Hs.63290	NP_036392
,		mRNA /cds=(100,1836) /gb=NM_012260			
		/gi=6912417 /ug=Hs.63290 /len=1976	*	••	*
6772	0.018081	hypothetical protein FLJ22301	NM 024836	Hs.181406	NP_079112
		(FLJ22301), mRNA /cds=(696,2054)			
		/gb=NM_024836 /gi=13376246			
		/ug=Hs 181406 /len=2952			
6774	0.012262	echinoderm microtubule associated	NM_019063	Hs.333555	NP_061936
0111	0.01202	protein like 4 (EML4), mRNA		110.00000	- 40 1000
	ε.	/cds=(237,3182) /gb=NM_019063			
	**	/gi=19923496 /ug=Hs.333555 /len=5539			-
6788	0.004203	S100 calcium binding protein A6	NM_014624	Hs.275243	NP_055439
0,00	0.00-1200	(calcyclin) (S100A6), mRNA	14141_014024	13.27 02-10	-000400
٠		/cds=(103,375) /gb=NM_014624	,		
		/gi=9845517 /ug=Hs.275243 /len=470			Α.
6793	0.018081	transforming growth factor, beta receptor	NM_003243	Hs.342874	NP_003234
0,00	1 0.0 10001	III (betaglycan, 300kDa) (TGFBR3),	11111_000240	113.042074	141 _00020
		mRNA /cds=(349,2898) /gb=NM_003243			
		/gi=4507470 /ug=Hs.342874 /len=4208		ľ	
			*		
6810	0.003803	KIAA0538 protein, partial cds	AB011110		NP_008920
6811		pleckstrin domain interacting protein	NM_017934	Hs.10177	NP_060404
5011	0.00709	(PHIP), mRNA /cds=(306,2429)	11111_01/304	113.10177	-000404
		/gb=NM_017934 /gi=20149647	÷		
		/ug=Hs.10177 /len=2573			l .
6813	0.013001	constitutive photomorphogenic protein	NM 022457	Hs.105737	NP 071902
0013	0.013991	(COP1), mRNA /cds=(1,2196)	141VI_UZZ401	[:13.100707	_07 1902
	'	/gb=NM 022457 /gi=21359962			
		/gb=NM_022457 /gl=21359962  /ug=Hs.105737 /len=2196	* .		
6816	0.00242		AF185705	<del> </del>	ļ
00 10	0.00242	oxysterol binding protein 1 (OSBP1)			
		gene, exons 13 and 14, and complete cds	1		
6004	0.000400	ribocomol protoin L45 (DDL45) DNA	NIM 002049	Hs.74267	NP_002939
6821	0.020482	ribosomal protein L15 (RPL15), mRNA	NM_002948	HS.14201	145_002939
		/cds=(37,651) /gb=NM_002948	÷	1	
	<u> </u>	/gi=15431292 /ug=Hs.74267 /len=2018	L	<u> </u>	<u> </u>

		nding To Differentially Expressed Gen s			
Spot	p-value	Description	Gen	Unig ne	Protein
-			Acc ssion	Accession	Accession
T- 1	*		No.	No.	No.
6840	0.031117	FK506 binding protein 7 (FKBP7), mRNA	NM_016105	Hs.344379	NP_851939
,		/cds=(96,875) /gb=NM_016105			
-2-		/gi=23618828 /ug=Hs.344379 /len=1067			
6850	0.043576	jumping translocation breakpoint (JTB),	NM_006694	Hs.6396	NP_006685
		mRNA /cds=(433,873) /gb=NM_006694	. A.	*	
· .		/gi=5729888 /ug=Hs.6396 /len=1040			
6862	0.006566	golgi apparatus protein 1 (GLG1), mRNA	NM_012201	Hs.78979	NP_036333
-		/cds=(27,3560) /gb=NM_012201		,	
		/gi=6912389 /ug=Hs.78979 /len=3909	,		
6873	0.00189	coated vesicle membrane protein	NM_006815	Hs.75914	NP_006806
		(RNP24), mRNA /cds=(24,629)			
		/gb=NM_006815 /gi=21314646			٠.
		/ug=Hs.75914 /len=2060			
6875	0.016974	cDNA FLJ12924 fis, clone	AK022986	Hs.38034	. V. 10 (10)
	1	NT2RP2004709. /gb=AK022986		, ,	
		/gi=10434694 /ug=Hs.38034 /len=2667			
6880	0.023148	cytochrome c oxidase subunit VIIa	NM 001864	Hs.421621	NP 001855
<del>0</del> 000	0.020149	polypeptide 1 (muscle) (COX7A1),	11001001	10.12.102.1	-00.000
		nuclear gene encoding mitochondrial			
		protein, mRNA /cds=(463,702)			
	*	/gb=NM_001864 /gi=18105034	*		
		·			•
6889	0.001222	/ug=Hs.421621 /len=783 clone MGC:9929 IMAGE:3873001,	BC040341	Hs.314169	
0009	0.001232		DC040341	115.514109	1
-		mRNA, complete cds /cds=(142,3333)			ē
٠,.		/gb=BC040341 /gi=25955484			
0000	0.000.400	/ug=Hs.314169 /len=5328	NINA 040000	11- 200007	ND OCCE
6892	0.020482	hypothetical protein FLJ10420	NM_018090	Hs.289087	NP_060560
		(FLJ10420), mRNA /cds=(34,825)			
	×	/gb=NM_018090 /gi=20127581	,	-6	
		/ug=Hs.289087 /len=2046		113 10 10 10 10	
6897	0.043576	FLJ14613 fis, clone NT2RP1001113,	AK027519	Hs.105509	NP_06516
		highly similar to Homo sapiens CTL2	·		1.
		gene /cds=UNKNOWN /gb=AK027519	a 10	0.	
		/gi=14042254 /ug=Hs.105509 /len=3310			
6903	8.63E-04	Similar to expressed sequence	BC041167	Hs.72242	NP_06582
		AU043625, clone MGC:48919			
		IMAGE:5575580, mRNA, complete cds	•		
		/cds=(170,2206) /gb=BC041167			-
		/gi=27371019 /ug=Hs.72242 /len=4941			<u></u>
6906	0.00489	polymerase (RNA) II (DNA directed)	NM_021974	Hs.46405	NP_06880
		polypeptide F (POLR2F), mRNA			
	1	/cds=(79,462) /gb=NM 021974			
		/gi=14602451 /ug=Hs.46405 /len=546		<u> </u>	1
		/u - 400245  /uu-ns.40405/lell-J40			
6910	0.043576		NM 012127	Hs.23476	NP 036259
6910	0.043576	Cip1-interacting zinc finger protein (CIZ1),	NM_012127	Hs.23476	NP_036259
6910	0.043576		NM_012127	Hs.23476	NP_03625

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigen	Protein
			Accession	Acc ssion	Accession
			No.	No.	No.
6920	0.043576	thioredoxin (TXN), mRNA /cds=(64,381)	NM_003329	Hs.432922	NP_003320
		/gb=NM_003329 /gi=4507744			1
		/ug=Hs.432922 /len=501			-
6921	0.002054	drebrin 1 (DBN1), transcript variant 2,	NM 080881	Hs.89434	NP 543157
		mRNA /cds=(611,2566) /gb=NM_080881	_	,	
		/gi=18426912 /ug=Hs.89434 /len=3383			
	@			·	
6930	0.021781	HMT1 hnRNP methyltransferase-like 1	NM_001535	Hs.235887	NP 001526
		(S. cerevisiae) (HRMT1L1), mRNA	_		_
	,	/cds=(166,1467) /gb=NM_001535			70
. :		/gi=4504494 /ug=Hs.235887 /len=2093	_ Y	•	
6935	0.014931	FtsJ 3 (E. coli) (FTSJ3), mRNA	NM 017647	Hs.257486	NP_060117
		/cds=(72,2615) /gb=NM 017647			
		/gi=17017990 /ug=Hs.257486 /len=2999			
6938	0.001737	guanine nucleotide binding protein (G	NM_002074	Hs.215595	NP 002065
3000	0.001707	protein), beta polypeptide 1 (GNB1),	vozo/	110.21000	_002000
	* *	mRNA /cds=(333,1355) /gb=NM_002074		1 .	
		/gi=20357526 /ug=Hs.215595 /len=3147	1	·	1
	, .	/gi=2000/020/dg=113.210000/icii=014/			
3956	0.001232	DNA from chromosome 19-cosmid	AD000684		1 - 11
	0.001232	R30879 containing USF2, genomic	/ LD000004	-	
	•	sequence			,
3957	0.007578	ATP synthase, H transporting,	NM_001697	Hs.433960	NP 001688
)	0.007070	mitochondrial F1 complex, O subunit	14141_001007	113.400000	100.1000
	-	(oligomycin sensitivity conferring protein)			9
		(ATP50), mRNA /cds=(37,678)			
٠,		/gb=NM_001697 /gi=4502302	i -		
		/ug=Hs.433960 /len=772			
6958	0.003844	origin recognition complex, subunit 5-like	NM_002553	Hs.153138	NP_002544
J330	0.002044	(yeast) (ORC5L), mRNA /cds=(89,1396)	TVIVI_002333	113.100100	141 _002544
	,	/gb=NM_002553 /gi=4505524			
		/ug=Hs.153138 /len=1901			-
6073	7 58E 05		AL832702	He 125010	11.2
6973	7.56⊑-05	mRNA; cDNA DKFZp313P0434 (from	ALOSZIUZ	Hs.125019	,
1	-	clone DKFZp313P0434) /gb=AL832702	3		*
0007	0.045024	/gi=21733281 /ug=Hs.125019 /len=2995	NM 000098	Hs.274336	ND 000000
6987	0.015924	carnitine palmitoyltransferase II (CPT2),	MM_000090	IDS.274330	NP_000089
		nuclear gene encoding mitochondrial	· .		
		protein, mRNA /cds=(517,2493)			
	.]-	/gb=NM_000098 /gi=4503022	1		
2000	0.004507	/ug=Hs.274336 /len=3090	NIM 040500	11- 400005	ND 000500
6999	0.024587	ring finger protein 20 (RNF20), mRNA	NM_019592	Hs.168095	NP_062538
	· .	/cds=(91,3018) /gb=NM_019592		] · · · · · · · · · · · · · · · · · · ·	
		/gi=16554452 /ug=Hs.168095 /len=3936			
7019	2.63E-05	hypothetical protein MGC10986	NM_030576	Hs.50601	NP_085053
	,	(MGC10986), mRNA /cds=(145,528)			
		/gb=NM_030576 /gi=22095372	1 30		
		/ug=Hs.50601 /len=3178		:	

		nding To Diff r ntially Expressed Genes	in Figure 12 -	<u>Hypertension</u>	. 0
	p-value	Description	Gene	Unigene	Protein
	(		Accession	Accession	Accession
•		6	No.	No.	No.
7032	0.01925	NADH:ubiquinone oxidoreductase MLRQ	NM_020142	Hs.110024	NP_064527
		subunit (LOC56901), mRNA	ζ.		
		/cds=(274,537) /gb=NM_020142			
		/gi=20127589 /ug=Hs.110024 /len=1284			·
7048	0.031117	twisted gastrulation 1 (Drosophila)	NM_020648	Hs.247302	NP_065699
-		(TWSG1), mRNA /cds=(106,777)			<u> </u>
	•	/gb=NM_020648 /gi=21314788			1
		/ug=Hs.247302 /len=3693			
7052	0.013991	SUMO-1-specific protease (SUSP1),	NM_015571	Hs.27197	NP_056386
. 1		mRNA /cds=(1,3339) /gb=NM_015571			
		/gi=7662311 /ug <sup>2</sup> Hs.27197 /len=4210			·
7092	0.048543	chromosome condensation 1 (CHC1),	NM 001269	Hs.84746	NP 001260
		mRNA /cds=(287,1552) /gb=NM_001269	<del>-</del> ·		
		/gi=20149512 /ug=Hs.84746 /len=2559	*.		
			·		/
7103	0.014931	sialidase 1 (lysosomal sialidase) (NEU1),	NM_000434	Hs.118721	NP_000425
- 1		mRNA /cds=(130,1377) /gb=NM_000434			
***		/gi=4557790 /ug=Hs.118721 /len=1894			
		, g			*
7105	0.001344	PRO0657	AAF24054		
7137		DEAD (aspartate-glutamate-alanine-	NM_007841		
		aspartate) box polypeptide 6 (Ddx6)			
7142	0.007578	eukaryotic translation elongation factor 1	NM_001402	Hs.422118	NP 001393
		alpha 1 (EEF1A1), mRNA /cds=(63,1451)			
*		/gb=NM_001402 /gi=25453469 \			
· .		/ug=Hs.422118 /len=1837			
7149	0.023148	solute carrier family 25 (mitochondrial	NM 002635	Hs.78713	NP_005879
		carrier; phosphate carrier), member 3			
		(SLC25A3), nuclear gene encoding		·	,
		mitochondrial protein, transcript variant			2
	* *	1b, mRNA /cds=(49,1134)		. 1	
	. `	/gb=NM_002635 /gi=4505774			* -
		/ug=Hs.78713 /len=1330	*		
7159		myosin, heavy polypeptide 3, skeletal	NM_002470	Hs.173084	NP 002461
		muscle, embryonic (MYH3), mRNA	) · · · · · · · · · · · · · · · · · · ·	110.170001	J
		/cds=(85,5907) /gb=NM 002470			
		/gi=11342671 /ug=Hs.173084 /len=6032			
7163	0.032959	KIAA0652 gene product (KIAA0652),	NM 014741	Hs.79672	NP_055556
. 1		mRNA /cds=(309,1862) /gb=NM_014741	514741		
	,	/gi=7662225 /ug=Hs.79672 /len=4040			
	- *	1 302220 /ug=113./ 30/ 2 /ici1=4040	*		
7165	0.0261	zinc finger protein 25 (KOX 19) (ZNF25),	NM 145011	Hs.5856	NP_659448
100	3.0201	mRNA /cds=(106,1476) /gb=NM_145011	140011	13.0000	1.41 _053440
	I .		I '	I .	-81
		/gi=24462252 /ug=Hs.5856 /len=3736	į		

Snot		nding To Differentially Expr ssed Genes			Drote:-
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
7477	0.005074		No.	No.	No.
7177	0.005674	aminomethyltransferase (glycine	NM_000481	Hs.102	NP_000472
		cleavage system protein T) (AMT), mRNA	,		
		/cds=(146,1357) /gb=NM_000481	·		
	:	/gi=4502082 /ug=Hs.102 /len=2119			
7199	8.63E-04	putative dimethyladenosine transferase	NM_014473	Hs.125819	NP_055288
		(HSA9761), mRNA /cds=(79,1020)	<u> </u>		-
		/gb=NM_014473 /gi=7657197		10	
		/ug=Hs.125819 /len=1505	·/		,
7216	0.046005	cDNA FLJ37923 fis, clone	AK095242	Hs.382858	
	,	CTONG1000283, weakly similar to BETA-			ľ
	*	CATENIN. /gb=AK095242 /gi=21754455		0	
		/ug=Hs.382858 /len=2791			7
7221	0.041254	602410168F1 NIH_MGC 92 cDNA clone	BG394022	Hs.421597	
		IMAGE:4538560 5', mRNA sequence			
		/clone=IMAGE:4538560 /clone_end=5'			
		/gb=BG394022 /gi=13287470			
		/ug=Hs.421597 /len=1059			*
7224	0.046005	hypothetical protein FLJ20312	NM_017761	Hs.7862	NP 060231
		(FLJ20312), mRNA /cds=(384,803)	_		_
		/gb=NM_017761 /gi=20127576	0.	_	
	ì	/ug=Hs.7862 /len=2382	· ·		
7228	3.02E-04	hypothetical protein FLJ10254 (RefSeq	NP_060511		,
		aa 7e-30)			
7231	0.048543	clone MGC:29744 IMAGE:3347567,	BC021250	Hs.29645	NP_612373
		mRNA, complete cds /cds=(1622,2545)			
		/gb=BC021250 /gi=20987353	* -,		- *-
		/ug=Hs.29645 /len=2712		/	
7232	0.048543	protein tyrosine phosphatase, non-	NM_002835	Hs.62	NP_002826
		receptor type 12 (PTPN12), mRNA		***	
		/cds=(30,2372) /gb=NM_002835		- 30	· ·
		/gi=18375651 /ug=Hs.62 /len=3161			
7240	0.03489	block of proliferation 1 (BOP1), mRNA	NM_015201	Hs.30736	NP_056016
		/cds=(43,2283) /gb=NM_015201			
		/gi=21389316 /ug=Hs.30736 /len=2396	*		<u> </u>
7245	0.005674	cDNA FLJ90297 fis, clone	AK074778	Hs.405809	
		NT2RP2000447, moderately similar to			
		GOLGIN-95. /cds=(333,728)	-		
		/gb=AK074778 /gi=22760446	·		ĺ
		/ug=Hs.405809 /len=2520			
7282		glutaminase isoform C mRNA, 3'UTR	AF097494		NP_055720
7283	0.031117	HSPC056 protein (HSPC056), mRNA	NM_014154	Hs.422287	NP_054873
		/cds=(145,972) /gb=NM_014154			
		/gi=7661763 /ug=Hs.422287 /len=2879		-	
7284	0.048543	GK003 protein (GK003), mRNA	NM_020192	Hs.83313	NP_064577
		/cds=(10,690) /gb=NM_020192		,	. 92
	1	/gi=21281666 /ug=Hs.83313 /len=901		1	

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene Accession	Protein Accession
			Accession		
			No.	No.	No.
7306	0.043576	golgi autoantigen, golgin subfamily b,	NM_004487	Hs.7844	NP_004478
	-	macrogolgin (with transmembrane		-	
		signal), 1 (GOLGB1), mRNA			9
		/cds=(127,9906) /gb=NM_004487			
	* .	/gi=4758453 /ug=Hs.7844 /len=10300			ì
7315	0.013103	Hypothetical protein(cDNA: FLJ20994 fis,	AK024647		
1313	0.013102	clone CAE02453)	AK024047	*	r-
7319	0.040046		D87466	Un 040440	<del></del>
1319	0.010015	mRNA for KIAA0276 gene, partial cds.	D67400	Hs.240112	
	i i	/cds=(1,932) /gb=D87466 /gi=1665816		20	
		/ug=Hs.240112 /len=4185	30		
7327	0.012262	tumor endothelial marker 6 (TEM6),	NM_022748	Hs.12210	NP_07358
		mRNA /cds=(93,3710) /gb=NM_022748			
		/gi=17511208 /ug=Hs.12210 /len=6702			
7332	0.027691	a disintegrin-like and metalloprotease	NM_006988	Hs.8230	NP_00891
		(reprolysin type) with thrombospondin			
		type 1 motif, 1 (ADAMTS1), mRNA		• 10	ļ
	ĺ	/cds=(294,3146) /gb=NM_006988		*	
		/gi=11038653 /ug=Hs.8230 /len=4459			
7367	0.000340	cDNA: FLJ21488 fis, clone COL05445.	AK025141	Hs.406852	
1301	0.009349	/gb=AK025141 /gi=10437599	- ANO23141	115.400032	
		= '		1	
7070		/ug=Hs.406852 /len=2677	41.447.470		NID 05044
7372	0.032959	mRNA, cDNA DKFZp727l051 (from clone	AL11/4/8	Hs.239370	NP_05641
		DKFZp727l051); partial cds			
-	- %-	/cds=(1,2099) /gb=AL117478	ĺ		Ì
:	•	/gi=5911952 /ug=Hs.239370 /len=2480		, i	
7376	0.016974	KIAA1805 protein (KIAA1805), mRNA	NM_032434	Hs.294122	NP_11581
		/cds=(55,1758) /gb=NM_032434		-0-	
		/gi=24308327 /ug=Hs.294122 /len=2873			
7383	0.006566	mannose receptor, C type 1 (MRC1),	NM 002438	Hs.75182	NP 00242
, 000		mRNA /cds=(104,4474) /gb=NM_002438		1,100102	
		/gi=4505244 /ug=Hs.75182 /len=5185	*		
		/gi=4505244 /dg=118./5102 /ieii=5105	1.		
720E	0.004536	v-maf musculoaponeurotic fibrosarcoma	NM_005360	He 20250	NP_00535
7385	0.004536	1	NINI_002300	Hs.30250	NP_00535
		oncogene (avian) (MAF), mRNA			: 1
		/cds=(808,2019) /gb=NM_005360	[ ·	,	
	2 11 11 11	/gi=5453735 /ug=Hs.30250 /len=2145			-
7392	0.031117	cDNA FLJ30250 fis, clone	AK054812	Hs.318977	
•		BRACE2002304. /gb=AK054812			
		/gi=16549424 /ug=Hs.318977 /len=2148			·
7394	7.18E-04	cDNA FLJ10785 fis, clone	AK001647	Hs.96513	*
		NT2RP4000457, weakly similar to			
	,	UBIQUITIN CARBOXYL-TERMINAL		8	
		HYDROLASE 15 (EC 3.1.2.15).			
		/cds=(383,3424) /gb=AK001647			
7005	0.000400	/gi=7023028 /ug=Hs.96513 /len=3424	NINA 470005	Us 204407	ND ZOCOS
7395	0.006106	PDZ domain protein (Drosophila inaD-	NM_170605	Hs.321197	NP_79535
	,	like) (INADL), mRNA /cds=(1,5406)			
		/gb=NM_170605 /gi=24850118			
	1	/ug=Hs.321197 /len=5406			i

Spot	p-value	D scription	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7407	4 48E-04	myosin phosphatase target subunit 2	AF324892	(110)	110.
,		(MYPT2) gene, exons 11 through 24, and			l
		complete cds			
7409	0.046005	similar to glycoprotein 330 (H. sapiens)	XM_060698	:	
1400	0.01000	(LOC127827), mRNA	/	· .	e .
7425	0.013991	FLJ32759 fis, clone TESTI2001793,	AK057321	Hs.351657	
1420	0.010001	moderately similar to Human B219/OB	741007021	110.001001	, ,
		receptor isoform HuB219.1 precursor	- (1)	[·	
		mRNA /cds=UNKNOWN /gb=AK057321			00
		/gi=16552966 /ug=Hs.351657 /len=1763	*	*	
	*	10002000 / ug=113:001007 / lell=1700			
7435	0 039034	spastic paraplegia 7, paraplegin (pure	NM_003119	Hs.296847	NP_003110
1400	0.00004	and complicated autosomal recessive)	14141_000110	113.2000-77	111 _00011
	*	(SPG7), mRNA /cds=(13,2400)	* *	a gradi	
		/gb=NM_003119 /gi=4507172	9		ē
		/ug=Hs.296847 /len=3087	,	0	
7452	7 88F-04	hypothetical protein PRO1051	NM 018572	Hs.326548	NP 061042
1402	7.00L-04	(PRO1051), mRNA /cds=(755,1003)	111111_010072	113.020040	
	0	/gb=NM_018572 /gi=8924004	4.		
	1	/ug=Hs.326548 /len=1393			
7459	0.004536	proteasome (prosome, macropain) 26S	NM 002817	Hs.279554	NP 787128
1400	0.004550	subunit, non-ATPase, 13 (PSMD13),	14141_002017	113.273004	107 120
	*	mRNA /cds=(70,1200) /gb=NM_002817			
		/gi=4506222 /ug=Hs.279554 /len=1584	]		J
7471	0.013102	clone IMAGE:5302140, mRNA	BC041960	Hs.442622	· · · · · ·
1-11	0.010102	/gb=BC041960 /gi=27469467	00041000	113.442022	
		/ug=Hs.442622 /len=1510	Y)		÷
7473	0.043576	enhancer of polycomb 1, (Drosophila)	NM_025209	Hs.129998	NP 07948
1415	0.075570	(EPC1), mRNA /cds=(271,2781)	14141_020200	113.123330	_0/340
	'	/gb=NM_025209 /gi=24475703	•	1.	ł
		/ug=Hs.129998 /len=2913	·	-	
7490	0.00480	troponin T2, cardiac (TNNT2), mRNA	NM 000364	Hs.296865	NP 00035
1430	0.00403	/cds=(51,917) /gb=NM_000364	14141_000304	113.230003	
		/gi=4507626 /ug=Hs.296865 /len=1124			
7491	0.031117	chromosome 20 open reading frame 149	NM_024299	Hs.79625	NP 07727
7401	0.001117	(C20orf149), mRNA /cds=(150,494)	14141_02-4200	113.70020	-07727
		/gb=NM 024299 /gi=13236523	8		
		/ug=Hs.79625 /len=803			
7492	0.046005	ni59g06.s1 NCI_CGAP_Ov2 cDNA clone	AA526325	Hs.404464	<del> </del>
1732	0.040000	IMAGE:981178 similar to contains Alu	1,47050050	13.707707	
	1	repetitive element,, mRNA sequence	}	1	
		/clone=IMAGE:981178 /gb=AA526325			
		/gi=2268394 /ug=Hs.404464 /len=503			
	1	/g 000004 /uq-  10.404404 /1011-000	I	1	1

		nding To Diff r ntially Expressed Genes			
Spot-	p-value	Description	Gene	Unigene	Prot in
*			Accession .	Accession	Acc ssion
1	`		No.	No.	No.
7498	0.036914	UI-H-DF1-auj-I-12-0-UI s1	BM991698	Hs.355489	
		NCI_CGAP_DF1 cDNA clone			
		IMAGE:5870363 3', mRNA sequence		· .	
	2	/clone=IMAGE:5870363 /clone end=3'			
		/gb=BM991698 /gi=19711087			
		/ug=Hs.355489 /len=1105	- 0		
7508	0.021781	mRNA for RCC1-like protein (TD-60	AJ421269	Hs.284146	NP 061185
		gene) /cds=(236,1804) /gb=AJ421269			_
		/gi=27526612 /ug=Hs.284146 /len=4114	*	·	
7515	4.06E-04	FLJ11708 fis, clone HEMBA1005123	AK021770	**	NP 803882
7518		FLJ21950 fis, clone HEP04949	AK025603	10.00	NP 054900
7520		hypothetical protein FLJ10350	NM 018067	Hs.177596	NP_060537
	,	(FLJ10350), mRNA /cds=(676,2340)	_		
	4.	/gb=NM_018067 /gi=21361780	'		
		/ug=Hs.177596 /len=2811		0.0	
7532	0.011469	a disintegrin and metalloproteinase	NM 025220	Hs.173716	NP_694882
		domain 33 (ADAM33), transcript variant			
	:	1, mRNA /cds=(88,2529)			
		/gb=NM_025220 /gi=24041037			
		/ug=Hs.173716 /len=3594			
7535	0.046005	hypothetical protein MGC5242	NM 024033	Hs.77365	NP_076938
		(MGC5242), mRNA /cds=(267,656)			,,,,,,,,
	*	/gb=NM_024033 /gi=13162284			
		/ug=Hs.77365 /len=1498			
7536	0.039034	inhibitor of growth family, member 1	NM 005537	Hs.46700	NP 005528
,	, , , , , ,	(ING1), mRNA /cds=(433,1701)			
		/gb=NM_005537 /gi=19923770			
	,	/ug=Hs.46700 /len=2886			
7543	0.032959	hypothetical protein FLJ20255.	NM 017728	Hs.15797	NP_060198
		(FLJ20255), mRNA /cds=(146,1090)			
		/gb=NM_017728 /gi=8923229			
		/ug=Hs.15797 /len=1769			7
7548	0.048543	methionine adenosyltransferase II, beta	NM_013283	Hs.54642	NP_037415
		(MAT2B), mRNA /cds=(73,1077)		1.10.0 1.0	
		/gb=NM_013283 /gi=20127525			
		/ug=Hs.54642 /len=2054			
7553	0.023148	hypothetical protein FLJ10276	NM 018045	Hs.333149	NP 060515
- , , , ,		(FLJ10276), mRNA /cds=(18,1310)		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
		/gb=NM_018045 /gi=8922323		1	
_		/ug=Hs.333149 /len=2826			
7554	0.01072	mRNA IRO40627 full length insert cDNA	AL109779	· · · · · ·	NP 075379
		clone EUROIMAGE 40627		*	_5,55,6
7564	0.018081	paired basic amino acid cleaving system	NM_002570	Hs.170414	NP_612198
. 554		4 (PACE4), transcript variant 1, mRNA		1.0.170-717	_012130
		/cds=(315,3224) /gb=NM 002570			
		/gi=20336178 /ug=Hs.170414 /len=4553			
•		rg. 2000017074g-110-110-11-11011-1000	÷	[	1

Spot		nding To Differentially Expressed G nes			
	p-value	Description	G ne	Unig n	Protein
			Accession	Accession	Accession
			No.	No.	No.
7591	0.002844	glioma tumor suppressor candidate	NM_015710	Hs.421907	NP_056525
l	*	region gene 2 (GLTSCR2), mRNA	,	100	
		/cds=(53,1489) /gb=NM_015710		*	
1 1		/gi=21359905 /ug=Hs.421907 /len=1610	0 .		,
7592	0.012262	KIAA1221 protein (KIAA1221), mRNA	NM_032186	Hs.173001	NP_115562
		/cds=(129,4037) /gb=NM_032186		·	
		/gi=24496786 /ug=Hs.173001 /len=5531			
7599		fibrinogen, B beta polypeptide (FGB),	NM_005141	Hs.7645	NP_005132
٠,		mRNA /cds=(9,1484) /gb=NM_005141	*		
*		/gi=11761630 /ug=Hs.7645 /len=1918			
7608	0.002844	WW45 protein (WW45), mRNA	NM_021818	Hs.288906	NP_068590
		/cds=(339,1490) /gb=NM_021818			
		/gi=18860913 /ug=Hs.288906 /len=3031	<u> </u>		
7618	0.031117	hypothetical protein FLJ11240	NM_018368	Hs.339833	NP_060838
	·	(FLJ11240), mRNA /cds=(26,1648)			-
		/gb=NM_018368 /gi=8922955		•	
		/ug=Hs.339833 /len=1947			
7630	8.63E-04	synaptonemal complex protein 2	NM_014258	Hs.202676	NP_055073
		(SYCP2), mRNA /cds=(14,4606)		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	[ ·
7.7		/gb=NM_014258 /gi=7657634			
		/ug=Hs.202676 /len=4967	15.		,
7631	2.47E-04	mRNA for KIAA0794 protein, partial cds.	AB018337	Hs.127287	7
	•	/cds=(1,1473) /gb=AB018337	* •	,*	
		/gi=3882308 /ug=Hs.127287 /len=4656			
7632	0.020482	nuclear factor of kappa light polypeptide	NM 020529	Hs 81328	NP_065390
٠.		gene enhancer in B-cells inhibitor, alpha	_		
	*	(NFKBIA), mRNA /cds=(95,1048)			
		/gb=NM 020529 /gi=10092618	1 .	9.0	
		/ug=Hs.81328 /len=1550			
7637	0.008722	serum response factor (c-fos serum	NM_003131	Hs.155321	NP_003122
	,	response element-binding transcription			· <del>-</del> · ·
		factor) (SRF), mRNA /cds=(359,1885)		0	,
		/gb=NM 003131 /gi=4507204			
•		/ug=Hs.155321 /len=4201	· ·		
7640	0.002625	clone IMAGE:5264837, mRNA	BC035149	Hs.247309	NP 003839
		/gb=BC035149 /gi=23242682		: \	
		/ug=Hs.247309 /len=2127			- 14 m
7647	0.0261	BCL2/adenovirus E1B 19kD interacting	AL132665	Hs.132955	NP 004322
		protein 3-like, DKFZp566E034 (from			
		clone DKFZp566E034); complete cds			
		/cds=UNKNOWN /gb=AL132665			
		/gi=6137021 /ug=Hs.132955 /len=3481	_		7
7663	0.001737	cDNA FLJ10131 fis, clone	AK000993	Hs.274128	<b>†</b>
1003	3.55,757	HEMBA1003041. /gb=AK000993	1	1.3.27.4120	*
	I	. =	0.3		
		OOD - 7 17 1990 710 - 6% 777 178 790 - 7165			
7665		/gi=7021996 /ug=Hs.274128 /len=2065	NIM: 020143	He 103384	ND 064529
7665		putatative 28 kDa protein (LOC56902), mRNA /cds=(21,779) /gb=NM_020143	NM_020143	Hs.193384	NP_064528

Cnot	p-value	nding To Differentially Expressed Genes Description	Gene	Unigene	Protein
Shor	p-value	Description	Accession	Acc ssion	Accession
			No.	No.	No.
7666	5.38E-05	FLJ14102 fis, clone MAMMA1000940	AK024164	Hs.301811	110.
	,,,,,,,	/cds=UNKNOWN /gb=AK024164			
		/gi=10436477 /ug=Hs.301811 /len=1878	- 10		
7673	0.024587	hypothetical protein FLJ10970	NM_018286	Hs.173233	NP 060756
, 0, <del>0</del>		(FLJ10970), mRNA /cds=(229,633)	11111_010200	110.170200	
		/gb=NM_018286 /gi=8922795	•		
		/ug=Hs.173233 /len=1670			
7675	0.013991	polymerase (DNA directed), gamma	NM_002693	Hs.80961	NP_002684
, 0, 0	0.0,10001	(POLG), nuclear gene encoding		1.0.0000	
		mitochondrial protein, mRNA	***	}	*
		/cds=(283,4002) /gb=NM_002693	,		
		/gi=4505936 /ug=Hs.80961 /len=4465			
7678	0.031117	hypothetical protein FLJ14007	NM_024699	Hs.99519	NP 07897
, 0, 0	10.001717	(FLJ14007), mRNA /cds=(15,821)	11111_02 1000	110.00010	-07007
		/gb=NM_024699 /gi=13375984	·		
		/ug=Hs.99519 /len=1793	1		·
7684	0.030034	UI-CF-FN0-aeu-d-04-0-UI.s1 UI-CF-FN0	BU607402	Hs.405846	1
	0.000004	cDNA clone UI-CF-FN0-aeu-d-04-0-UI 3',	00007402	113.400040	
		mRNA sequence /clone=UI-CF-FN0-aeu-			
	2	d-04-0-UI /clone_end=3' /gb=BU607402	·		• 8 • 7
		/gi=23270719 /ug=Hs.405846 /len=1176	-		-
7685	0.003416	lymphocyte antigen 75 (LY75), mRNA	NM_002349	Hs.153563	NP 00234
1,000	0.005410	/cds=(54,5222) /gb=NM_002349	14141_002545	113.10000	
		/gi=4505052 /ug=Hs.153563 /len=6928			1.
7692	0.012262	ribosomal protein L41 (RPL41), mRNA	NM_021104	Hs.356795	NP 066927
7,002	0.012202	/cds=(84,161) /gb=NM_021104	02	110.000100	
		/gi=10863874 /ug=Hs.356795 /len=478	}		*.
7693	9.44E-04	KIAA1396 protein, partial cds	AB037817	Hs.230188	* 6
		/cds=UNKNOWN /gb=AB037817		, , , , , , , , , , , , , , , , , , , ,	
		/gi=7243172 /ug=Hs.230188 /len=5041		·	
7694	0.0261	cDNA FLJ25013 fis, clone CBL01365.	AK057742	Hs.380091	1 111 21
	9.525	/gb=AK057742 /gi=16553667			* -
		/ug=Hs.380091 /len=2200		1	
7699	3.02E-04	mRNA full length insert cDNA clone	AL109691	Hs.306330	- · · · ·
		EUROIMAGE 239714. /gb=AL109691			
		/gi=5689821 /ug=Hs.306330 /len=1453			,
7716	0.001232	IFNAR gene (HSIFNAR) for interferon	X60459		<del> </del>
		alpha/beta receptor		÷	1
7719	0.013102	endothelial differentiation,	NM 057159	Hs.75794	NP 47650
		lysophosphatidic acid G-protein-coupled	_		
	1	receptor, 2 (EDG2), transcript variant 2,	l	1	2
	1 .	mRNA /cds=(394,1488) /gb=NM_057159	a de la	y*	1
		/gi=16950637 /ug=Hs.75794 /len=2732			
7722	8.63E-04	Similar to hypothetical protein MGC4707,	BC013988	Hs.348323	
		clone MGC:19860 IMAGE:3349493,	13.1	ļ ·	· .,
		mRNA, complete cds /cds=(38,1051)	V.		
		/gb=BC013988 /gi=15559264	•		
	1	/ug=Hs.348323 /len=1684		1	1

Snot	p-value	nding To Differentially Expressed Genes Description	Gene	Unigene	Protein
Spot	p-value	Description		-	I .
			Accession	Accession	Accession
770.4	0.007050		No.	No.	No.
7724	0.007056	tumor necrosis factor receptor	NM_002546	Hs.81791	NP_00253
		superfamily, member 11b			-
		(osteoprotegerin) (TNFRSF11B), mRNA	. 8		
		/cds=(252,1457) /gb=NM_002546	,		. )
		/gi=22547122 /ug=Hs.81791 /len=2291	- ,		
7731	0.043576	cDNA FLJ14844 fis, clone	AK027750	Hs.93748	
		PLACE1000133, highly similar to			·
		TRANSCRIPTION FACTOR BTF3.	*)(**	0	* -
		/cds=(91,567) /gb=AK027750			
		/gi=14042660 /ug=Hs.93748 /len=2203			,
7732	0.01925	hypothetical protein FLJ20265	NM_017733	Hs.7099	NP_06020
		(FLJ20265), mRNA /cds=(40,1854)			
	10	/gb=NM_017733 /gi=8923239			
		/ug=Hs.7099 /len=2039			
7748	0.024587	Hypothetical protein HSPC232, clone	BC025306	Hs.281428	NP_05757
		IMAGE:4893383, mRNA, partial cds			
	·	/cds=UNKNOWN /gb=BC025306			
		/gi=19263704 /ug=Hs.281428 /len=3392			
7753	0.007056	SAC1 suppressor of actin mutations 1-	NM 014016	Hs.5867	NP 05473
		like (yeast) (SACM1L), mRNA			· -
	(X)	/cds=(70,1833) /gb=NM_014016			
•		/gi=7662337 /ug=Hs.5867 /len=3572	- Y		
7765	0.041547	hypothetical protein LOC51234	NM_016454	Hs.250905	NP 05753
		(LOC51234), mRNA /cds=(72,623)		,	
	*	/gb=NM_016454 /gi=24475963	·		
		/ug=Hs.250905 /len=1013	÷	. *	
7773	0.004536	SM-11044 binding protein (SMBP),	NM_020123	Hs.8203	NP_06450
	0.001000	mRNA /cds=(20,1780) /gb=NM_020123	1111_020120	110.0200	
	·	/gi=10047129 /ug=Hs.8203 /len=3389		, :	
7801	0.03480	bx02b08.x1 Iris cDNA (Un-normalized,	BF724206	Hs.221024	<del>                                       </del>
7001	0.05409	unamplified): BX cDNA clone bx02b08 3',	DI 724200	113.221024	
		mRNA sequence /clone=bx02b08			:
•			. 37		
	-	/clone_end=3' /gb=BF724206			
7002	0.042576	/gi=12040115 /ug=Hs.221024 /len=645	AVAIOCOE 12		ND 05705
7802	0.043576	EST 380589 MAGE resequences, MAGJ	AW968513		NP_05725
		cDNA= (xj42h09.x1	`		4
٠.	·	Soares_NFL_T_GBC_S1)=( tt93e04.x1			
	i e	NCI_CGAP_Pr28			ĺ
: '		)=(Soares_fetal_heart_NbHH19W)=(	•		
		Soares melanocyte 2NbHM )			ļ
7812	0.001232	EST(nw29b03.s1 NCI_CGAP_GCB0	AA714698		
		clone IMAGE:1241837 contains Alu			
		repeat)			ļ
7825	0.01925	retinol dehydrogenase 14 (all-trans and 9-	NM_020905	Hs.288880	NP_06595
		cis) (RDH14), mRNA /cds=(64,1074)			
		/gb=NM_020905 /gi=10190745	: .	<b>1</b> • • • • • • • • • • • • • • • • • • •	
	1	/ug=Hs.288880 /len=1538	,		

Spot	p-value	Description	Gene	Unigene	Protein
Opot	p-value	Description	Accession	Accession	Accession
•					1
7020	0.046074	DV006472	<b>No.</b> BX096472	<b>No.</b> Hs.20799	No.
7830	0.016974	BX096472	BA090472	HS.20799	j
		Soares_fetal_liver_spleen_1NFLS_S1			1
		cDNA clone IMAGp998P16979, mRNA			,
	,	sequence			
,		/clone=IMAGp998P16979_;_IMAGE:4184	Y	-0	
	-	31 /gb=BX096472 /gi=27842824	÷		1
		/ug=Hs.20799 /len=696			
7839	0.013102	EST(xc43h04.x1 NCI_CGAP_Co20 clone	AW081723		NP_003251
•		IMAGE:2587063 3' gb:M99436	4		
		TRANSDUCIN-LIKE ENHANCER			. 1
		PROTEIN 2)		*	
7843	9 48F-05	EST(qu23h09.x1 NCI CGAP Br12 clone	Al284640		
1010	0.102.00	IMAGE:1965665 contains Alu repeat)	/20 1.0		
		invivide: 1000000 oomano 7 na repeaty			
7854	0.001506	EST fetal brain (TFujiwara) Human	D81944		NP_07921
1004	0.001390	sapiens cDNA clone GEN-425D02 5'	001944	0.0	NP_0/921
7057	0.042402	EST(PM4-SN0016-030400-002-c05	V/V/06/1/33		
7857	0.013102	l ,	AW864432		
7000	0.000400	SN0016)	41070400		· · · · · ·
7862	0.020482	EST(ap61c03.x1 Stanley Frontal SN	Al272136	٠,	
		individual clone IMAGE:2022052)			
7871.	0.046005	clone IMAGE:5267224, mRNA	BC045644	Hs.425116	
		/gb=BC045644 /gi=28279007		:	
		/ug=Hs.425116 /len=4064			
7889	0.039034	piwi-like 2 (Drosophila) (HIWI2), mRNA	NM_152431	Hs.58248	NP_68964
	. *	/cds=(152,2710) /gb=NM_152431			
	·	/gi=22748904 /ug=Hs.58248 /len=3138	· ·		
7890	0.00189	likely ortholog of Xenopus dullard	NM 015343	Hs.84359	NP_056158
		(HSA011916), mRNA /cds=(31,765)			·
	,	/gb=NM_015343 /gi=7661721	, ,		. •
		/ug=Hs.84359 /len=1356			
7895	0.015924	EST(zw54g08.r1	AA463590		<del>                                     </del>
, 000	0.01002	Soares total fetus Nb2HF8 9w clone	, , , , , , , , , , , , , , , , , , , ,		v €
:		IMAGE:773918 5' contains Alu and			
		MER22 repeat)	•		*
7908	0.020262	EST EST43399 Fetal brain I cDNA 3' end	V V 3 3 6 4 4 8		NP_11257
7900	0.029303	EST EST45599 Fetal brail TODINA'S end	AA330440	I	NF_11257
7000	0.047005	oa19h06.s1 NCI_CGAP_GCB1 cDNA	AA736852	Hs.318618	
7922	0.017885		AA730032	IUS.2 100 10	
		clone IMAGE:1305467 3', mRNA	,,,		·
		sequence /clone=IMAGE:1305467			
	1	/clone_end=3' /gb=AA736852	J		.0.
	<u></u>	/gi=2768086 /ug=Hs.318618 /len=315			ļ
7925	0.039034	EST(ng19d12.s1 NCI_CGAP_Lip2 cDNA	AA501823		·
		clone IMAGE:929879 similar to contains		1	
	r ·	Alu repetitive element; contains element			
	`	MSR1 repetitive element)			
7930	0.048543	EST (nz09e04.s1 NCI_CGAP_GCB1	AA761167		
		IMAGE:1287294 3')	1		

		nding To Diff rentially Expressed Gen s			
Spot	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
7938	9.44E-04	UI-H-EU1-bai-b-07-0-UI.s1	BQ448117	Hs.8705	1
		NCI_CGAP_Ct1 cDNA clone UI-H-EU1-			
		bai-b-07-0-UI 3', mRNA sequence	-00	J	
		/clone=UI-H-EU1-bai-b-07-0-UI	0	1	
	] : [	/clone_end=3' /gb=BQ448117	*		]
*1.		/gi=21251229 /ug=Hs.8705 /len=1171	·	1.	*
7939	2.47E-04	EST (IL-BT003-221198-003 BT003)	AI902209		
7947	0.013102	EST (AV690707 GKC H.sapiens cDNA	AV690707		NP_004577
7948	0.039034	mRNA; cDNA DKFZp686J072 (from	AL832207	Hs.255938	
		clone DKFZp686J072) /gb=AL832207			
		/gi=21732752 /ug=Hs.255938 /len=7028		1	**
7956	0.039267	EST(zu24g05.s1 Soares_NhHMPu_S1	AA421768		
	,	cDNA clone IMAGE:738968 3' similar to		1	
		gb:Z13009_rna1 EPITHELIAL-			-
		CADHERIN PRECURSOR; contains Alu			
•		repetitive element;)			
7961	0.00527	FtsJ 2 (E. coli) (FTSJ2), mRNA	NM_013393	Hs.279877	NP_803191
		/cds=(30,770) /gb=NM_013393	i ·		
		/gi=7019376 /ug=Hs.279877 /len=1605			
7983	0.006106	proteasome (prosome, macropain) 26S	NM_005047	Hs.193725	NP_005038
		subunit, non-ATPase, 5 (PSMD5), mRNA	_		
		/cds=(20,1534) /gb=NM_005047	*		
		/gi=25777613 /ug=Hs.193725 /len=3411		, .	
8017	0.01925	secreted frizzled-related protein 5	NM_003015	Hs.279565	NP_003006
		(SFRP5), mRNA /cds=(182,1135)	. 0		_
		/gb=NM_003015 /gi=8400734	-		1
		/ug=Hs.279565 /len=1905	•		
8037	0.013991	hypothetical protein DKFZp564C236	NM_152392	Hs.378856	NP_689605
•		(DKFZp564C236), mRNA		1	
		/cds=(1590,2003) /gb=NM_152392	* *		
		/gi=22748838 /ug=Hs.378856 /len=2161			
8039		BX090877 NCI_CGAP_Ut3 cDNA clone	BX090877	Hs.359704	
	* . *	IMAGp998N165642; IMAGE:2278479,			
		mRNA sequence			
	10	/clone=IMAGp998N165642_;_IMAGE:227			
	="=.	8479 /gb=BX090877 /gi=27824565		1 .	-4-
		/ug=Hs.359704 /len=471			
8050	0.004536	hypothetical protein FLJ22557	NM_024713	Hs.106101	NP_078989
		(FLJ22557), mRNA /cds=(87,1001)		ĺ	
		/gb=NM_024713 /gi=13376012			,
		/ug=Hs.106101 /len=2676			
8056	0.001344		NM_001618	Hs.177766	NP_001609
•		ribose) polymerase) (ADPRT), mRNA	4-5	w **	
	1	/cds=(160,3204) /gb=NM_001618		1.	
		/gi=11496989 /ug=Hs.177766 /len=3859		1	
				+	
8062	0.014481	p53-induced protein PIGPC1 (PIGPC1),	NM_022121	Hs.303125	NP_071404
	ł	mRNA /cds=(73,654) /gb=NM_022121			
	L	/gi=11545842 /ug=Hs.303125 /len=1098			

		nding To Differentially Expressed Genes				
Spot	p-value	Description	Gene	Unigene	Protein	
			Accession	Accession	Accession	
-			No.	No.	No.	
8069	0.027691	Similar to nuclear localization signals	BC016981	Hs.244624		
		binding protein 1, clone MGC:21810				
		IMAGE:4183576, mRNA, complete cds				
		/cds=(58,375) /gb=BC016981				
		/gi=16877469 /ug=Hs.244624 /len=2059				
8079	0.01072	tripartite motif-containing 38 (TRIM38),	NM_006355	Hs.59545	NP_006346	
		mRNA /cds=(436,1833) /gb=NM_006355	· · .	*		
		/gi=24497622 /ug=Hs.59545 /len=3286			ļ	
8095	8.63E-04	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM 004728	Hs.169531	NP_004719	
		polypeptide 21 (DDX21), mRNA	_		- '	
		/cds=(266,2413) /gb=NM_004728				
	}	/gi=13787208 /ug=Hs.169531 /len=3319				
8157	0.048543	protection of telomeres 1 (POT1), mRNA	NM 015450	Hs.31968	NP 056265	
0.07	0.010010	/cds=(24,1928) /gb=NM_015450	10.0.00	110.07000		
:	17	/gi=13123773 /ug=Hs.31968 /len=2631				
8166	0.031117	epidermal growth factor (beta-	NM_001963	Hs.2230	NP 001954	
0100	0.031117	urogastrone) (EGF), mRNA	14141_001303	113.2250	-00 1337	
	1	/cds=(443,4066) /gb=NM_001963	10		1	
9.1		, , , , <u> </u>				
0400	0.027604	/gi=6031163 /ug=Hs.2230 /len=4877	Al934154	Hs.215019		
8180	0.027691	wn97f10.x1 NCI_CGAP_Ut1 cDNA clone	A1934 154	HS.215019		
		IMAGE:2453803 3' similar to TR:076003	960			
		O76003 THIOREDOXIN-LIKE PROTEIN.				
•		;, mRNA sequence				
		/clone=IMAGE:2453803 /clone_end=3'				
••		/gb=Al934154 /gi=5673024				
		/ug=Hs.215019 /len=425			2.00	
8182	0.036914	general transcription factor IIH,	NM_001515	Hs.191356	NP_001506	
	<b>]</b> .	polypeptide 2, 44kDa (GTF2H2), mRNA	] .			
		/cds=(1,1188) /gb=NM_001515			]	
		/gi=6681761 /ug=Hs.191356 /len=1188		<u> </u>		
8186	0.029363	Arkadia (ARK), mRNA /cds=(374,1486)	NM_017610	Hs.12504	NP_060080	
*	1,	/gb=NM_017610 /gi=24111229		е.		
		/ug=Hs.12504 /len=3010		•		
8187	0.026033	calcium channel, voltage-dependent, L	NM_000719	Hs.89925	NP_000710	
	-	type, alpha 1C subunit (CACNA1C),				
		mRNA /cds=(266,6682) /gb=NM_000719	90			
		/gi=27597079 /ug=Hs.89925 /len=8374	. *	e · ·		
			-			
8194	8.63E-04	mRNA for KIAA0876 protein, partial cds.	AB020683	Hs.301011		
		/cds=(150,3509) /gb=AB020683				
•	*	/gi=14133222 /ug=Hs.301011 /len=5595			-	
8198	0.031117	PHD zinc finger protein XAP135	NM 133325	Hs.7759	NP 579866	
5150	3.331117	(XAP135), transcript variant 2, mRNA		1.5.7.05		
		/cds=(222,1448) /gb=NM_133325				
	ŀ	/gi=19747275 /ug=Hs.7759 /len=1583			-4-	
8206	6 77E 05	mRNA for KIAA0640 protein, partial cds.	AB014540	Hs. 153026	NP_055870	
0200	0.776-05		\rightarrow   14540	113.103020	INF_000070	
	· ·	/cds=(1,1813) /gb=AB014540				
	1	/gi=3327093 /ug=Hs.153026 /len=4824		, , , , , , , , , , , , , , , , , , ,	<u>L</u>	

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
		, ,	No.	No.	No.
8215	0.010015	zinc finger protein 141 (clone pHZ-44)	NM_003441	Hs.193677	NP_003432
٠ ٦		(ZNF141), mRNA /cds=(157,1581)			· -
	,	/gb=NM_003441 /gi=4507992			1
		/ug=Hs.193677 /len=2985	8		
8220	0.008133	hypothetical protein FLJ23560	NM 024685	Hs.96322	NP 078961
0220	0.006133	(FLJ23560), mRNA /cds=(185,640)	14141_024000	1113.30322	_070301
	,				
		/gb=NM_024685 /gi=13375955			
2004	0.00144	/ug=Hs.96322 /len=2050	115040	U 055000	ND 000000
8231	0.031117	peptide-histidine transporter 4 (PTR4),	NM_145648	Hs.355660	NP_663623
× **		mRNA /cds=(59,1792) /gb=NM_145648			
		/gi=21717815 /ug=Hs.355660 /len=2807			<u> </u>
8232	0.01072	early hematopoietic zinc finger (EHZF),	NM_015461	Hs.26799	NP_056276
•	1	mRNA /cds=(150,4085) /gb=NM_015461	: -		
		/gi=24308068 /ug=Hs.26799 /len=4869		-0.0	
		. <b>3</b>			
8269	0.012262	clone IMAGE:5243705, mRNA	BC043383	Hs.439631	
0200	0.012202	/gb=BC043383 /gi=27695948	100010000	110.100001	٠.
		/ug=Hs.439631 /len=2177			
0074	0.475.04		AW887541	<u> </u>	
8271	2.47E-04	EST (RC3-OT0091-170300-011-c12	AVV007541		1
	<u> </u>	ОТ0091)	=======		110 000 100
8272	0.004536	EST(PM4-BT0650-010400-002-a06	BE083882	. (	NP_060487
	1	BT0650)	310		
8278	1.81E-04	EST(wf82e10.x1	AI873423		
``	,	Soares_NFL_T_GBC_S1 clone	*		
•		IMAGE:2362122 3')			
8296	0.014931	EST(zk44a11.r1 Soares pregnant uterus	AA040238	1	NP_057250
		NbHPU clone 485660 5')			
8298	0.008722	EST(0007a03.x1	Al218719	· · · · · · · · · · · · · · · · · · ·	
,QZQQ	0.000722	Soares_NSF_F8_9W_OT_PA_P_S1	"210110	+X+	
·		IMAGE:1565452 3')	. *	'	
0207	0.002602		NIM 002944	Hs.79005	NP_002835
8307	0.003603	protein tyrosine phosphatase, receptor	NM_002844	ns./9005	INP_002033
	·· ·	type, K (PTPRK), mRNA /cds=(221,4543)			
		/gb=NM_002844 /gi=18860901			1
	<u> </u>	/ug=Hs.79005 /len=5982			*
8308	0.001232	EST(ty24e09.x1 NCI_CGAP_Ut3 clone	A1758800		ì
		IMAGE:2280040 3' contains Alu repeat)			
8310	0.036914	phosphatidylinositol-3 phosphate 3-	NM 019061	Hs.93872	NP 061934
		phosphatase adaptor subunit (3PAP),	_		——————————————————————————————————————
		mRNA /cds=(132,2375) /gb=NM_019061		·ľ	1.
•		/gi=27477131 /ug=Hs.93872 /len=5064	, ,		
		191 27477 10 7749 110.00072 11011 0001	÷	1	
8329	0.00242	ECT/ECT12622 Utorus tumor L6!	AA300027	<del> </del>	<del> </del>
0329	0.00242	EST(EST12632 Uterus tumor I 5'	AA300027		ł ·
0000	0.00=0==	transaldolase)	Descen		ND 00700-
8339	0.007056	EST (Clontech human placenta polyA	D63238		NP_067635
		mRNA (#6572)GEN-511B02	ļ .		ļ
8340	0.031156	hypothetical protein MGC5306	NM_024116	Hs.301732	NP_077021
-		(MGC5306), mRNA /cds=(207,1043)	*		= .
		/gb=NM_024116 /gi=13129135	: '	[ . ·	[:
	1 ;	/ug=Hs.301732 /len=2336			

Smot	p-value	nding To Differentially Expressed Genes Description			
Shôr	p-value	Description	Gene	Unigene	Protein
		,	Acc ssion	Accession	Accession
		•	No.	No.	No.
8360	0.003603	EST(zf51h11.r1 Soares retina N2b4HR	AA044938		
ľ		clone IMAGE:380517 5' contains			
•		MER17.b2 MER17 repeat)			1
8365	0.048543	hypothetical protein FLJ10702	NM 018184	Hs.104222	NP 060654
0000	0.040040	(FLJ10702), mRNA /cds=(175,735)	14W_010104	1115,104222	INF_00003
	1			·	
	* 1	/gb=NM_018184 /gi=8922600	•		*
		/ug=Hs.104222 /len=2944			<u></u>
8373	0.002625	NISC_gj17d11.x1 NCI_CGAP_Pr28	CB050438	Hs.435309	
		cDNA clone IMAGE:3272108 31, mRNA			1
		sequence /clone=IMAGE:3272108			
		/clone_end=3' /gb=CB050438			-
	·	/gi=27788725 /ug=Hs.435309 /len=534		O.	
8382	8 63F-04	hypothetical protein clone 23745 mRNA,	U79260		-
0002	0.002-04	complete cds	073200		
0205	0.002070		A)A/0704E7		
8395	0.003079	EST xp73h11.x1 NCI_CGAP_Ov40 cDNA	AVV270457	,	•
	ļ	clone IMAGE:2746053 3' similar to		. "	Į · .
		contains Alu repetitive element;contains			
•		element MER32 repetitive element ;	[	,	
1.				*	, ,
8399	0.006566	EST(nc26d02.r1 NCI_CGAP_Pr1 cDNA	AA226526	-	
		clone IMAGE:1009251 similar to contains			. 20
		Alu repetitive element)			
8404	1 81E 05	Hypothetical protein(cDNA sequence	AK001911		ND 06597
0404	1.61E-03		AKOUTSTI		NP_06587
		FLJ11049 fis, clone PLACE1004548)	1	1	
8406	0.00489	erythroblast membrane-associated	NM_018538	Hs.410294	NP_06100
	i	protein (ERMAP), mRNA /cds=(167,1594)			
	<i>'</i>	/gb=NM_018538 /gi=19923535			
		/ug=Hs.410294 /len=3381	•		
8407	0.00223	EST (cDNA clone IMAGE:344153 3'	W69999	2	<del></del>
		similar to			•
8411	0.003079	UI-1-BB1p-aya-d-12-0-UI.s1	BU754499	Hs.432873	·
0411	0.000073	NCI_CGAP_PI6 cDNA clone UI-1-BB1p-	100754499	113.432073	1
		aya-d-12-0-UI 3', mRNA sequence		-	
	*	/clone=UI-1-BB1p-aya-d-12-0-UI	-		
•	,	/clone_end=3' /gb=BU754499			
		/gi=23713459 /ug=Hs.432873 /len=1196			
8417	0.029363	EST QV4-FT0005-110500-203-e03	AW949100		
		FT0005			
8420	0.001033	hypothetical protein FLJ10774	NM 024662	Hs.71472	NP 07893
2 17 7		(FLJ10774), mRNA /cds=(207,3284)			
		/gb=NM_024662 /gi=13399321			
0.400	0.475.01	/ug=Hs.71472 /len=4002	A14000051	115 454554	
8422	2.4/E-04	cDNA FLJ13792 fis, clone	AK023854	Hs.154751	
	4	THYRO1000072, weakly similar to			
		MYOSIN LIGHT CHAIN KINASE,			
		SMOOTH MUSCLE AND NON-MUSCLE		1	
		ISOZYMES (EC 2.7.1.117). /cds=(9,1337)	,		
		/gb=AK023854 /gi=10435918	•		
	l	/ug=Hs.154751 /len=2184		1 .	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	G ne	Unigene	Protein
		. 00	Accession	Accession	Accession
			No.	No.	No.
8423	0.014931	ot96g10.s1	AA993566	Hs.369984	. *
		Soares_total_fetus_Nb2HF8_9w cDNA			
		clone IMAGE:1624674 3', mRNA		,	
		sequence /clone=IMAGE:1624674		-	
		/clone_end=3' /gb=AA993566	•		
		/gi=3180111 /ug=Hs.369984 /len=498			1
8436	0.003603	EST 7e76f05.x1 NCI CGAP Pr28 cDNA	BE645808		NP 065105
		clone IMAGE:3288417 3' similar to	•	* .	
		contains element MER36 repetitive	' -		
		element;			
8437	0.010015	EST (yl83h07.r1 Soares infant brain 1NIB	H06795		
0.07	0.010010	IMAGE:44845 5')			
8438	0.003893	mRNA sequence /gb=L26969	L26969	Hs.362852	
0430	0.00000	/gi=16905391 /ug=Hs.362852 /len=1738	E20005	113.002002	
8448	0.003603	EST MR1-UM0111-030400-002-h07	AW806236	* 1 × 1	· · · · · · · · · · · · · · · · · · ·
0440	0.003603	UM0111	744000230		
0440	0.042570	1	NIM 019156	Un 101426	ND 00000
8449	0.043576	hypothetical protein FLJ10619	NM_018156	Hs.191436	NP_060626
		(FLJ10619), mRNA /cds=(65,1894)	9.7	*	
		/gb=NM_018156 /gi=8922552			
· · ·	1 1 1 1 1 1 1 1	/ug=Hs.191436 /len=3989			<b> </b>
8451	0.003332	EST (PM1-HT0422-170100-005-c12	BE160711		'
		HT0422)		ļ. ·	
8454	0.018081	EST ae93d05.s1 Stratagene schizo brain	AA780434		
	[	S11 H.sapiens cDNA clone		[ ·	
<u> </u>		IMAGE:1020489 3'			
8456	0.00223	EST (CM0-ST0189-081099-074-f09	AW813135		e 1
		ST0189)			
8458	0.020482	cDNA FLJ35666 fis, clone	AK092985	Hs.233382	
		SPLEN2017781./gb=AK092985	1		
,		/gi=21751702 /ug=Hs.233382 /len=2153			
8465	2.23E-04	likely ortholog of Xenopus dullard	NM_015343	Hs.84359	NP_056158
•		(HSA011916), mRNA /cds=(31,765)		-	:
		/gb=NM_015343 /gi=7661721			
		/ug=Hs.84359 /len=1356			
8472	0.002844	cDNA FLJ14188 fis, clone	AK024250	Hs.288671	
		NT2RP2005980. /gb=AK024250		,	٠.
		/gi=10436579 /ug=Hs.288671 /len=2289			
8482	0.002678	EST (7q71c12.x1 NCI_CGAP_Lu24	BF433956	1	†
	0.002010	cDNA clone IMAGE:3703702 3')		,	
8489	0.041254	CLK4 mRNA sequence /cds=(154,1515)	AF212224	Hs.406557	
J-0J	0.071234	/gb=AF212224 /gi=9437514	1 2 12227	1,13.400007	}
		/ug=Hs.406557 /len=1865			
8499	0.041254	hypothetical protein FLJ30999	NM 152461	Hs.129166	NP 689674
0499	0.041254	(FLJ30999), mRNA /cds=(302,703)	132401	1115. 128 100	1.4L _009014
		1,		*	
		/gb=NM_152461 /gi=22748964			
	1	/ug=Hs.129166 /len=2067			1

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
8500	0.00189	•	AW963571	Hs.182962	
		cDNA, mRNA sequence /gb=AW963571			
		/gi=8153407 /ug=Hs.182962 /len=672		*	- 3
			<u></u>		*
8522	0.023148	Enah/Vasp-like (EVL), mRNA	NM_016337	Hs.241471	NP_057421
		/cds=(62,1318) /gb=NM_016337			
		/gi=7706686 /ug=Hs.241471 /len=1833			
8525	0.00223	7f26a06.x1 NCI CGAP CLL1 cDNA	BE676253	Hs.436350	
	20	clone IMAGE:3295762 3' similar to			,
		contains Alu repetitive element;contains		. *	
		element MER22 repetitive element;		1.	7
		mRNA sequence /clone=IMAGE:3295762			· ·
		/clone end=3' /gb=BE676253		1:	
		_ : : :			
		/gi=10036794 /ug=Hs.436350 /len=492	9	4	
0504	0.00000	DNA 51 140045 5	414000004	11 007070	
8531	0.00223	cDNA FLJ40915 fis, clone	AK098234	Hs.207079	,
		UTERU2005450. /gb=AK098234		٠.	
		/gi=21758205 /ug=Hs.207079 /len=2739	*		
8537	0.048539	BX110006 Soares fetal liver spleen	BX110006	Hs.440742	***
. *		1NFLS cDNA clone IMAGp998K05525,			
•		mRNA sequence	~ .		
		/clone=IMAGp998K05525_;_IMAGE:2439			
		64 /gb=BX110006 /gi=27836130			·
		/ug=Hs.440742 /len=683		. 0	
8559	0.008722	clone MGC:5564, mRNA, complete cds	BC003697	Hs.188757	
		/cds=(227,304) /gb=BC003697			
		/gi=13277575 /ug=Hs.188757 /len=2145			
8560	0.024587	ribosomal protein L28 (RPL28), mRNA	NM 000991	Hs.356371	NP_000982
ĢOĢO	0.02-307	/cds=(43,456) /gb=NM 000991		1113.000,071	
					- V
OFCE	0.04005	/gi=13904865 /ug=Hs.356371 /len=500	AL599090		-
8565	0.01925	EST(DKFZp313E1524_r1 313 (synonym:	ALS99090		
		hlcc2) Homo sapiens cDNA clone		•	
		DKFZp313E1524 5')		<del> </del>	
8574	0.01072	EST(EST386869 MAGE resequences,	AW974779	:	NP_061008
		MAGN)			<u> </u>
8584	0.003603	AGENCOURT_6417307 NIH_MGC_67	ВМ799896	Hs.304926	·
	-	cDNA clone IMAGE:5492062 5', mRNA			
		sequence /clone=IMAGE:5492062			
	- 30	/clone_end=5' /gb=BM799896			1
	-	/gi=19116719 /ug=Hs.304926 /len=913			
8586	0.039034	UPF3 regulator of nonsense transcripts A	NM_023011	Hs.399740	NP_542418
		(yeast) (UPF3A), transcript variant 1,			_
•		mRNA /cds=(38,1468) /gb=NM_023011			
		/gi=18375523 /ug=Hs.399740 /len=2381			
8588	0.011460	EST(hz62d05.x1 NCI_CGAP_Lu24 cDNA	BE467153	7 : -	NP_059996
0900	0.011408		DE-407 100		1.11 -009990
0500	0.004244	clone IMAGE:3212553 3')	DE886334		ND 777504
8590	0.001344	EST (601509721F1 NIH_MGC_71 cDNA	BE886324		NP_777581
	l	clone IMAGE:3911140 5')	<u> </u>	1	

	p-value	nding To Differentially Expressed Genes D scription	Gene	Unigene	Protein
Shor	p-value	Discription	Accession	Accession	Accession
0502	0.445.04	as26a08 v1 Datical nigmont	<b>No.</b> CA392625	No. Hs.389253	No.
8593	9.446-04	cs26g08.y1 Retinal pigment	CA392025	FIS.309233	j
		epithelium/choroid cDNA (Un-normalized,	-		
		unamplified): cs cDNA clone cs26g08 5',		]/	- ) -
		mRNA sequence /clone=cs26g08	-	**	
		/clone_end=5' /gb=CA392625		9	
	*	/gi=24725520 /ug=Hs.389253 /len=648`	·	=	
8594	0.0261	EST(nh89a01.r1 NCI_CGAP_Br1.1 cDNA	AA513780	7	****
	0.020	clone IMAGE:965640 5' similar to			
	=	contains Alu repetitive element)	*		
8595	0.011460	ribosomal protein L3 (RPL3), mRNA	NM_000967	Hs 119598	NP 00095
0000	0.011403	/cds=(27,1238) /gb=NM 000967	14141_000001	113.113030	1.41 _00000
		/gi=16507968 /ug=Hs.119598 /len=1311	• **		
8619	0.015024	FLJ11481 fis, clone HEMBA1001803	AK021543	Hs.135159	1/21
0019	0.013924	/cds=UNKNOWN /gb=AK021543	ARUZ 1545	1 13. 133 133	. 1
	٠				
8621	7 00E 04	/gi=10432744 /ug=Hs.135159 /len=1539 ah42f05.s1 Soares_testis_NHT cDNA	AA705851	Hs.443872	
8621	7.88E-04	clone 1292193 3' similar to P54687	AA703631	ITS.443072	
			=		
	9	BRANCHED-CHAIN AMINO ACID	* .	*	
		AMINOTRANSFERASE, CYTOSOLIC ;,			
	•	mRNA sequence /clone=1292193	171		
:		/clone_end=3' /gb=AA705851	<b>6</b> -		
	- 10- 11	/gi=2715769 /ug=Hs.443872 /len=412	70047000		. ,
8631		clone IMAGE:4615963, mRNA	BC017826		ND 77750
8632		cDNA clone IMAGE:4769918 5'	BG623330	100	NP_77756
8635	9.44E-04	ESTs, cDNA, 3' end /clone_end=3'	B1789108	Hs.304928	
		/gb=BI789108 /gi=15816833		* '	
		/ug=Hs.304928 /len=529			
8646	0.032959	cDNA FLJ39413 fis, clone	AK096732	Hs.194339	
		PLACE6015729. /gb=AK096732	,	1	
	ļ	/gi=21756291 /ug=Hs.194339 /len=1957		. '	
8647	0.001344	tm62d04.x1 NCI_CGAP_Brn25 cDNA	Al475033	Hs.36915	
	٠.	clone IMAGE:2162695 3', mRNA			
		sequence /clone=IMAGE:2162695			
		/clone_end=3' /gb=Al475033 /gi=4328078	6	}	} .
		/ug=Hs.36915 /len=453			-
8649	0.031117	nah90b12.x1 NCI_CGAP_HN19 cDNA	BG272785	Hs.440690	
		clone IMAGE:4257766 similar to P39194			
	*	ALU SUBFAMILY SQ SEQUENCE			
•		CONTAMINATION WARNING ENTRY.	* -		
	.[	[1] ;contains Alu repetitive element;,	[	•	
		mRNA sequence /clone=IMAGE:4257766			
	ii.	/gb=BG272785 /gi=12982288		1	20
		/ug=Hs.440690 /len=360			
8650	0.021781	ah55e11.s1 Soares testis NHT cDNA	AA757094	Hs.191365	
5550	0.021701	clone 1309580 3', mRNA sequence	0.000		J
		/clone=1309580 /clone_end=3'	1		
		//gb=AA757094 /gi=2804957	[		
	1	/ug=Hs.191365 /len=379			

		nding To Differentially Expressed Genes			Protein
Spot	p-value	Description	Gene	Unigene	
	0		Acc ssion	Accession	Accession
	1 2 2 2 2 2		No.	No.	No.
8653	0.00527	EST, cDNA /clone=DKFZp586F2021	AL047579	Hs.310753	
		/gb=AL047579 /gi=4728575		• .	
		/ug=Hs.310753 /len=431		-	
8660	0.002844	nk74h02.s1 NCI_CGAP_Sch1 cDNA	AA551072	Hs.368624	,
		clone IMAGE:1019283 3' similar to			121
	• •	contains Alu repetitive element;contains			f. =
	·	element LTR5 repetitive element ;, mRNA		1	· ·
		sequence /clone=IMAGE:1019283		/	. 3
	9	/clone_end=3' /gb=AA551072			· ,
÷.		/gi=2321324 /ug=Hs.368624 /len=477	-	- 00	
				1	
8665	0:03489	wk57f04.x1 NCI_CGAP_Pan1 cDNA	AI829133	Hs.226780	
	•	clone IMAGE:2419519 3' similar to	• .	,	
7 0		contains Alu repetitive element,, mRNA		-	
		sequence /clone=IMAGE:2419519	* .	*	1
•	9.7	/clone_end=3' /gb=Al829133 /gi=5449804			
		/ug=Hs.226780 /len=518			
8669	0.014931	cDNA FLJ10190 fis, clone	AK001052	Hs.274546	1
		HEMBA1004753. /gb=AK001052	1,0		
	<u>'</u>	/gi=7022081 /ug=Hs.274546 /len=1318		*	
8672	6.55E-04	FLJ22781 fis, clone KAIA1958	AK026434	Hs.213236	
	8	/cds=UNKNOWN /gb=AK026434			
		/gi=10439298 /ug=Hs.213236 /len=2599			
8674	0.012262	EST, nu27f02.s1 NCI_CGAP_Pr2 cDNA	AA687557		,
		clone IMAGE:1211931 similar to contains			
		Alu repetitive element;			<u> </u>
8688	0.008722	mitogen-activated protein kinase kinase	NM_006301	Hs.211601	NP_006292
		kinase 12 (MAP3K12), mRNA			
		/cds=(99,2678) /gb=NM_006301		13.1	/
	,	/gi=21735551 /ug=Hs.211601 /len=3365			
8689	0.002054	ESTs, cDNA, 3' end	AL044007	Hs.95663	
		/clone=DKFZp434I2028 /clone_end=3'		. *	-
	. ,	/gb=AL044007 /gi=5432235			
		/ug=Hs.95663 /len=535			
8694	0.043576	protein kinase, cAMP-dependent,	NM_002734	Hs.183037	NP_002725
		regulatory, type I, alpha (tissue specific			
		extinguisher 1) (PRKAR1A), mRNA			
		/cds=(88,1233) /gb=NM_002734			1
		/gi=4506062 /ug=Hs.183037 /len=3036		,	
8699	0.00242	clone IMAGE:3909623, mRNA, partial	BC015894	Hs.33264	
		cds /cds=(1,178) /gb=BC015894			
		/gi=16198445 /ug=Hs.33264 /len=2980	*	,	
8707	0.015924	tc93c11.x1 NCI_CGAP_CLL1 cDNA	AI475669	Hs.309348	
		clone IMAGE:2073716 3' similar to			·
		contains Alu repetitive element;, mRNA			
	<b>.</b>	sequence /clone=IMAGE:2073716	}		
		/clone_end=3' /gb=Al475669 /gi=4328714			
	1	/ug=Hs.309348 /len=487			

Genes	Correspoi	nding To Diff rentially Expr ssed Genes	in Figure 12 -	Hypertension	
	p-value	Description	Gen	Unigene	Protein
			Accession	Accession	Accession
		***	No.	No.	No.
8714	0.031117	eukaryotic translation elongation factor 1	NM 001402	Hs.422118	NP 001393
		alpha 1 (EEF1A1), mRNA /cds=(63,1451)			
		/gb=NM_001402 /gi=25453469	10		
		/ug=Hs.422118 /len=1837	•		
8719	3.02F-04	clone UWGC:y17c090 from 6p21,	AC004188	1	
07.10	0.022 0	complete sequence	, (000), (00		
8725	0.024587	clone IMAGE:5288537, mRNA	BC043190	Hs.108806	3 12
0.20	0.024001	/gb=BC043190 /gi=27693257	30010100		
		/ug=Hs.108806 /len=3270			
8728	0.002054	DKFZp547N166_r1 547 (synonym: hfbr1)	AL134698	Hs.272048	
0/20	0.002034	cDNA clone DKFZp547N166 5', mRNA	  AL 134090	1115.272040	
} '					
	} .	sequence /clone=DKFZp547N166			
		/clone_end=5' /gb=AL134698	8		
· .		/gi=6602885 /ug=Hs.272048 /len=586	1		
070	5 405 0	5. 100440.5	A14057745	11-04004	
8734	5.42E-04	FLJ33148 fis, clone	AK057710	Hs.61304	· · · · · · · · · · · · · · · · · · ·
	[	UTERU2000238/cds=UNKNOWN			
		/gb=AK057710 /gi=16553627			
		/ug=Hs.61304/len=2347			
8738	5.96E-04	tb26b01.x1 NCI_CGAP_Kid12 cDNA	Al308217	Hs.177064	
(-	. *	clone IMAGE:2055433 3' similar to		4.	
	1	contains Alu repetitive element;, mRNA		80	
1		sequence /clone=IMAGE:2055433	٠,		
		/clone_end=3' /gb=Al308217 /gi=4002852			,
		/ug=Hs.177064 /len=421		*	
8739	0.039034	UI-H-FG1-bgk-p-20-0-UI s1	BU624684	Hs.235402	
		NCI_CGAP_FG1 cDNA clone UI-H-FG1-	. **		
		bgk-p-20-0-UI 3', mRNA sequence	1		
		/clone=UI-H-FG1-bgk-p-20-0-UI			*
	,	/clone_end=3' /gb=BU624684			].,
,		/gi=23290899 /ug=Hs.235402 /len=1150			-
8747	0.0261	EST(cDNA IL3-CT0674-210201-486-G12	BG956818	<del>                                     </del>	
		CT0674 cDNA, mRNA sequence)			-
8753	0.039034	UI-H-EU1-bai-b-07-0-UI.s1	BQ448117	Hs.8705	
3.00	J	NCI_CGAP_Ct1 cDNA clone UI-H-EU1-		1.0.0.0	
	1	bai-b-07-0-UI 3', mRNA sequence			
)		/clone=UI-H-EU1-bai-b-07-0-UI		. **	
	;	/clone_end=3' /gb=BQ448117			
Ť		/gi=21251229 /ug=Hs.8705 /len=1171		-X-	
8754	0.021701	602072454F1 NCI_CGAP_Brn67 cDNA	BF530944	Hs.319823	-
07.54	0.021781		DF330944	113.313043	
	}	clone IMAGE:4215325 5', mRNA		-	
		sequence /clone=IMAGE:4215325	Y e		
1		/clone_end=5' /gb=BF530944	1		
9	<u> </u>	/gi=11618307 /ug=Hs.319823 /len=686		<u> </u>	<u> </u>

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
•			Accession	Accession	Accession
			No.	No.	No.
8756	0.007578	7m95c07.x1 NCI_CGAP_Brn23 cDNA	BF197659	Hs.289387	- **
	120	clone IMAGE:3562764 3' similar to			
		contains Alu repetitive element;contains			· ·
	- 33	element MER33 repetitive element;	0		
•	-	mRNA sequence /clone=IMAGE:3562764	*		
		/clone_end=3' /gb=BF197659	•		·
	<b>J</b>	/gi=11086958 /ug=Hs.289387 /len=516		· ·	1
		rg			
8757	0.0261	602319564F1 NIH_MGC_89 cDNA clone	BG249501	Hs.281067	*
J. J.	0.020	IMAGE:4415078 5, mRNA sequence	BOF 1009 1	110.201007	
		/clone=IMAGE:4415078 /clone end=5'	4		'.
		/gb=BG249501 /gi=12759329			-
				*	
0750	0.04070	/ug=Hs.281067 /len=976	DM044074	11- 050407	
8758	v.v10/2	ESTs, cDNA, 3' end /clone_end=3'	BM314871	Hs.352487	- 3
		/gb=BM314871 /gi=18049216			
0701	0.04:55	/ug=Hs.352487 /len=451	0000000		
8761	0.041254	UI-H-DT1-awb-g-11-0-UI.s1	BQ016101	Hs.438666	
•		NCI_CGAP_DT1 cDNA clone		ł	
		IMAGE:5887138 3', mRNA sequence	2	-1	
	1	/clone=IMAGE:5887138 /clone_end=3'			, .,
		/gb=BQ016101 /gi=19751378		. *	
		/ug=Hs.438666 /len=800	• • • • • • • • • • • • • • • • • • • •		
8766	0.020482	BX107527 Soares_testis_NHT cDNA	BX107527	Hs.187615	
		clone IMAGp998E231862, mRNA		1	ì
		sequence			
:		/clone=IMAGp998E231862_;_IMAGE:757		• *	
		246 /gb=BX107527 /gi=27847429			·
		/ug=Hs.187615 /len=775		*	
8767	0.01925	UMP-CMP kinase (UMP-CMPK), mRNA	NM 016308	Hs.11463	NP 05739
0101	0.01323	/cds=(31,717) /gb=NM_016308	14141_0 10000	1113.11403	1111 _007 00
	<u>'</u>	/gi=7706496 /ug=Hs.11463 /len=2836		•	
8772	0.04005	<u> </u>	DO000000	110 202265	
0112	0.01925	Ül-1-BB1p-avb-a-02-0-Ul.s1	BQ023333	Hs.222365	
		NCI_CGAP_PI6 cDNA clone UI-1-BB1p-	1 /A		. /
	- 1	avb-a-02-0-UI 3', mRNA sequence	•		·
		/clone=UI-1-BB1p-avb-a-02-0-UI			1
		/clone_end=3' /gb=BQ023333			
		/gi=19758612 /ug=Hs.222365 /len=1133			
8773	0.012262	nn16d07.s1 NCI_CGAP_Co12 cDNA	AA593988	Hs.270630	
. 0		clone IMAGE:1084045 3' similar to	•		}
		contains Alu repetitive element;contains			]
		element MER26 repetitive element ;,	• @		,
		mRNA sequence /clone=IMAGE:1084045			
		/clone_end=3' /gb=AA593988			
	· ·	/gi=2409338 /ug=Hs.270630 /len=560			
8788	0.008133	ESTs, cDNA /gb=AW978555	AW978555	Hs.92448	
J. UU	1 3.555,55	/gi=8169822 /ug=Hs.92448 /len=754			
	i .				
8816	2 01F-04	mRNA; cDNA DKFZp586G1922 (from	AL080110		NP_80323

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
<u>:</u>			No.	No.	No.
8827	0.039034	ob11d04.s1 NCI_CGAP_Kid3 cDNA	AA872730	Hs.125229	
		clone IMAGE:1323367 3' similar to			
		contains Alu repetitive element; contains	*-	4 -	,
	-1-	element LTR5 repetitive element ;, mRNA	*		
•	٠,	sequence /clone=IMAGE:1323367		ł	
* .		/clone_end=3' /gb=AA872730			
		/gi=2968852 /ug=Hs 125229 /len=586		· ·	
8832	0.01072	yz39c12.s1 Morton Fetal Cochlea cDNA	N63237	Hs.269296	
		clone IMAGE:285430 3', mRNA			9
	,	sequence /clone=IMAGE:285430			· .
*		/clone_end=3' /gb=N63237 /gi=1211066		*	
	,	/ug=Hs.269296 /len=444			· · · —
8837	0.039034	no significant match	SEQ.ID.No.39		
8845		No significant match	SEQ.ID.No.82		- ;
8851		No significant match			
		(ORF:+3:3~167[166]; +1:49~167[120])	SEQ.ID.No.14		
8856	0.046005				
8863		EST(cDNA clone IMAGE:290115 3'	N63269		
		similar to contains Alu repetitive			
		element;contains element MSR1	-0.0		
		repetitive element ; )	• • • • •		
8874	0.002625	No significant match			*
		(ORF:+1:256~491[237])	SEQ.ID.No.26	1	
8899	0.019424	mRNA for KIAA1503 protein, partial cds.	AB040936	Hs.284274	
	*	/cds=(1350,3833) /gb=AB040936			
		/gi=7959266 /ug=Hs.284274 /len=4119			
8900	0.013102	hypothetical protein FLJ10252	NM_018040	Hs.53913	NP_060510
		(FLJ10252), mRNA /cds=(99,1685)			
		/gb=NM_018040 /gi=8922312			
		/ug=Hs.53913 /len=2338		• •	
8903	0.01925	EST(xg71d09.x1 NCI_CGAP_Ut4 cDNA	AW167136		
		clone IMAGE:2633777 3' similar to			
		contains Alu repetitive element)			<u> </u>
8904	4.06E-04	EST yx44d02.s1 Soares melanocyte	N20222		
		2NbHM cDNA clone IMAGE:264579 3'			
8911	0.00633	cDNA sequence (cDNA sequence	AL122062		NP_060691
		DKFZp727M031 (from clone cDNA	**		
		sequence DKFZp727M031)	.'		
8917	0.007056	EST (hs96b03.x1 NCI_CGAP_Kid13	BE463624		
		IMAGE:3145037 3')		ļ	
8922	0.03489	EST RC3-CT0197-100999-021-F10	AW177654	1	
		CT0197 H.sapiens cDNA			ļ
8923	0.029363	cDNA sequence (cDNA FLJ11671	AK021733		
		fis,clone HEMBA1004730)	1	1	

		nding To Differentially Expr ssed Genes Description	Gene		Protein
Spot	p-value	Describtion		Unigene	
			Accession	Accession	Accession
8924	0.008722	BX112599 Soares fetal liver spleen	<b>No.</b> BX112599	No. Hs.424205	No.
0924	0.000722	1NFLS cDNA clone IMAGp998N15537,	DA 1 12099	FIS.424205	
		mRNA sequence			÷.
		•	o ₹	\$ °	
		/clone=IMAGp998N15537_;_IMAGE:2486			
		54 /gb=BX112599 /gi=27837735 /ug=Hs.424205 /len=606			
8926	0.001222	clone IMAGE:5001859, mRNA	BC040072	Hs.194051	
0920.	0.001232	/gb=BC040072 /gi=25303948	BC040072	IDS. 19400 1	
	• .	/ug=Hs.194051 /len=3016			
8932	0.026022	PTEN induced putative kinase 1 (PINK1),	NM 032409	Hs.6163	NP_115785
0932	0.020033	mRNA /cds=(95,1840) /gb=NM_032409	14101_032409	IU8'0162	NE LISTOR
		/gi=14165271 /ug=Hs.6163 /len=2700			
		/gi=1416527-17ug=HS.01637left=2700		ŀ	
8942	0.041254	mRNA for Sec24 protein (Sec24A	AJ131244	Hs.211612	-
0342	0.041254	isoform), partial /cds=(1,3237)	1012 <del>94</del>	113.21 1012	
	11	/gb=AJ131244 /gi=3947687	* -		-
		/ug=Hs.211612 /len=5967	E		
8943	0.44F-04	hypothetical protein FLJ13213	NM_024755	Hs.331328	NP 079031
Q943	3.446-04	(FLJ13213), mRNA /cds=(234,1670)	14141_0247.55	113.551520	1117 _07 900
	* .	/gb=NM_024755 /gi=13376087			
		/ug=Hs.331328 /len=2617			-8-
8946	0.043576	hypothetical protein FLJ33282	NM_152388	Hs.346509	<del> </del>
0340	0.045570	(FLJ33282), mRNA /cds=(225,1523)	132300	113.040003	
		/gb=NM_152388 /gi=22748830	}		1
		/ug=Hs.346509 /len=2078			
8947	0.046005	EST (SsS0759 Suaeda salsa ZAP cDNA)	BF145070		
0041	0.04000	Coo   Coo   Co   Cadeda Salsa 27 (1   55   17   7	DI 140070	-	
8948	0.010015	ribosomal protein, large, P1 (RPLP1),	NM_001003	Hs.424299	NP 000994
00 10	0.010010	mRNA /cds=(130,474) /gb=NM 001003	11111_001000	110.12.1200	]
		/gi=16905511 /ug=Hs.424299 /len=512			
8962	1 23F-05	UI-H-BW0-ajq-g-03-0-UI.s1	AW298806	Hs.438211	
0002		NCI CGAP Sub6 cDNA clone			·
		IMAGE:2732740 3', mRNA sequence			
٠.		/clone=IMAGE:2732740 /clone_end=3'			
		/gb=AW298806 /gi=6705442	:	}	ł
		/ug=Hs.438211 /len=615		,	
8966	0.001941	EST (AV764100 MDS cDNA clone	AV764100		
		MDSBAE09 5')		w <sup>*</sup>	
8967	0.003505	hypothetical protein FLJ13231	NM_023073	Hs.156148	NP 07556
		(FLJ13231), mRNA /cds=(134,1255)			
		/gb=NM 023073 /gi=12751482			
		/ug=Hs.156148 /len=2642	200		
8968	0.013102	xc57a09.x1 NCI_CGAP_Eso2 cDNA	AW084739	Hs.445134	† <del></del>
		clone IMAGE:2588344 3' similar to			1
		contains Alu repetitive element, mRNA			
		sequence /clone=IMAGE:2588344	ā .	1	
		/clone_end=3' /gb=AW084739		100	
		/gi=6039891 /ug=Hs 445134 /len=509			

		nding T Differentially Expressed Genes			
Spot	p-value	Description	Gen	Unigene	Protein
		*	Acc ssion	Accession	Accession
		*	No.	No.	No.
8970	0.031117	on43h10.y5 NCI_CGAP_Co8 cDNA clone	A1793153	Hs.58262	
		IMAGE:1559491 5', mRNA sequence			9
		/clone=IMAGE:1559491 /clone_end=5'			•
	-	/gb=AI793153 /gi=5340869 /ug=Hs.58262			
		/len=521			
8971	0.041254	EST (yr72f10.r1 Soares fetal liver spleen	H65663		
		1NFLS cDNA clone IMAGE:210859 5'			
		similar to contains MER1 repetitive		· ·	
	l	element);			
8983	0.048543	eukaryotic translation elongation factor 1	NM 001402	Hs.422118	NP_001393
	0,010010	alpha 1 (EEF1A1), mRNA /cds=(63,1451)			,
		/gb=NM_001402 /gi=25453469	+()	,	
: · ·	•	/ug=Hs.422118 /len=1837		٠.	{
8987	0.007086	hypothetical protein MGC4562	NM 133375	Hs.269496	NP_588616
0907	0.007000	(MGC4562), mRNA /cds=(166,3081)	14141_100070	113.203430	141 _000010
		/gb=NM_133375 /gi=19115965	* *	*	•
	ſ				
0000	0.405.05	/ug=Hs.269496 /len=3694	PO636304	Hs.135613	
9000	9.48E-05	hd05h05.y1 Retina cDNA (Un-normalized,	BQ030204	IUS: 199019	
	1	unamplified): hd/he cDNA clone hd05h05			
	1 :	5', mRNA sequence /clone=hd05h05			
		/clone_end=5' /gb=BQ636204			
		/gi=21760663 /ug=Hs.135613 /len=544			
	7		<u> </u>		
9011	0.00223	EST(yb62b08.r1 Stratagene ovary	T58561		NP_002088
		(#937217) cDNA clone IMAGE:75735 5')			L
9015	0.018081	ubiquitin C (UBC), mRNA	NM_021009	Hs.183704	NP_066289
1		/cds=(136,2193) /gb=NM_021009	1		ľ
	<u> </u>	/gi=20149305 /ug=Hs.183704 /len=2309			
9019	0.023027	EST(UI-H-BW0-aiu-h-04-0-UI.s1	AW296071		
		NCI_CGAP_Sub6 cDNA clone			
		IMAGE:2730846 3')	•		
9029	0.007056	ol54a01.s1 Soares_NFL_T_GBC_S1	AA917705	Hs.190264	
	,	cDNA clone IMAGE:1527240 3' similar to			-
	ľ	contains Alu repetitive element,, mRNA			1
		sequence /clone=IMAGE:1527240			i .
		/clone_end=3' /gb=AA917705			ļ .
		/gi=3057595 /ug=Hs.190264 /len=515			Œ
	}	3			
9030	0.001465	EST(cDNA RC0-NT0113-300500-011-	BF366806		The second second
""	10,00	g05 NT0113)			
9041	0.027691	7I40g01.x1	BF112131	Hs.288083	<u> </u>
55-1	3.52, 55	Soares_NSF_F8_9W_OT_PA_P_S1	1		] .
1		cDNA clone IMAGE:3524136 3', mRNA		1	
		sequence /clone=IMAGE:3524136			1
	1.	•			
}		/clone_end=3' /gb=BF112131	**		1
0040	0.040045	/gi=10941821 /ug=Hs.288083 /len=620	NIM 022970	He 19269	ND 116050
9048	0.010015	SR rich protein (DKFZp564B0769),	NM_032870	Hs.18368	NP_116259
		mRNA /cds=(33,2450) /gb=NM_032870			1
1	1 '	/gi=18699723 /ug=Hs.18368 /len=2663	1	1	1

Smal	p-value	nding To Differentially Expressed Genes Description	Gene	Unigene	Protein
Spot	p-value			_	
- 1	1		Accession	Accession	Accession
9051	0.012262	EST384051 MAGE resequences, MAGL	<b>No.</b> AW972067	No. Hs.443703	No.
9031	0.012202	cDNA, mRNA sequence /gb=AW972067	AVV972007	105.443703	
			4. *	-00	, , ,
-		/gi=8161808 /ug=Hs.443703 /len=640	*	1	
9053	0.003332	UI-H-FL1-bgw-f-18-0-UI.s1	BU634141	Hs.32163	
0000	0.00002	NCI_CGAP_FL1 cDNA clone UI-H-FL1-	0000	110.02100	
		bgw-f-18-0-UI 3', mRNA sequence	-		
		/clone=UI-H-FL1-bgw-f-18-0-UI	• •	,	
		/clone_end=3' /gb=BU634141		1	
	,	/gi=23301396 /ug=Hs.32163 /len=1068			*
9061	0.001915	cDNA FLJ33960 fis, clone	AK091279	Hs.126465	
3001	0.00 1915   .	CTONG2018843. /gb=AK091279	12/3	1,13,120400	
		/gi=21749612 /ug=Hs.126465 /len=2849		1	1
9072	0.002625	clone MGC:20469 IMAGE:4554554,	BC012182	Hs.82508	<del> </del>
9012	0.002023	mRNA, complete cds /cds=(208,1149)	BC012102	115.02300	
		/gb=BC012182 /gi=15082546		-	
				ĺ	
9082	0.041254	/ug=Hs.82508 /len=1862 EST(cDNA clone IMAGE:2062168 3' )	Al343411		
9088		clone IMAGE:3875308, mRNA, partial	BC013784	Hs.351379	
9000	0.012016	cds /cds=UNKNOWN /gb=BC013784	DC013704	IDS.331379	
0005	4.405.04	/gi=15489380 /ug=Hs.351379 /len=2872	AW969151	Un 470004	- <del></del>
9095	4.465-04	EST381228 MAGE resequences, MAGK	Avvaoa 15 1	Hs.178604	
		cDNA, mRNA sequence /gb=AW969151		*.	ł
	_	/gi=8158992 /ug=Hs.178604 /len=623			
9098	0.001596	cDNA clone IMAGE:1045828 similar to	AA559186		
0000	0.001000	contains Alu	, , , , , , , , , , , ,		
9102	0.009349	cDNA FLJ10071 fis, clone	AK000933	Hs.28661	<u> </u>
0102	0.000040	HEMBA1001702. /gb=AK000933	/ 11000000	113.20001	}
		/gi=7021908 /ug=Hs.28661 /len=2570			9
9124	6.55F-04	UI-H-EZ1-bbf-I-14-0-UI.s1	BQ575680	Hs.257044	1
0 12.1	0.002 04	NCI CGAP Ch2 cDNA clone UI-H-EZ1-	150070000	110.207044	1
		bbf-l-14-0-UI 3', mRNA sequence			0.
		/clone=UI-H-EZ1-bbf-I-14-0-UI		00.	
		/clone_end=3' /gb=BQ575680	ì		F
		/gi=21478997 /ug=Hs.257044 /len=1036	2		*
9130	0.01072	CGI-18 protein (CGI-18), mRNA	NM_015947	Hs.121599	NP_057031
ÿ 100	0.01072	/cds=(421,1491) /gb=NM 015947	14141_010047	113.12.1000	_007001
	ľ.	/gi=7705601 /ug=Hs.121599 /len=2305	·	-	
9133	0.036014	UI-H-BW1-anh-g-07-0-UI.s1	BF514691	Hs.437157	<del> </del>
3 100	0.050514	NCI CGAP Sub7 cDNA clone		113.407 107	ł
	,	IMAGE:3082548 3', mRNA sequence		-	1
		/clone=IMAGE:3082548 /clone_end=3'			
		<u> </u>			
	α.	/gb=BF514691 /gi=11599870			
0425	0.000004	/ug=Hs.437157 /len=608	NIM 031440	Ho 54200	ND 44000
9135	0.039034	hypothetical protein DKFZp762D096	NM_031448	Hs.54320	NP_113636
		(DKFZP762D096), mRNA /cds=(123,356)			
		/gb=NM_031448 /gi=24308311	8 , 1	,	
	1	/ug=Hs.54320 /len=1925			1

	p-value	nding To Differentially Expr ssed Genes Description	Gene	Hypertension Unigen	Protein
		* ,	Accession	Accession	Accession
			No.	No.	No.
9137	0.032959	cDNA FLJ31919 fis, clone	AK056481	Hs.400872	140.
		NT2RP7004964. /gb=AK056481			
		/gi=16551895 /ug=Hs.400872 /len=4013			
9143	0.015704	mRNA; cDNA DKFZp434N185 (from	AL117645	Hs.33032	NP_07948
. ,	1	clone DKFZp434N185) /gb=AL117645		1.15.55552	10. 9.10
		/gi=5912235 /ug=Hs.33032 /len=1641			F
9151	0.01072	mRNA; cDNA DKFZp564A2164 (from	AL117611	Hs.19150	
		clone DKFZp564A2164) /gb=AL117611		1.	
		/gi=5912187 /ug=Hs.19150 /len=1908		1	ľ
9152	0.023148	cDNA FLJ31610 fis, clone	AK056172	Hs.196379	
		NT2RI2002865. /gb=AK056172			
		/gi=16551502 /ug=Hs.196379 /len=2194	-		·
9156	0.004536	AV700727 GKC cDNA clone GKCGRD12	AV700727	Hs.446006	
=.; = =	1	3', mRNA sequence /clone=GKCGRD12			1)
		/clone_end≈3' /gb=AV700727			•
	0	/gi=10302698 /ug=Hs.446006 /len=494	*		
9166	0.039034	FLJ23172 fis, clone	AK026825	Hs.306885	2 * * :
		LNG10005/cds=UNKNOWN			-X-
		/gb=AK026825 /gi=10439771			
		/ug=Hs.306885/len=1882	·		
9169	0.013102	EST(placenta Nb2HP cDNA clone	R25670		
		IMAGE: 132920 3' similar to contains Alu			9
		repetitive element; contains L1 repetitive	·	1	
		element;)			
9173	7.58E-05	EST381780 MAGE resequences, MAGK	AW969703	Hs.142074	
		cDNA, mRNA sequence /gb=AW969703	,		
		/gi=8159547 /ug=Hs.142074 /len=651		1	
9178	0.043576	EST(cDNA clone IMAGE:2954041 3')	AW612522		NP 06589
9180		cDNA FLJ30816 fis, clone	AK055378	Hs.350229	T
	•	FEBRA2001571. /gb=AK055378			
	•	/gi=16550091 /ug=Hs.350229 /len=2296			
9187	0.048543	LL5 beta (LL5beta), mRNA	NM 145753	Hs.7378	NP_66569
		/cds=(116,3748) /gb=NM_145753		·	_
		/gi=21955171 /ug=Hs.7378 /len=5491		-	
9190	0.027691	DKFZP564D116 protein	NM 015631	Hs.181185	NP 05644
		(DKFZP564D116), mRNA			_ · · · ·
		/cds=(676,1965) /gb=NM_015631			*
		/gi=24308108 /ug=Hs.181185 /len=2637	·	· · ·	
9196	0.048543	7n20h11.x1 NCI_CGAP_Lu24 cDNA	BF195340	Hs.279193	
		clone IMAGE:3565316 3', mRNA	·		
•		sequence /clone=IMAGE:3565316	*		*
		/clone_end=3' /gb=BF195340			,
		/gi=11082134 /ug=Hs.279193 /len=463		1 .	

Cmat	n volue	nding To Differentially Expressed Genes			
Spot	p-value	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
0040	0.0004	DV40C400 Carray fatal lives and an	<b>No.</b> BX106122	No.	No.
9213	0.0261	BX106122 Soares fetal liver spleen	BX 106122	Hs.194290	
		1NFLS cDNA clone IMAGp998I16420,	,	7	
	٠.	mRNA sequence		·	
		/clone=IMAGp998I16420_;_IMAGE:2139	,		
•		75 /gb=BX106122 /gi=27833926			
0000	0.044004	/ug=Hs.194290 /len=747	11.510705		ND 000400
9222	0.014931	EST(cDNA clone CS0DI054YF18 5 prime	AL549795		NP_003109
		) 			20
9225	1.06E-04	UI-H-DT0-atx-c-08-0-UI.s1	BM992885	Hs.436581	
		NCI_CGAP_DT0 cDNA clone	-		
	i	IMAGE:5865535 3', mRNA sequence	0	9.9	
		/clone=IMAGE:5865535 /clone_end=3'			
	· ·	/gb=BM992885 /gi=19712274			
		/ug=Hs.436581 /len=1301			
9228	0.039267	wn36h11 x1 NCI_CGAP_Gas4 cDNA	AI888818	Hs.213958	•
	*.	clone IMAGE:2447589 3' similar to	·		
	. 1	contains Alu repetitive element;, mRNA			
		sequence /clone=IMAGE:2447589		1 .	
, .		/clone_end=3' /gb=Al888818 /gi=5593982		,	
		/ug=Hs.213958 /len=538			
9230	0.031117	hn49c02.x1 NCI_CGAP_Co17 cDNA	AW770800	Hs.371969	
		clone IMAGE:3026978 3' similar to	١	•	*
4.		contains MER5.b1 MER5 repetitive	* * * * * * * * * * * * * * * * * * * *	90	
		element ;, mRNA sequence	* *		
		/clone=IMAGE:3026978 /clone_end=3'			
		/gb=AW770800 /gi=7702847	, ·•	<b>.</b>	
		/ug=Hs.371969 /len=463	•		
9232	0.01925	clone IMAGE:5265853, mRNA	BC037736	Hs.397840	
•		/gb=BC037736 /gi=23337068			·
		/ug=Hs.397840 /len=3811		40	
9233	0.009349	AGENCOURT 10227215 NIH MGC 141	BU536672	Hs.380933	
		cDNA clone IMAGE:6565196 5', mRNA			- 4.
		sequence /clone=IMAGE:6565196		*.))	*
		/clone_end=5' /gb=BU536672			
		/gi=22847113 /ug=Hs.380933 /len=1275			
		ligit === 0		•	İ
9245	0.001232	EST, cDNA, 5' end /clone=ADCAVF02	AV708876	Hs.330985	
0		/clone_end=5' /gb=AV708876			
		/gi=10726141 /ug=Hs.330985 /len=414			
9246	3.34F-04	EST(T-cells V Homo sapiens cDNA 5'	AA355092		+
02 10	0.012 01	lend)	7 4 1000002		
9252	0.00489	cDNA FLJ31169 fis, clone	AK055731		
J_UZ	5.55453	KIDNE2000026		'	
9257	0.014031	602246637F1 NIH MGC 62 cDNA clone	BF690692	Hs.442332	<del> </del>
J2.01	0.014931	IMAGE:4331985 5', mRNA sequence	151 030032	113.772332	
		/clone=IMAGE:4331985 /clone end=5'			
		/gb=BF690692 /gi=11976100			
	1	/ug=Hs.442332 /len=929		1	L

		nding To Differentially Expressed Genes			
Spot	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
9259	0.021781	th92f12.x1	AI435504	Hs.443955	
.,		Soares_NSF_F8_9W_OT_PA_P_S1	,	*	1
		cDNA clone IMAGE:2126159 3' similar to	o.		
		SW:DOC2_MOUSE P98078 MITOGEN-			
	4.	RESPONSIVE PHOSPHOPROTEIN			·
		ISOFORMS P96, P93 AND P67.;, mRNA		0.00	
•	9	sequence /clone=IMAGE:2126159			
•		/clone end=3'/gb=Al435504/gi=4303646			*
		/ug=Hs.443955 /len=545	٠	•	
, ,		*	4		
9267	8.63E-04	ESTs, cDNA, 3' end	Al683884	Hs.213763	
	-15.	/clone=IMAGE:2263506 /clone_end=3'		11012	F 4 (1987)
		/gb=Al683884 /gi=4894066	* .		* · · · · · · · · · · · · · · · · · · ·
		/ug=Hs.213763 /len=485			
9287	0.03489	UI-H-DT1-avz-k-14-0-UI.s1	BQ015886	Hs.22607	
٥٤٥١	0.00-100	NCI_CGAP_DT1 cDNA clone	DQ010000	113.22007	
.;	* .	IMAGE:5886469 3', mRNA sequence	*.		
	t.	/clone=IMAGE:5886469 /clone_end=3'			
		/gb=BQ015886 /gi=19751163		· ·	
			Sel .	00000000	1
0004	0.007000	/ug=Hs.22607 /len=1207	A1 050044	11. 50445	
9294	0.007886	mRNA; cDNA DKFZp761J1112 (from	AL353944	Hs.50115	
		clone DKFZp761J1112) /gb=AL353944		1	
	<del> </del>	/gi=7669984 /ug=Hs.50115 /len=3563			
9295	0.046005	EST(fetal liver spleen 1NFLS Homo	R98733		1
•		sapiens cDNA clone IMAGE:206946 3'			ļ
	}	similar to contains L1 repetitive element;	*		
			· · · · · · · · · · · · · · · · · · ·		
9298	0.032959	ad47h05 s1 Stratagene lung carcinoma	AA669458	Hs 445542	
	±*,	937218 cDNA clone IMAGE:884889 3'	4	]	
		similar to gb:X51956_rna1 GAMMA	-		
	1 %	ENOLASE Alu repetitive element contains	·		1
		element TAR1 repetitive element;			1
		mRNA sequence /clone=IMAGE:884889		١.	e.
	1				
		/clone_end=3' /gb=AA669458			
					-
9302	4.06E-04	/clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs.445542 /len=926			
9302	4.06E-04	/clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs.445542 /len=926 No significant match, ORF-	SEO ID No.11		
		/clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs 445542 /len=926 No significant match, ORF- 1(1~102,214~317)	SEQ.ID.No.11		
9302 9319		/clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs.445542 /len=926 No significant match, ORF- 1(1~102,214~317) No significant match	*		
9319	0.020482	/clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs.445542 /len=926 No significant match, ORF- 1(1~102,214~317) No significant match (ORF:+2:2~226[225]), low complexity	SEQ.ID.No.11 SEQ.ID.No.17		
	0.020482	/clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs.445542 /len=926  No significant match, ORF- 1(1~102,214~317)  No significant match (ORF:+2:2~226[225]), low complexity  No significant match	SEQ.ID.No.17		
9319 9320	0.020482	/clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs.445542 /len=926 No significant match, ORF- 1(1~102,214~317) No significant match (ORF:+2:2~226[225]), low complexity No significant match (ORF:+1:208~366[159])	SEQ.ID.No.17 SEQ.ID.No.62		
9319	0.020482	/clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs.445542 /len=926 No significant match, ORF- 1(1~102,214~317) No significant match (ORF:+2:2~226[225]), low complexity No significant match (ORF:+1:208~366[159]) EST(CM4-CT0310-170300-114-f06	SEQ.ID.No.17		
9319 9320	0.020482	/clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs.445542 /len=926  No significant match, ORF- 1(1~102,214~317) No significant match (ORF:+2:2~226[225]), low complexity No significant match (ORF:+1:208~366[159]) EST(CM4-CT0310-170300-114-f06 CT0310 cDNA, MRNA sequence)	SEQ.ID.No.17 SEQ.ID.No.62		

Genes	Correspo	nding To Diff rentially Expr ssed Genes	in Figure 12 -	Hypertensior	
Spot	p-value	Description	Gene	Unigen	Protein
		*	Accession	Accession	Accession
			No.	No	No.
9362	0.010015	UI-E-CR1-adz-a-04-0-UI.r1 UI-E-CR1	BM706524	Hs.421063	-
•		cDNA clone UI-E-CR1-adz-a-04-0-UI 5',			
		mRNA sequence /clone=UI-E-CR1-adz-a-		9.0	
		04-0-UI /clone_end=5' /gb=BM706524	9		
		/gi=19019782 /ug=Hs.421063 /len=1149			
9368	0.03489	fms-related tyrosine kinase 1 (vascular	NM_002019	Hs.381093	NP_002010
		endothelial growth factor/vascular			1
		permeability factor receptor) (FLT1),			
		mRNA /cds=(250,4266) /gb=NM_002019.			
		/gi=4503748 /ug=Hs.381093 /len=7680		XI.	
			<u></u>		
9383	0.00189	phosphoinositide-3-kinase, regulatory	NM_005027	Hs.211586	NP_005018
	:	subunit, polypeptide 2 (p85 beta)			
		(PIK3R2), mRNA /cds=(242,2428)			
	1 .	/gb=NM_005027 /gi=4826907			
·	1	/ug=Hs.211586 /len=3201			
9385	0.005674	ATP-binding cassette, sub-family F	NM_001090	Hs.9573	NP_001081
		(GCN20), member 1 (ABCF1), mRNA	·		1
		/cds=(95,2518) /gb=NM_001090			
		/gi=10947134 /ug=Hs.9573 /len=3141		`	l
9388	0.041254	Hpall tiny fragments locus 9C (HTF9C),	NM_022727	Hs.63609	NP_073564
		mRNA /cds=(340,2028) /gb=NM_022727		•	Ì
		/gi=21361611 /ug=Hs.63609 /len=2498		1	
0000	0.000400		NIN 004040	11 407405	ND 440000
9396	0.020482	fenestrated-endothelial linked structure	NM_031310	Hs.107125	NP_112600
		protein; PV-1 protein (PV1), mRNA	·		1
		/cds=(51,1379) /gb=NM_031310			1
9416	0.010015	/gi=13775237 /ug=Hs.107125 /len=2317 striatin, calmodulin binding protein 4	NIM 042402	Un 400005	ND 007505
9410	0.010015	(STRN4), mRNA /cds=(1,2262)	NM_013403	Hs.108665	NP_037535
	<b>.</b>	/gb=NM_013403 /gi=7019572			-
•		l =			1
9443	0.00223	/ug=Hs.108665 /len=3188 synapse associated protein 1, SAP47	NM_032796	Hs.47334	NP_116185
· · ·	0.00223	(Drosophila) (SYAP1), mRNA	14141_032780	13.41334	11.0.102
		/cds=(94,1152) /gb=NM_032796		[ .	į
		/gi=19923854 /ug=Hs.47334 /len=2030	2	•	-
9459	0.01072	ubiquinol-cytochrome c reductase binding	NM 006294	Hs.131255	NP_006285
0400	0.01072	protein (UQCRB), mRNA /cds=(54,389)	14141_000294	113. 191233	_000203
		/gb=NM_006294 /gi=20070231	<b>!</b>		
•		/ug=Hs.131255 /len=965			
9460	0.002054	FLJ10254 (FLJ10254), mRNA	NM 018041	Hs.326551	<del> </del>
3.00	5.552554	/cds=(172,993) /gb=NM_018041	1.1101_0 10041	1.15.020001	[
		/gi=8922314 /ug=Hs.326551 /len=2134			
9475	0.039034	hypothetical protein FLJ20624	NM 017906	Hs.52256	NP 060376
2 0	0.000004	(FLJ20624), mRNA /cds=(80,1255)	1, 1111_0 1 7 3000	10.02200	1.4000076
		/gb=NM_017906 /gi=8923576		[	
		/ug=Hs,52256 /len=1554			
	<u> </u>	1109-110,02200 /ICH-1004	ـــــــــــــــــــــــــــــــــــــ	L	ل

Genes	Correspon	nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
		·	Accession	Accession:	Accession
			No.	No.	No.
9478	0.0261	FLJ23558 (FLJ23558), mRNA	NM 025095	Hs.288552	NP_079371
,		/cds=(498,959) /gb=NM_025095	_		_
		/gi=13376657 /ug=Hs.288552 /len=2365			
9479	0.002625	ALS2CR18 mRNA (=cDNA FLJ12667	AB053320	-	NP_079528
		fis)			: · · , — · · · · · · · · · · ·
9482		mRNA for KIAA1367 protein, partial cds.	AB037788	Hs.224961	. *** 1.
	0.007.0	/cds=(1,1741) /gb=AB037788			
		/gi=7243114 /ug=Hs.224961 /len=4196			
9504	0.009349	serum/glucocorticoid regulated kinase	NM 005627	Hs.296323	NP 005618
000 .	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	(SGK), mRNA /cds=(58,1353)	55552.	110.200020	
	ļ	/gb=NM 005627 /gi=25168262		ļ	
	-	/ug=Hs.296323 /len=2386			
9518	2 73F-04		K00627	Hs.203776	
3310	2.734-04	3' end. /gb=K00627 /gi=337653	100027	113.200770	
	[ ·	/ug=Hs.203776 /len=2126			
9530	0.036014	hypothetical protein FLJ10856	NM 018247	Hs.108530	NP_060717
9530	0.0369 14	(FLJ10856), mRNA /cds=(148,1233)	INIVI_010247	IHS. 100000	NF_000717
		/gb=NM_018247 /gi=8922719			*
0504	0.000400	/ug=Hs.108530 /len=3720	AE505200	11- 004004	
9534	0.006106	codanin I mRNA, partial cds.	AF525398	Hs.334834	
		/cds=(1,3798) /gb=AF525398			
05.45	0.040540	/gi=27451597 /ug=Hs.334834 /len=4725	41.000770	11 100510	
9545	0.048543	mRNA; cDNA DKFZp686C117 (from	AL832773	Hs.433512	
	]	clone DKFZp686C117) /gb=AL832773			
0500	2 22 122	/gi=21733355 /ug=Hs 433512 /len=5984	1111 004045	11 0000	110 00 1000
9568	0.00489	estrogen receptor binding site associated,	NM_004215	Hs.9222	NP_004206
		antigen, 9 (EBAG9), mRNA			*
		/cds=(362,1003) /gb=NM_004215			i
		/gi=14577926 /ug=Hs 9222 /len=1182		11 05 160	
9584	3.69E-04	hypothetical protein FLJ20522	NM_017861	Hs.35406	NP_060331
,	1	(FLJ20522), mRNA /cds=(213,866)	^		<u>.</u> 1
		/gb=NM_017861 /gi=23680884		,	
1-3		/ug=Hs.35406 /len=1876			
9594	0.027691	serine (or cysteine) proteinase inhibitor,	NM_006216	Hs.21858	NP_006207
		clade E (nexin, plasminogen activator			
*		inhibitor type 1), member 2 (SERPINE2),			I
340		mRNA /cds=(210,1406) /gb=NM_006216			
		/gi=24307906 /ug=Hs.21858 /len=2129		, w	
9596	0.012262	vimentin (VIM), mRNA /cds=(123,1523)	NM_003380	Hs.297753	NP_000995
	*	/gb=NM_003380 /gi=4507894	1		
	12000	/ug=Hs.297753 /len=1851		ļ	
9617	0.002625	mRNA; cDNA DKFZp761B0823 (from	AL157462	Hs.306484	1
		clone DKFZp761B0823) /gb=AL157462	l .		ļ
		/gi=7018477 /ug=Hs.306484 /len=5085			
9619	7.18E-04	hypothetical protein MGC14817	NM_032338	Hs.124813	NP_115714
		(MGC14817), mRNA /cds=(53,442)	1.	1	
		/gb=NM_032338 /gi=14150123		}	
	I	/ug=Hs.124813 /len=1010			ŀ

		nding To Differ ntially Expr ssed Genes			
Spot	p-value	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
	-	11	No.	No.	No.
9627	0.029363	hypothetical protein DKFZp564B1162	NM_031305	Hs.93589	NP_11259
		(DKFZP564B1162), mRNA			
	' '	/cds=(661,2628) /gb=NM_031305			
	÷	/gi=13775229 /ug=Hs.93589 /len=4593	*		2
9628	0.048543	similar to weakly similar to glutathione	BC029424	Hs.283072	<del> </del>
0020		peroxidase 2, clone MGC:32677		1.0.2000.2	
		IMAGE:4285958, mRNA, complete cds		100	-
		/cds=(35,664) /gb=BC029424	10	4	-
		/gi=20810222 /ug=Hs.283072 /len=1398			
0664	0.002222		A1642000	· · · · ·	ND CEO44
9661	0.003332	. ,	Al613080		NP_65941
0000	0.0014.47	IMAGE:2284373 3')	1111	111 040500	t
9662	0.031117	hypothetical protein FLJ33282	NM_152388	Hs.346509	٠.
	1	(FLJ33282), mRNA /cds=(225,1523)		-	
	- 50	/gb=NM_152388 /gi=22748830		.*	
	<u> </u>	/ug=Hs.346509 /len=2078	,		
9665	0.036914	EST(df64h05.y1 Morton Fetal Cochlea	AW024055		
		clone IMAGE:2488569 5') (5e-06 match)			
9677	6.03E-05	EST(QV3-NN1023-260400-168-a04	AW902143		NP_06596
,		NN1023)			
9680	0.004536	clone 114 tumor rejection antigen mRNA,	AF445027	Hs.24723	
7 7		complete cds /cds=(3482,3544)		1	1-
		/gb=AF445027 /gi=17386079		ĺ	-
		/ug=Hs.24723 /len=3648			
9682	0.010015	BX091044 Soares retina N2b4HR cDNA	BX091044	Hs.435655	+
000 <u>2</u>	0.010010	clone IMAGp998D18828 ;	DX031044	113.40000	
		IMAGE:360161, mRNA sequence	ί,		
			• *		
		/clone=IMAGp998D18828_;_IMAGE:3601			•
		61 /gb=BX091044 /gi=27826224			
	1.	/ug=Hs.435655 /len=644			
9683	1.63E-04	cDNA FLJ12246 fis, clone	AK022308	Hs.188853	·
		MAMMA1001343. /gb=AK022308		·	
		/gi=10433677 /ug=Hs.188853 /len=1766			
9684	0.003893	cDNA FLJ40989 fis, clone	AK098308	Hs.325568	
		UTERU2015108. /gb=AK098308			
		/gi=21758297 /ug=Hs.325568 /len=2316			
9697	2.32E-05	EST(wc77f09.x1 NCI_CGAP_Pan1 clone	AI674873		1
	•	IMAGE:2324681 3' contains Alu repeat)		8	
9702	0.020482	EST(yz87a01.s1 cDNA clone 289992 3')	N64638	· ·	†
9712		wI54c05.x1 NCI CGAP Brn25 cDNA	AI864553	Hs.371597	1
	1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	clone IMAGE:2428712 3', mRNA	-		1
		sequence /clone=IMAGE:2428712			
		/clone_end=3' /gb=Al864553 /gi=5528660		· ·	
		, –		1.	
0747	0.04047	/ug=Hs.371597 /len=474	1104200	·	<del> </del>
9717	0.01047	EST(yu74g03.s1 clone 239572 3'	H81306	1.	
	A 6 4 . S =	contains Alu repeat)	112 1222	ļ.,	<del> </del>
9719	0.021781	EST(qp43d06.x1 NCI_CGAP_Co8 clone	Al346089		
		IMAGE:1925771 3')			<u> </u>
9721	1 0 008722	EST(yj01e06.r1 clone 147490 5')	R81297	1	NP_05770

		nding To Diff r ntially Expr ss d Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
		<u> </u>	N .	No.	No.
9723	4.48E-04	yx53g06.s1 Soares melanocyte 2NbHM	N21311	Hs.433011	
•	7	cDNA clone IMAGE:265498 3', mRNA			
		sequence /clone=IMAGE:265498			
	*	/clone_end=3' /gb=N21311 /gi=1126481	*	() F +	
•	1.	/ug=Hs.433011 /len=570		0.5	*
9724	0.03489	hypothetical protein BC012010	NM 138421	Hs.183733	NP. 612430
	1.	(LOC113174), mRNA /cds=(30,1457)	· ·		T .
		/gb=NM_138421 /gi=19923942			
- 8	*	/ug=Hs:183733 /len=1527	*		* *
9729	0.005674		AAD38784	7 1	
9732		AV719651 GLC cDNA clone GLCEBH07	AV719651	Hs.337318	
		5', mRNA sequence /clone=GLCEBH07			
•		/clone_end=5' /gb=AV719651	*		
-		/gi=10816803 /ug=Hs.337318 /len=680		='	
,			8		, i i
9739	0.027691	ribosomal protein L5 pseudogene	U66589		NP 000960
9741		EST UI-H-BI0p-aau-a-05-0-UI.s1	AW015507		NP 037442
0.41	0.04000	NCI_CGAP_Sub2 Human sapiens cDNA	7,000	- 4	141 _037 442
		clone IMAGE:2710544 3'			
9743	0.004203	hypothetical protein FLJ20507	NM_017849	Hs.202955	NP_060319
9143	0.004203	(FLJ20507), mRNA /cds=(258,974)	14141_017049	IU8.505829	NE_0002   s
	,	/gb=NM_017849 /gi=8923465	, , , , , ,		÷ +
		/ug=Hs.202955 /len=4223			
9746	0.027691	clone IMAGE:4182947, mRNA	BC016962	Hs.16193	- p-
37.40	0.027091	/gb=BC016962 /gi=16877432	DC010902	ns. 10 193	4
* -	1 3				
9749	0.016074	/ug=Hs.16193 /len=1866 TBC1 domain family, member 2	NM 049424	Up 125017	ND 00000
9/49	0.010974		NM_018421	Hs.135917	NP_060891
1,		(TBC1D2); mRNA /cds=(1622,3028)		,	
		/gb=NM_018421 /gi=8922166	* **		
0700	0.000440	/ug=Hs.135917 /len=3431	NIA 000000	11 400044	N.D. 540000
9762	0.023148	poly(A) binding protein, cytoplasmic 5	NM_080832	Hs.190614	NP_543022
£ .		(PABPC5), mRNA /cds=(441,1589)		*	
		/gb=NM_080832 /gi=18201887	)		
		/ug=Hs.190614 /len=3521			
9763	0.005674	EST(ze13e01.r1	W94505		
		Soares_fetal_heart_NbHH19WcDNA			
,		clone IMAGE:358872 5')			
9772	0.043576	hypothetical protein FLJ30596	NM_153013	Hs.81907	NP_694558
		(FLJ30596), mRNA /cds=(223,1062)			-
3 <sup>1</sup>		/gb=NM_153013 /gi=23308514			
		/ug=Hs.81907 /len=1978			
9774	0.010015	cDNA FLJ36605 fis, clone	AK093924	Hs.379100	
		TRACH2015316, highly similar to			1
		VIMENTIN. /cds=(631,1317)	σ.		1
		/gb=AK093924 /gi=21752883			1
		/ug=Hs.379100 /len=2665		*	
9783	5.34E-04	EST(tx54b12.x1 NCI_CGAP_Lu24 clone	Al630984		
		IMAGE:2273375 3' contains L1.t2 L1			
	*	repeat)			

Genes	Correspoi	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	
Spot	p-value	D scription	Gene	Unigen	Protein
* .		·	Accession	Accession	Accession
			No	No.	No.
9805	0.043576	EST (qh12h02.x1	Al240516		
		Soares_NFL_T_GBC_S1	-		
		IMAGE:1844499 3')		1	
9807	0.01072	UI-E-CK0-aap-a-05-0-UI.s1 UI-E-CK0	BU726073	Hs.170264	
		cDNA clone UI-E-CK0-aap-a-05-0-UI 3',			
•		mRNA sequence /clone=UI-E-CK0-aap-a-			
		05-0-UI /clone_end=3' /gb=BU726073		×*	
		/gi=23645560 /ug=Hs.170264 /len=1266			
9808	0.002844	EST HS_5436_B2_H08_T7A RPCI-11	AQ670656		
		Human Male BAC Library genomic clone	٠.	1	ŀ
	. ,	Plate=1012 Col=16 Row=P	·	<u> </u>	
9812	1.06E-04	mRNA; cDNA DKFZp313C1042 (from	AL833436	Hs.376859	
٠,	,	clone DKFZp313C1042) /gb=AL833436	>=		
-		/gi=21734078 /ug=Hs.376859 /len=2103			
9819	0.03489	EST (yq42a05.r1 Soares fetal liver spleen	R94397		
				<u> </u>	
9823	0.013991	hypothetical protein MGC2560	NM_031452	Hs.80624	NP_113640
	· · ·	(MGC2560), mRNA /cds=(195,551)			
		/gb=NM_031452 /gi=13899288		1 ' '*	
	9	/ug=Hs.80624 /len=1229			
9827	0.001465	EST CB H.sapiens cDNA clone	AV743921		
		CBCCHD05 5'			<u> </u>
9850	0.003893	cDNA FLJ11946 fis, clone	AK022008	Hs.323231	
		HEMBB1000709. /gb=AK022008	,		- *
1.		/gi=10433321 /ug=Hs.323231 /len=3241		J	
9856	0.029363	repressor of estrogen receptor activity	NM_007273	Hs.7771	NP_009204
		(REA), mRNA /cds=(81,980)			
• •	v 0	/gb=NM_007273 /gi=20149589		,	
		/ug=Hs.7771 /len=1342		1	
9883	0.024587	chromosome 11 open reading frame2	NM_013265	Hs.5258	NP_008917
		(C11orf2), mRNA /cds=(40,2388)		·	
	1 .	/gb=NM_013265 /gi=8393008	1	0.0	
		/ug=Hs.5258 /len=2546			ļ
9890	0.041254		AF338199	Hs.143740	1
		/cds=(66,440) /gb=AF338199			
		/gi=12802898 /ug=Hs.143740 /len=916		l	100 000 100
9891	0.003332	isocitrate dehydrogenase 2 (NADP),	NM_002168	Hs.5337	NP_002159
		mitochondrial (IDH2), nuclear gene	1		
	1	encoding mitochondrial protein, mRNA			1
	<b>)</b> '	/cds=(87,1445) /gb=NM_002168			
0000		/gi=28178831 /ug=Hs.5337 /len=1740	000000	41. 40000	100 00000
9928	2.47E <del>-</del> 04	LIM domain containing preferred	NM_005578	Hs.180398	NP_005569
		translocation partner in lipoma (LPP),	+		
		mRNA /cds=(247,2085) /gb=NM_005578		1	1
		/gi=5031886 /ug=Hs.180398 /len=5656	÷		
	1	L	ــــــــــــــــــــــــــــــــــــــ	<u> </u>	<u> L</u>

		nding To Differentially Expressed Genes	Gene		Protein
Spot	p-value	Description	7	Unigene	2
	ł	η.	Accession	Accession	Accession
00.10			No.	No.	No.
9940	2.47E-04	BRF2, subunit of RNA polymerase III	NM_018310	Hs.274136	NP_060780
	*	transcription initiation factor, BRF1-like			
	(	(BRF2), mRNA /cds≃(111,1370)	6		
	1	/gb=NM_018310 /gi=22035561			
		/ug=Hs.274136 /len=1978			
9960	0.011469	similar to weakly similar to glutathione	BC029424	Hs.283072	
	!	peroxidase 2, clone MGC:32677	. •	-	
		IMAGE:4285958, mRNA, complete cds	· ·		<b>.</b>
. ,		/cds=(35,664) /gb=BC029424	*		
		/gi=20810222 /ug=Hs.283072 /len=1398			
9990	0.041254	hypothetical protein FLJ23467	NM_024575	Hs.16179	NP 078851
	}	(FLJ23467), mRNA /cds=(103,657)	· ·	}	
	<u> </u>	/gb=NM_024575 /gi=13375749			ł
•	٠.	/ug=Hs.16179 /len=1196			
10019	0.01072	serologically defined colon cancer antigen	NM 005786	Hs.284217	NP 00577
		33 (SDCCAG33), mRNA /cds=(295,2358)	-		_
	-	/gb=NM_005786 /gi=15451922			
		/ug=Hs.284217 /len=2858	,		ĺ
10049	7.18E-04	FLJ12209 fis, clone MAMMA1000962	AK022271	Hs.366548	
		/cds=UNKNOWN /gb=AK022271			
		/gi=10433630 /ug=Hs.366548 /len=1239		*	1
10054	0.01925	similar to hypothetical protein FLJ10883	NM 052937	Hs.60293.	NP 443169
		(LOC115294), mRNA /cds=(98,1171)			
	ł	/gb=NM_052937 /gi=24308385			
		/ug=Hs.60293 /len=3967			1
10058	0.029363	ribosomal protein L36a-like (RPL36AL),	NM_001001	Hs:419465	NP 000992
.,	0.02000	mRNA /cds=(95,415) /gb=NM_001001	001001	110.110.100	
- 7	· .	/gi=16306559 /ug=Hs.419465 /len=537			*
10064	7 18F-04	KIAA0570 gene product (KIAA0570),	XM 002692		<del></del>
	1	mRNA	/002,002		
10087	2 23F-04	cDNA FLJ30064 fis, clone	AK054626	Hs.188504	
10007	2.202 04	ADRGL2000323. /cds=(118,516)	711004020	1113.100004	
		/gb=AK054626 /gi=16549205	1		×.
		/ug=Hs.188504 /len=2081	Ξ		
10094	1.81E-04	nuclear factor of kappa light polypeptide	NM_013432	Hs.323834	NP_038460
10034	1.01104	Igene enhancer in B-cells inhibitor-like	14141_015452	1115.525654	1117_050400
	( ;	2(NFKBIL2), mRNA /cds=(473,4132)			
	*	/gb=NM 013432/gi=15718771			÷ ,
	} '			-	ł
10100	0.015024	/ug=Hs.323834 /len=4501	NIM 024820	110 470470	NID 07040
10100	0.015924	hypothetical protein FLJ22662	NM_024829	Hs.178470	NP_07910
		(FLJ22662), mRNA /cds=(66,1586)		{ ·	İ
	1	/gb=NM_024829 /gi=13376231	-	1	1
10155	1 2 2 2 2 2 2 2	/ug=Hs.178470 /len=1707			1.5
10103	J 0.018081	eukaryotic translation elongation factor 1	NM_001404	Hs.256184	NP_00139
		gamma (EEF1G), mRNA /cds=(38,1351)			·
,	1	/gb=NM_001404 /gi=25453475	·	0.	1
	i	/ug=Hs.256184 /len=1429		(	1

		nding To Differentially Expressed Genes			
Spot	p-valu	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No	No.	No.
10108	0.008722	myosin, heavy polypeptide 9, non-muscle	NM_002473	Hs.146550	NP 002464
		(MYH9), mRNA /cds=(1,5883)	<b>-</b>	, . Del 1	<u> </u>
		/gb=NM_002473 /gi=22507396			
•		/ug=Hs.146550 /len=7274			,
10111	0.016974	ubiquitin-conjugating enzyme E2G 2	NM 003343	Hs.192853	NP_003334
		(UBC7 yeast) (UBE2G2), mRNA			
	.	/cds=(56,553) /gb=NM_003343	•		
	ļ	/gi=4507780 /ug=Hs.192853 /len=2900			
10133	0.001737	hypothetical protein FLJ13576	NM 022484	Hs.334335	NP_071929
		(FLJ13576), mRNA /cds=(365,2458)	· · · · · · · · ·		
	÷.	/gb=NM 022484 /gi=21362101		•	
•	·	/ug=Hs.334335 /len=3973			*
10145	9.48F-05	EST(fi21a05.x1 Sugano Kawakami	AW116880		<del></del>
,	J.#JL-09	zebrafish DRA clone 2601776 3')	7.44110000		f
10146	0.006106	EST qz90a06.x1	AI493872	<del>                                     </del>	NP_008878
10170	0.000100	Soares_pregnant_uterus_NbHPU cDNA	71433072		1141 _000070
		clone IMAGE:2041810 3'		1	
10148	0.004303	EST(qo26g10.x1 NCI_CGAP_Lu5 clone	AI342863		
10140	0.004203	IMAGE:1909698 3' contains Alu repeat)	A 342003		
10151	0.01025	cDNA FLJ36605 fis, clone	AK093924	Hs.379100	<del></del>
10151	0.01925	TRACH2015316, highly similar to	AN093924	ns.379100	*
		VIMENTIN. /cds=(631,1317)			
		/gb=AK093924 /gi=21752883			
10152	G EEE OA	/ug=Hs.379100 /len=2665	A A 760200	<u> </u>	
10152	0.555-04	EST(oa36e01.s1 NCI_CGAP_GCB1	AA766399	• *	, , , , ,
		clone IMAGE:1307064 contains Alu		· .	
40470	0.004000	repeat) (low match)	NOOFEAR		
10170	0.001033	EST (ts95a10.x1 NCI_CGAP_GC6 cDNA	Al635513		
10470	0.000010	clone IMAGE:2239002 3')			100000000000000000000000000000000000000
10179	0.009349	EST (wq27e08.x1 NCI_CGAP_Kid11	Al953360		NP_620149
		IMAGE:2472518 3')			
10186	0.023148		NM_003270	Hs.121068	NP_003261
		(TM4SF6), mRNA /cds=(104,841)			
		/gb=NM_003270 /gi=21265115			1
40:		/ug=Hs.121068 /len=2069			
10194	0.008722	hypothetical protein FLJ11101	NM_018322	Hs.58382	NP_060792
		(FLJ11101), mRNA /cds=(1,552)			1
		/gb=NM_018322 /gi=8922866			h-
	1	/ug=Hs.58382 /len=1920	1		*
10195	0.003079	mRNA for KIAA1586 protein, partial cds.	AB046806	Hs.180663	
		/cds=(1481,3700) /gb=AB046806			1
Y-	- 44	/gi=10047246 /ug=Hs.180663 /len=4061			
10196	0.001737	UI-CF-DU1-aav-k-08-0-UI s1 UI-CF-DU1	BM983293	Hs.424609	
	1	cDNA clone UI-CF-DU1-aav-k-08-0-UI 3',			
		mRNA sequence /clone=UI-CF-DU1-aav-	1	;	1
		k-08-0-UI /clone_end=3' /gb=BM983293			
		/gi=19607660 /ug=Hs 424609 /len=684			

		nding To Diff r ntially Expressed Genes			
Spot	p-valu	Description	Gen	Unigene	Protein
		4	Accession	Accession	Accession
			No.	No.	No =
10197	0.007056	CDA02 protein (CDA02), mRNA	NM_032025	Hs.332404	NP 114414
		/cds=(3,1832) /gb=NM_032025			
		/gi=14042940 /ug=Hs.332404 /len=2179		- *	
10204	0.020482	BX109229 NCI_CGAP_GCB1 cDNA	BX109229	Hs.136841	
		clone IMAGp998K073291, mRNA			
		sequence	,	:	
		/clone=IMAGp998K073291_;_IMAGE:130			
		6110 /gb=BX109229 /gi=27835680	4 4	, J.	
		/ug=Hs.136841 /len=468			
10212	0.014931	EST(ye51h07.s1 Soares fetal liver spleen	T96639		
		1NFLS clone IMAGE:121309 3' similar to	10000	-	*
		contains Alu repetitive element; contains		6	
		L1 repetitive element)			·
10214	0.036914	DNA sequence (chromosome 8 clone	AC090131		
10214	0.000014	RP11-463G10 map 8)	7,0000101		,
10226	0.006106	wm98f08.x1 NCI_CGAP_Ut2 cDNA clone	Δ1889396	Hs.212245	***
10220	0.000	IMAGE:2444007 3' similar to contains Alu	A1003330	113.212240	
		repetitive element; contains element MIR		i.	
		repetitive element ;, mRNA sequence			,
	7	/clone=IMAGE:2444007 /clone_end=3'			
		/gb=Al889396 /gi=5594560			
	-				
10228	0.006566	/ug=Hs.212245 /len=434	NIM 0400C4	115 404544	ND 000524
10220	0.000000	hypothetical protein FLJ10342	NM_018064	Hs.101514	NP_060534
		(FLJ10342), mRNA /cds=(534,1145)		1	
4	- 32	/gb=NM_018064 /gi=14149717		=	
40000	0.000044	/ug=Hs.101514 /len=1506	DV004050	11. 407050	
10232	0.002844	BX094256	BX094256	Hs.407356	
		Soares_fetal_heart_NbHH19W cDNA	4		
		clone IMAGp998B20783, mRNA			
	. *	sequence			<i>'</i>
	0	/clone=IMAGp998B20783_;_IMAGE:3428			* ~
	ı	35 /gb=BX094256 /gi=27841884			[
100 11	0.007004	/ug=Hs.407356 /len=477	4.400.50.50		<u> </u>
10241	0.02/691	EST (nc21a04.r1 NCI_CGAP_Pr1 cDNA	AA225070		
4004=	0.040001	clone IMAGE:1008750)	1110005		ļ
10247		vimentin (VIM) gene	M18895		
10272	5.42E-04	EST yc21h02.r1 Stratagene lung	T63815	38	
		(#937210) cDNA clone IMAGE:81363 5'			1
10276	0.043576	Hypothetical protein(cDNA sequence	AK002173	*	NP_689971
		FLJ11311 fis, clone PLACE1010102)			
		(=cDNA sequence DKFZp566J2146)			<u> </u>
10277	0.006106	likely ortholog of mouse embryonic	NM_017611	Hs.274453	NP_060081
		epithelial gene 1 (EEG1), mRNA			-24-1
	].	/cds=(319,1794) /gb=NM_017611			
		/gi=18252046 /ug=Hs.274453 /len=2630	·		
10000	0.027691	EST RC3-HT0593-170300-011-c10	BE177303		
10289	0.027031	HT0593			

<u>Genes</u>	Correspo	nding To Diff rentially Expressed Genes	in Figure 12 -		
Spot	p-value	D scription	Gene	Unig ne	Prot in
			Accession	Acc ssion	Accession
		* * * * * * * * * * * * * * * * * * * *	No.	No.	No
10291	0.021781	cDNA FLJ33775 fis, clone	AK091094	Hs.325625	
		BRSSN2000498. /gb=AK091094			
	*	/gi=21749382 /ug=Hs.325625 /len=2431			18
10293	0.023148	BX102130 NCI_CGAP_Pr3 cDNA clone	BX102130	Hs.433046	- E'
.0_00	0.0201	IMAGp998P072795, mRNA sequence	DX 102 100	110.4000-10	
		/clone=IMAGp998P072795_;_IMAGE:111		1	Ì
	]	5766 /gb=BX102130 /gi=27831621	9.	,	
		/ug=Hs.433046 /len=450			,
10294	0.01072		AK002420		ND 000EE0
10294	0.01072	unnamed protein product [Homo sapiens]	AKUU2 129		NP_062553
10296	4 25E 05	cDNA sequence (cDNA sequence	AV024665	<u> </u>	<del></del>
10290	4.25E-05		AK021665		
40204	0.045004	FLJ11603 fis, clone HEMBA1003926)	A 1400 4007	11- 000040	
10304	0.015924	cDNA FLJ14175 fis, clone	AK024237	Hs.288613	i
	·	NT2RP2002979. /gb=AK024237			
1000=	2.22.122	/gi=10436564 /ug=Hs.288613 /len=3493		<del>                                     </del>	
10307	0.00189	EST(ti95f04.x1 NCI_CGAP_Gas4 cDNA	Al445690		
		clone IMAGE:2139775 3')			
10322	0.00489	cDNA sequence FLJ11479 fis, clone	AK021541		
		HEMBA1001784		·	
10325	0.006106	EST IL2-UM0076-130500-084-A01	AW802834		
	L	UM0076 cDNA	·		L
10330	8.48E-05	EST xa58b09.x1 NCI_CGAP_HSC2	AW073612		
		cDNA clone IMAGE:2570969 3' similar to			
		contains Alu repetitive element;	2.9		
10331	7.18E-04	EST QV4-UM0094-060400-159-f11	AW804948		NP_112180
		UM0094			_
10344	0.002625	clone IMAGE:5260918, mRNA	BC035085	Hs.250448	
	*	/gb=BC035085 /gi=23958865			
	ŀ	/ug=Hs.250448 /len=3052			
10350	0.039034	hypothetical protein FLJ90013	NM_153365	Hs.25119	NP 699196
		(FLJ90013), mRNA /cds=(15,1703)	-	- 81	7
	}	/gb=NM_153365 /gi=23503310		].~	
		/ug=Hs.25119 /len=3382			
10356	0.008722		BG494113	Hs.47122	
,.,		IMAGE:4672494 5', mRNA sequence	70.01.10		4
	1	/clone=IMAGE:4672494 /clone end=5'			
	,	/gb=BG494113 /gi=13455627			
		/ug=Hs.47122 /len=744			
10357	0.012262	ribosomal protein L23 (RPL23), mRNA	NM 000978	Hs.234518	NP_000969
10007	0.012202	/cds=(27,449) /gb=NM_000978	14141_000970	115.234310	145-000909
•				· ·	
10372	0.00242	/gi=14591907 /ug=Hs.234518 /len=493	COECOO	110 202470	
10372	0.00242	C05683 pancreatic islet cDNA clone	C05683	Hs.323472	
		hbc5035, mRNA sequence	* * *		Y.
	}	/clone=hbc5035 /gb=C05683 /gi=1502459	· ·	.	
40070	0.044400	/ug=Hs.323472 /len=428	100445	<del> </del>	110 0000
10379	J U.U11469	EST (tc71e05.x1 Soares_NhHMPu_S1	Al804457	7	NP_002067
	1	cDNA clone IMAGE:2070080 3')		0.00	

G nes	Correspo	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	
	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
*	* .		No.	No	No.
10392	5.42E-04	ribosomal protein, large, P1 (RPLP1),	NM_001003	Hs.424299	NP 000994
	. *	mRNA /cds=(130,474) /gb=NM_001003			
.,		/gi=16905511 /ug=Hs.424299 /len=512			•
10400	0.001128	EST (602616324F1 NIH_MGC_79 cDNA	BG619143		
		clone IMAGE:4730333 5')	1 20 10 10	-	
10401	0.001232	EST (Clontech human aorta polyA	C14262		
		mRNA (#6572) cDNA clone GEN-041E02			
		(5')			
10430	0.046005	EST(ha63a03.x1 NCI_CGAP_Pan1	AW338626	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	NP_006826
		cDNA clone IMAGE:2878348 3')			- 6
10433	0.018081	clone IMAGE:5275753, mRNA	BC044623	Hs.418416	
		/gb=BC044623 /gi=27882398			
		/ug=Hs.418416 /len=1997			10
10436	0.00223	Indian hedgehog (Drosophila), clone	BC034757	Hs.115274	E
		MGC:34815 IMAGE:5182642, mRNA,			*
		complete cds /cds=(74,955)	,		
		/gb=BC034757 /gi=21961329			
:		/ug=Hs.115274 /len=1760	× •		
10452	0.0261	EST(nf83g03.s1 NCI_CGAP_Co3 cDNA	AA535420		
		clone IMAGE:926548 3')		•	
10460	0.004536	neuroepithelial cell transforming gene 1	NM_005863	Hs.25155	NP_005854
	٠. ٠.	(NET1), mRNA /cds=(147,1775)		-	
	5.4	/gb=NM_005863 /gi=19923326	*		₹, 0
. 4 0 0	7	/ug=Hs.25155 /len=3236			
10471	0.013102	hypothetical protein FLJ14596	NM_\032809	Hs.325309	NP_116198
	,	(FLJ14596), mRNA /cds=(1324,1968)			~
	٠.	/gb=NM_032809 /gi=19923651			
	1.	/ug=Hs.325309 /len=3597			
10488	3.34E-04	FLJ11842 fis, clone HEMBA1006652,	AK021904	Hs.26966	
• •		weakly similar to 60S RIBOSOMAL			1
		PROTEIN L7 /cds=UNKNOWN		-	
	,	/gb=AK021904 /gi=10433196			
<del></del>	, K <sup>1</sup>	/ug=Hs.26966 /len=1861		•	
10491	6.55E-04	UI-H-DH0-aul-j-10-0-UI.s1	BM994461	Hs.434057	
c		NCI_CGAP_DH0 cDNA clone			
	1	IMAGE:5871081:3', mRNA sequence			,
	*	/clone=IMAGE:5871081 /clone_end=3'			] .
1.0.		/gb=BM994461 /gi=19719362	(		ļ ' · ·
·		/ug=Hs.434057 /len=2059			
10495	0.002844	7q35h07.x1 NCI_CGAP_GC6 cDNA	BF478238	Hs.356203	
		clone IMAGE:3700476 3' similar to	<b>,</b>		1
		contains element MER4 MER4 repetitive	· ,		
		element ;, mRNA sequence		-	1
		/clone=IMAGE:3700476 /clone_end=3'	·		
		/gb=BF478238 /gi=11549065	(	Ì	1
,		/ug=Hs.356203 /len=400			

		nding To Diff rentially Expr ssed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
10497	8.59E-04	UI-H-DF0-bek-n-06-0-UI.s1	CA426336	Hs.20300	
. 4		NCI_CGAP_DF0 cDNA clone UI-H-DF0-			1
		bek-n-06-0-UI 3', mRNA sequence			
.1	}	/clone=UI-H-DF0-bek-n-06-0-UI	-		-
	, v	/clone_end=3' /gb=CA426336			
		/gi=24789062 /ug=Hs.20300 /len=1060	)	0	
10498	3 44F-05	wo45d05.x1 NCI_CGAP_Gas4 cDNA	AI926493	Hs.213840	
		clone IMAGE:2458281 3' similar to	,,,,,,		
	1	contains element XTR repetitive element	1		
		;, mRNA sequence	" , ,	l	
*	٠.	/clone=IMAGE:2458281 /clone_end=3'	: *		
	ł	/gb=Al926493 /gi=5662457	, .		
			,	,	
10.400	0.04400	/ug=Hs.213840 /len=509	AK025400	11- 02022	
10499	0.01122	cDNA: FLJ21545 fis, clone COL06195.	AK025198	Hs.83623	
	1	/gb=AK025198 /gi=10437662	:	1	
		/ug=Hs.83623 /len=2176			
10506	0.032959	K-EST0187941 L14ChoiCK0 cDNA clone		Hs.435110	1
	,	L14ChoiCK0-30-C05 5', mRNA sequence	٠.	·	
		/clone=L14ChoiCK0-30-C05	[		
		/clone_end=5' /gb=CB135678			
		/gi=28102621 /ug=Hs.435110 /len=419	·		
10509	3.02E-04	UI-H-DF0-bek-k-02-0-UI.s1	CA426088	Hs.285174	
٠	l.	NCI_CGAP_DF0 cDNA clone UI-H-DF0-	. 0	* 1	
	l'	bek-k-02-0-UI 3', mRNA sequence	ļ	,	
i		/clone≈UI-H-DF0-bek-k-02-0-UI			
		/clone_ end=3' /gb=CA426088	,		
		/gi=24788814 /ug=Hs.285174 /len=1052	- X	- 0	
10510	0.046432	3'-5' RNA exonuclease (OLD35), mRNA	NM 033109	Hs.392004	NP 149100
		/cds=(19,2370) /gb=NM 033109			
	<b>]</b>	/gi=24308347 /ug=Hs.392004 /len=2616			·
10511	0.00113	cDNA FLJ34603 fis, clone	AK091922	Hs.304130	
10011	0.00113	KIDNE2013388. /gb=AK091922	71103 1322	113.004100	
	¥			· .	
10500	0.045004	/gi=21750400 /ug=Hs.304130 /len=1992 ribosomal protein L35a (RPL35A), mRNA	NIM COCCCC	110 2005 44	ND 00000
10520	0.015924		  им_000aae	Hs.288544	NP_000987
	* *	/cds=(74,406) /gb=NM_000996	^		
10500	2 2 2 2 2 2 4	/gi=16117790 /ug=Hs.288544 /len=511	45400004		NID COCTO
10523	0.014931	clone FLB6914 PRO1821 mRNA,	AF130061		NP_060783
		complete cds (=AL050083.1)		11 0 1000	
10524	0.018079	hypothetical protein FLJ30656	NM_152344	Hs.349887	NP_689557
		(FLJ30656), mRNA /cds=(52,639)			
		/gb=NM_152344 /gi=22748746		}	
		/ug=Hs.349887 /len=2212			
10525	0.011469	UI-H-DF0-beq-g-04-0-UI.s1	BU617513	Hs.25566	
		NCI_CGAP_DF0 cDNA clone UI-H-DF0-			- 0.0
		beq-g-04-0-UI 3', mRNA sequence	<u> </u>	-	1
		/clone=UI-H-DF0-beg-g-04-0-UI	1		
		/clone_end=3' /gb=BU617513	ì	1	}
		/gi=23283728 /ug=Hs.25566 /len=1170	I	1	8 8

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
10526	0.009349	UI-H-FH0-bch-m-20-0-UI.s1	BQ775028	Hs.445395	
		NCI_CGAP_FH0 cDNA clone UI-H-FH0-			
- 1		bch-m-20-0-UI 3', mRNA sequence	•		
		/clone=UI-H-FH0-bch-m-20-0-UI	* *		
		/clone_end=3' /gb=BQ775028	*	<b>J</b>	8
		/gi=21983504 /ug=Hs.445395 /len=1059			·
10536	0.01286	nascent-polypeptide-associated complex	NM_005594	Hs.32916	NP_005585
		alpha polypeptide (NACA), mRNA			
		/cds=(26,673) /gb=NM_005594	1		
		/gi=5031930 /ug=Hs.32916 /len=797			
10539	0.027691	ribosomal protein, large, P1 (RPLP1),	NM_001003	Hs.424299	NP_000994
	,	mRNA /cds=(130,474) /gb=NM_001003		7	*
		/gi=16905511 /ug=Hs.424299 /len=512	107		
10546	0.024587	cDNA FLJ13585 fis, clone	AK023647	Hs.43047	,
		PLACE1009150. /gb=AK023647		3	· ·
		/gi=10435632 /ug=Hs.43047 /len=3430			
10547	2.01E-04	mRNA; cDNA DKFZp564B032 (from	AL049975	Hs.274510	
. "		clone DKFZp564B032) /gb=AL049975			- 1
		/gi=4884225 /ug=Hs.274510 /len=1943		1	: -
10549	0.007056	UI-H-FH0-bcl-g-09-0-UI.s1	CA419491	Hs.293327	
		NCI_CGAP_FH0 cDNA clone UI-H-FH0-			
	· ·	bcl-g-09-0-UI 3', mRNA sequence		*	
		/clone=UI-H-FH0-bcl-g-09-0-UI		1	
	-	/clone_end=3' /gb=CA419491		;	} .
		/gi=24782146 /ug=Hs.293327 /len=693	]		]
10550	0.013991	clone IMAGE:4694038, mRNA, partial	BC020891	Hs.390440	
		cds /cds=(1,796) /gb=BC020891			1
		/gi=18088767 /ug=Hs.390440 /len=1333		9.00	
10564	0.00189	UI-1-BB1p-akj-h-02-0-UI.s1	BQ021906	Hs.317762	<u> </u>
	31.73.13	NCI_CGAP_Pl6 cDNA clone UI-1-BB1p-			
		akj-h-02-0-UI 3', mRNA sequence	0		
	[.	/clone=UI-1-BB1p-akj-h-02-0-UI			
		/clone_end=3' /gb=BQ021906			
		/gi=19757184 /ug=Hs.317762 /len=1296	100		
10565	0.003893	clone IMAGE:5284350, mRNA	BC037924	Hs.143061	
10,000	0.00000	/gb=BC037924 /gi=23138690	100001021	110:110001	
		/ug=Hs.143061 /len=2659	.8		
10569	9 48F-05	ESTs, cDNA, 5' end	R98534	Hs.293656	
.0000	0.402.00	/clone=IMAGE:201172 /clone_end=5'	11000011	115.200000	
		/gb=R98534 /gi=985051 /ug=Hs.293656	]	1	
,		/len=596		,	
10572	0.002678	EST 602708659F1 NIH MGC 43 Human	BG749918	<del>                                     </del>	<del> </del>
7012	1 3.0029.0	cDNA clone IMAGE:4845302 5'	20, 10010	. 4	
10574	0.002906	cDNA FLJ38300 fis, clone	AK095619	Hs.34969	<del> </del>
10074	3.002300	FCBBF3017288. /gb=AK095619	,	13.04303	J ·
		/gi=21754917 /ug=Hs.34969 /len=3695		· · · · · · · · · · · · · · · · · · ·	
	L	EST(Fetal Cochlea Homo sapiens cDNA	BI492586	<del>                                     </del>	NP_003109
10501	1 0 001506				
10591	0.001596	clone IMAGE:2484509 3')	1	* @	_003109

Genes	Correspon	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	
	p-value	Description	Gene	Unigene	Protein
0			Accession	Accession	Accession
	•		No.	No.	No.
10595	0.001344	FLJ14309 fis, clone PLACE3000221	AK024371	Hs.129013	
		/cds=UNKNOWN /gb=AK024371			
		/gi=10436741 /ug=Hs.129013 /len=4964			
10597	0.001344	BX106681	BX106681	Hs.293334	
	,	Soares_parathyroid_tumor_NbHPA cDNA			*
		clone IMAGp998F054235, mRNA		-	
		sequence			
		/clone=IMAGp998F054235_;_IMAGE:166			1
) -		8484 /gb=BX106681 /gi=27847079		ayer to	.0
	,	/ug=Hs.293334 /len=605			
10621	0.031117	EST (383946 MAGE resequences MAGL)	AW971857		
10623	0.007578	clone IMAGE:5276765, mRNA	BC031314	Hs.26766	
		/cds=UNKNOWN /gb=BC031314			*
		/gi=21410747 /ug=Hs.26766 /len=1000			
10624	0.001128	AGENCOURT_6417307 NIH_MGC_67	BM799896	Hs 304926	
e •		cDNA clone IMAGE:5492062 5', mRNA			
	610	sequence /clone=IMAGE:5492062	- 1	· .	
		/clone_end=5' /gb=BM799896	,	*	ļ ·
		/gi=19116719 /ug=Hs.304926 /len=913		<u> </u>	
10628	2.47E-04	ESTs, cDNA, 3' end	AI732470	Hs.191157	
į		/clone=IMAGE:565677 /clone_end=3'		_ '.	*
		/gb=AI732470 /gi=5053583	,	. 10	, (a)
<u> </u>		/ug=Hs.191157 /len=596	<u> </u>	<u> </u>	
10629	0.00242	ac74b05.x5 Stratagene lung (#937210)	AI791153	Hs.444952	100
'	`;	cDNA clone IMAGE:868305 3' similar to			
l		contains Alu repetitive element;, mRNA		t .	
,		sequence /clone=IMAGE:868305	×.		*.
ĺ		/clone_end=3' /gb=Al791153 /gi=5338869	C .		
		/ug=Hs.444952 /len=498			
10630	0.0261	UI-H-DF0-bet-j-17-0-UI.s1	BU626301	Hs.443120	
		NCI_CGAP_DF0 cDNA clone UI-H-DF0-		·	<u>.</u>
!	,	bet-j-17-0-UI 3', mRNA sequence		100	j
		/clone=UI-H-DF0-bet-j-17-0-UI		*	
		/clone_end=3' /gb=BU626301	;	1	,
	,	/gi=23292516 /ug=Hs.443120 /len=1130	· · · · · · · · · · · · · · · · · · ·		
10632	0.020482	UI-H-EI1-aze-g-21-0-UI.s1	BQ003542	Hs.190642	*
		NCI_CGAP_EI1 cDNA clone			
		IMAGE:5847596 3', mRNA sequence			
		/clone=IMAGE:5847596 /clone_end=3'		, ,	ľ .
. ,		/gb=BQ003542 /gi=19728442	0.	}	<b>)</b>
		/ug=Hs.190642 /len=1086			
10636	0.008722	cDNA FLJ13571 fis, clone	AK023633	Hs.116278	
]		PLACE1008405. /gb=AK023633			•
		/gi=10435617 /ug=Hs.116278 /len=2484			
10648	0.0261	EST, cDNA, 3' end	BQ002644	Hs.364307	
		/clone=IMAGE:5843665 /clone_end=3'			
ĺ		/gb=BQ002644 /gi=19727544		· .	·
J ' ·	1	/ug=Hs.364307 /len=762 ,		J	

Genes	Correspo	nding To Diff rentially Expressed Genes	in Figure 12 -	<b>Hypertension</b>	
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
10666	0.012262	EST384170 MAGE resequences, MAGL	AW971961	Hs.136340	
		cDNA, mRNA sequence /gb=AW971961			
		/gi=8161927 /ug=Hs.136340 /len=642		· .	
:	{	/gi=0101921 /dg=119.130340 /ieii=042			
10669	0.021791	EST(Hippocampus SN pool 1 cDNA clone	A1217029		
10009	0.021761	IMAGE:1948863 similar to contains L1.t2	AIZ 17030		
				1	
10075	0.000	L1 repetitive element ; )	414000474		
10675	0.036914	cDNA FLJ11309 fis, clone	AK002171	Hs.28005	
	[ .	PLACE1010076. /gb=AK002171			
		/gi=7023887 /ug=Hs.28005 /len=3232		<u> </u>	
10676	0.007578	ESTs, cDNA, 3' end	AI735488	Hs.111436	
		/clone=IMAGE:2354884 /clone_end=3'	30 .		
		/gb=AI735488 /gi=5057012			l
	1	/ug=Hs.111436 /len=514	*		
10693	0.036914	7f77g07.x1 Lupski_dorsal_root_ganglion	BG057970	Hs.405856	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
		cDNA clone IMAGE:3302989 3' similar to			}
		Q16465 HYPOTHETICAL PROTEIN;	·		
٠.	l	mRNA sequence /clone=IMAGE:3302989		1	<b>}</b>
:	Ì	/clone_end=3' /gb=BG057970		*	r-
			· ·		1
	}	/gi=12523993 /ug=Hs 405856 /len=363		1.0	
10000	0.045004	DNA 51 107070 5	11/00/1004	11. 105110	
10698	0.015924	cDNA FLJ37672 fis, clone	AK094991	Hs.125419	
, .		BRHIP2012059. /gb=AK094991		·	
		/gi=21754166 /ug=Hs.125419 /len=2342		ļ. <u>.</u>	
10705	0.0261	No significant match,			
		ORF+2(386~529),+3(3~107)	SEQ.ID.No.2	·	*
10714	0.02048	No significant match, ORF-1(226~461)	SEQ.ID.No.69		
10715	0.013991	No significant match, low complexity	SEQ.ID.No.73		
10777		EST (wm51f05.x1 NCI_CGAP_Ut2	AI871724	, ,	
		IMAGE:2439489 3')			*
10782	0.001465	EST (cDNA clone IMAGE:120476 3'	T95469		f
	}	similar to			
10787	0.001465	cDNA FLJ37147 fis. clone	AK094466	Hs.420088	
10,01	0.001400	BRACE2025316, weakly similar to tRNA-	7.11004400	113.420000	
	]		2. 4		
		splicing endonuclease subunit.	. *	•	
		/cds=(26,559) /gb=AK094466			
		/gi=21753534 /ug=Hs.420088 /len=1738		ļ	ļ
10792	0.01072	EST (hb87e12.x1 NCI_CGAP_Ut2 cDNA	AW439703		
		clone IMAGE:2890222 3' similar to			
		contains Alu repetitive element)	<u> </u>	1,00	
10798	0.021781	EST (ta16g05.x1 NCI_CGAP_Lym5	Al471814		
		IMAGE:2044280 3')			
10800	0.043576	actin related protein M1 (ARPM1), mRNA	NM 032487	Hs.135411	NP_115876
		/cds=(377,1495) /gb=NM 032487	-		
	{	/gi=19549324 /ug=Hs.135411 /len=2002	1	1	
		-g. 150 1552 1 14g 115. 1554 1 1 11511-2552			
10804	0.001737	EST (yr74c11.s1 Soares fetal liver spleen	H65780	<del> </del>	-
10004	0.001/3/		1100700		1
	1	1NFLS IMAGE:211028 3')		L · ·	I

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
	· ,		No.	No.	No.
10817	0.01072	EST(hz33h07.x1 NCI_CGAP_GC6 cDNA	BE504880		
	0	clone IMAGE:3209821 3')			
10820	0.004203	hypothetical protein MGC39497	NM_152436	Hs.406728	NP 689649
1		(MGC39497), mRNA /cds=(9,770)	_		_
	•	/gb=NM 152436 /gi=22748922			
		/ug=Hs.406728 /len=1745	1-		[ .
10821	0.008133	601584240F1 NIH_MGC_7 cDNA clone	BE798289	Hs.446578	
		IMAGE:3938912 5', mRNA sequence	•	. *	
0		/clone=IMAGE:3938912 /clone_end=5'			) <i>'</i>
		/gb=BE798289 /gi=10219487			
		/ug=Hs.446578 /len=793			
10823	0.023148	ribosomal protein L28 (RPL28), mRNA	NM 000991	Hs.356371	NP_000982
		/cds=(43,456) /gb=NM_000991			_
		/gi=13904865 /ug=Hs.356371 /len=500			7 7
10825	0.016974	ribosomal protein L13 (RPL13), transcript	NM 033251	Hs.431392	NP_150254
		variant 2, mRNA /cds=(238,873)			_
	* -	/gb=NM 033251 /gi=15431294			·
		/ug=Hs.431392 /len=1296			
10831	0.015924	EST (QV0-CT0179-240300-175-a03	AW846528	-	· · · · · · · · · · · · · · · · · · ·
•	,	Сто179)			
10840	0.001128	hypothetical protein FLJ11292	NM 018382	Hs.272246	NP_060852
		(FLJ11292), mRNA /cds=(151,615)	]	]	
		/gb=NM_018382 /gi=8922980	-		
		/ug=Hs.272246 /len=1948		1	
10843	0.004536	EST (QV0-ST0236-171299-075-c08	AW816517	-	
	·	ST0236 cDNA)		İ	
10848	0.012262	EST(yu63g11.r1 clone 238532 5')	H65434		
10857		EST (7n15h06.x1 NCI_CGAP_Brn23	BF195152		NP_005315
		DNA clone IMAGE:3564899 3')	* *		-
10861	0.048543	UI-CF-EC1-aea-g-11-0-UI.s1 ÚI-CF-EC1	BU688263	Hs.336400	
	,	cDNA clone UI-CF-EC1-aea-g-11-0-UI 3',			-
	- 4	mRNA sequence /clone=UI-CF-EC1-aea-			9=
ļ		g-11-0-UI /clone_end=3' /gb=BU688263			
-		/gi=23544886 /ug=Hs.336400 /len=528	,		
-			,		1
10862	0.021781	mitochondrion, complete genome	NC_001807		
10865		SCY1-like 1 (S. cerevisiae) (SCYL1),	NM 020680	Hs.238839	NP_065731
	,	mRNA /cds=(40,2400) /gb=NM_020680	_		<del>-</del> "
		/gi=19923565 /ug=Hs.238839 /len=2580			
10868	0.001737	EST (wa28d06.x1 NCI_CGAP_Kid11	AI916588		
9		clone IMAGE:2299403 3')	1		ł
10869	0.0261	EST DKFZp434D1916_r1 434	AL041117		
		(synonym:htes3) cDNA clone		Ì	1
		DKFZp434D1916 5'	*		
10873	2.01E-04	601156470F1 NIH_MGC_21 cDNA clone	BE279006	Hs.444551	
- 15 t, <del>5</del>		IMAGE:3140104 5', mRNA sequence			1.
		/clone=IMAGE:3140104 /clone_end=5'		[	-
			1	I	1
b		/gb=BE279006 /gi=9153993	9	]	J

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
		•	Accession	Accession	Accession
-1-			N	No.	No.
10876	0.001737	EST(HSC11G121 normalized infant brain	Z43048		
		cDNA H.sapiens cDNA clone c-11g12)			٠.
10888	0.006106	UI-H-DH0-aul-j-10-0-UI.s1	BM994461	Hs.434057	
		NCI CGAP DH0 cDNA clone		٠.	<b>3</b> 20
		IMAGE:5871081 3', mRNA sequence		1	
		/clone=IMAGE:5871081 /clone_end=3'			9
		/gb=BM994461 /gi=19719362	*		
		/ug=Hs.434057 /len=2059	<i>.</i>	• • • • • • • • • • • • • • • • • • • •	
10891	0.007578	EST(yh69b07.r1 Soares placenta Nb2HP	R31623		
10001	0.007.070	cDNA clone IMAGE:134965 5' similar to	1101020	*	-
	l ,	contains Alu repetitive element)			
	ļ. ' ·	Contains Aid repetitive element)		<u> </u>	
10899	0.003603	ad44d12.x5 Stratagene lung carcinoma	AI732123	Hs.446065	
10099	0.003003	937218 cDNA clone IMAGE:884567 3'	MI/32123	115.440003	
			•		g
	A 1 4	similar to contains Alu repetitive			
		element; contains L1.t1 L1 repetitive			
		element;, mRNA sequence			
	5.	/clone=IMAGE:884567 /clone_end=3'	*		. ,
	74. · · ·	/gb=AI732123 /gi=5053258		1	
		/ug=Hs.446065 /len=484	11101000		
10910	0.006566	EST (tg92b06.x1 NCI_CGAP_CLL1	Al401289	0 .	
	-	cDNA clone IMAGE:2116211 3' similar to			-
		contains Alu repetitive element;)			<u> </u>
10931	0.001737	MR2-CI0186-291100-010-a06 CI0186	BF814502	Hs.446594	
		cDNA, mRNA sequence /gb=BF814502			
·		/gi=12147047 /ug=Hs.446594 /len=530			
10935	0.029363	ribosomal protein S20 (RPS20), mRNA	NM_001023	Hs.8102	NP_00101
		/cds=(128,487) /gb=NM_001023	•*		
		/gi=14591915 /ug=Hs.8102 /len=539			
10937	0.015924	hypothetical protein MGC16384	NM_053048	Hs.274268	NP_44427
		(MGC16384), mRNA /cds=(450,602)			i .
		/gb=NM_053048 /gi=16596689	<b>.</b> .		
		/ug=Hs.274268 /len=1599			
10950	0.043576	cDNA FLJ38913 fis, clone	AK096232	Hs.50094	NP_83522
		NT2NE2008017. /gb=AK096232			. –
		/gi=21755673 /ug=Hs.50094 /len=2555	,		•
10966	0.013991	mRNA; cDNA DKFZp586C1723 (from	AL050192	Hs.80285	
		clone DKFZp586C1723) /gb=AL050192			
-		/gi=4884408 /ug=Hs.80285 /len=1797			
10967	0.003603	cDNA /clone=cD622 /gb=AF107454	AF107454	Hs.107537	NP 07190
		/gi=5052209 /ug=Hs.107537 /len=4850			
10970	0.018081	BX098252 Soares fetal liver spleen	BX098252	Hs.32171	-
.5510	3.5 10001	1NFLS cDNA clone IMAGp998P03536,		1. 10.02 1.7	
		mRNA sequence			
		/clone=IMAGp998P03536_;_IMAGE:2483			
		06 /gb=BX098252 /gi=27829319			
			. "	1	
	<u> </u>	/ug=Hs.32171 /len=626	100		<u> </u>

		nding To Differentially Expressed Genes D scription	Gene	Unigene	Protein
Spot	p-value	Discription	-2	7	
		"	Accession	Accession	Accession
10973	0.020262	IL3-HT0619-280600-191-F06 HT0619	<b>No.</b> BQ357271	No. Hs.232093	No.
10973	0.029303	· · · · · · · · · · · · · · · · · · ·	DQ33121	HS.232093	*
N.	*	cDNA, mRNA sequence /gb=BQ357271	*	,	
10070		/gi=21022994 /ug=Hs.232093 /len=580	DU 170400E	Hs.442971	
10976	0.008133	in56e04.x1 HR85 islet cDNA clone	BU784825	HS.442971	
3	. `	IMAGE:6126055 3', mRNA sequence	*		
		/clone=IMAGE:6126055 /clone_end=3'		·	V.
		/gb=BU784825 /gi=23830229		*	<i>,</i> "
10077		/ug=Hs.442971 /len=548	DC004000	11- 252200	
10977	3.34E-04	· · · · · · · · · · · · · · · · · · ·	BG261238	Hs.352289	
	1	IMAGE:4484347 5', mRNA sequence			*
		/clone=IMAGE:4484347 /clone_end=5'			\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
		/gb=BG261238 /gi=12771054	,		
,	10.000400	/ug=Hs.352289 /len=1003	NINA 007040	11- 455040	ND CESSO
10985	0.006106	E1B-55kDa-associated protein 5 (E1B-	NM_007040	Hs.155218	NP_65333
•	8	AP5), transcript variant 1, mRNA			1.
		/cds=(174,2744) /gb=NM_007040			
	12.00.00	/gi=21536325 /ug=Hs.155218 /len=3872	D 00 1000 1		30 2 1 1
10999	0.001465	ax37a08.x1 Proliferating Erythroid Cells	BG943384	Hs.339555	, · · · ·
,		(LCB:ax library) cDNA clone ax37a08		-0-	
		random, mRNA sequence			
		/clone=ax37a08 /gb=BG943384			
		/gi=14342756 /ug=Hs.339555 /len=555		<u> </u>	
11000	0.001033	EST(cDNA clone IMAGE:796136 5'	AA461279	100	
	,	similar to contains L1.t1 L1 repetitive		1	
		element;)	1	11 100500	
11010	0.041254	ESTs, cDNA, 3' end	AI123563	Hs.166593	NP_06003
		/clone=IMAGE:1690154 /clone_end=3'			
	,	/gb=Al123563 /gi=3539329			
		/ug=Hs.166593 /len=530		100001	
11012	0.039034	cDNA FLJ12135 fis, clone	AK022197	Hs.130581	
••	1 1	MAMMA1000307. /gb=AK022197	:		-
		/gi=10433541 /ug=Hs.130581 /len=2356			.,
11013	0.009349	UI-H-FH0-bcl-g-09-0-UI.s1	CA419491	Hs.293327	
i		NCI_CGAP_FH0 cDNA clone UI-H-FH0-			
	100	bcl-g-09-0-UI 3', mRNA sequence		.,	ļ
		/clone=UI-H-FH0-bcl-g-09-0-UI			
		/clone_end=3' /gb=CA419491			
		/gi=24782146 /ug=Hs:293327 /len=693			
11014	2.05E-05	cDNA FLJ14135 fis, clone	AK024197	Hs:289037	
	,	MAMMA1002728. /gb=AK024197			. 3
		/gi=10436518 /ug=Hs.289037 /len=1784			
11015	0.00489	unidentified mRNA, partial sequence.	U43604	Hs.159901	
		/gb=U43604 /gi=1171236 /ug=Hs.159901			
		/len=1677		- 2	0.75
11019	0.009349	clone 23758 mRNA sequence	AF052140	Hs.141055	
		/gb=AF052140 /gi=3360449			^ '
	0.0	/ug=Hs.141055 /len=1498	*		1

Spot	p-value	nding To Differentially Expressed Genes Description	Gene Accession	Unigene Accession	Protein Accession
			No.	No.	No.
11021	6 55F-04	FLJ23302 fis, clone HEP11143	AK026955	Hs.367841	NP_115652
11021	U.UUL-04	/cds=UNKNOWN /gb=AK026955	741020300	113.007041	111 -110002
	. *	/gi=10439937 /ug=Hs.287737 /len=2509	Y		
11027	0.00189	cDNA FLJ12885 fis, clone	AK022947	Hs.36093	
11021	0.00103	NT2RP2003988. /gb=AK022947	71/02/2541	113.50055	
	i	/gi=10434630 /ug=Hs.36093 /len=2000	·		
11031	1.63F-04	cDNA: FLJ21228 fis, clone COL00739.	AK024881	Hs.306716	
11001	1.002 04	/gb=AK024881 /gi=10437293	, u(02-100 i	113.000710	
		/ug=Hs.306716 /len=1869			
11033	0.046005	FLJ30661 fis, clone DFNES2000526	AK055223	Hs.265540	NP 057178
11000	0.040003	/cds=UNKNOWN /gb=AK055223	٦١١٥٥٥٥٢٢٥	113.200040	
		/gi=16549904 /ug=Hs.265540 /len=2514	•.		
11034	0.003803	mRNA; cDNA DKFZp667P1423 (from	AL832809	Hs.288997	<del> </del>
11054	0.003033	clone DKFZp667P1423) /gb=AL832809	AE032009	113.200997	
	·	/gi=21733392 /ug=Hs.288997 /len=3567			
11048	0.005674	EST(placenta Nb2HP Homo sapiens	R68614	1.	
11040	0.003074	cDNA clone IMAGE:138431 5' similar to	100014		
		contains Alu repetitive element; )		8.5	
11049	0.006566	cs69c03.y2 Retinal pigment	CA395789	Hs.446106	
11049	0.000500	epithelium/choroid cDNA (Un-normalized,	CM393769	IUS:440100	
•		unamplified): cs cDNA clone cs69c03 5',		1	
			× .		
		mRNA sequence /clone=cs69c03	*	. *	100
•		/clone_end=5' /gb=CA395789			*
		/gi=24731580 /ug=Hs.446106 /len=585			
11052	0.002625	cDNA FLJ40815 fis, clone	AK098134	Hs.432620	
		TRACH2010600. /gb=AK098134			
		/gi=21758081 /ug=Hs.432620 /len=2814	-0-		
11058	0.027691	collagen, type XII, alpha 1 (COL12A1),	NM_004370	Hs.101302	NP_54237
	,	transcript variant long, mRNA	, =	*	
		/cds=(114,9305) /gb=NM_004370	. :		[ .
		/gi=18201922 /ug=Hs.101302 /len=11554			ĺ
				1	
11059	4.93E-04	UI-E-CQ1-aew-e-07-0-UI.s1 UI-E-CQ1	BU728934	Hs.436272	• • •
		cDNA clone UI-E-CQ1-aew-e-07-0-UI 3',			
		mRNA sequence /clone=UI-E-CQ1-aew-e-			2
	3.	07-0-UI /clone end=3' /gb=BU728934	. "		
	0.	/gi=23651308 /ug=Hs.436272 /len=1132		- 0	
11063	0.024587	clone alpha_est218/52C1 mRNA	AF001542	Hs.356442	<u> </u>
	1	sequence /gb=AF001542 /gi=2529714			
	*	/ug=Hs.356442 /len=2992			
11069	0.043576	ESTs, Stratagene ovarian cancer	AI732587	<u> </u>	
. 1000	0.070070	(#937219 cDNA clone IMAGE:595374 3'	02007	1.	
		similar to TR:Q13129 Q13129 ZN-15			
		RELATED ZINC FINGER PROTEIN;			
	1		E .	•	
11070	0.00222		AK001004	He 10/627	
11070	0.00223	cDNA FLJ34585 fis, clone KIDNE2008758. /gb=AK091904	AK091904	Hs.104627	

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
11071	0.041254	cDNA FLJ31335 fis, clone	AK055897	Hs.406914	
		MAMGL1000151. /gb=AK055897			
. 🐣		/gi=16550738 /ug=Hs.406914 /len=2180			
11091	0.015924	BX091936 Soares placenta Nb2HP cDNA	BX091936	Hs.24598	
		clone IMAGp998N02193;			
		IMAGE:135745, mRNA sequence			
	3	/clone=IMAGp998N02193_;_IMAGE:1357		٠.	
-	, ,	45 /gb=BX091936 /gi=27822661			ĺ
		/ug=Hs.24598 /len=688		* 4	
11092	0.003079	ESTs, cDNA, 5' end	BG741948	Hs.355530	NP_068747
		/clone=IMAGE:4779957 /clone end=5'		,	
		/gb=BG741948 /gi=14052601		0)(0	
		/ug=Hs.355530 /len=948		-	
11093	0.039034		BM929582	Hs.159153	***
	,.,	clone UI-E-EJ1-aje-j-02-0-UI 5', mRNA	* *		
	101	sequence /clone=UI-E-EJ1-aje-j-02-0-UI		, \	
		/clone end=5' /gb=BM929582	*		
0.0		/gi=19388755 /ug=Hs.159153 /len=1002		A.	
11097	0.008473	ESTs, cDNA, 3' end /clone=UI-E-EJ0-ahj-	BM674241	Hs.354662	
	1.000	f-02-0-UI /clone_end=3' /gb=BM674241	DIVIO1 12 1 1	110.00 1002	1 .
:_	-	/gi=18984139 /ug=Hs.354662 /len=684		. 16.	* 4. *
		1000 1100 74g 110.00 1002 710.11 00.1			
11104	0.006106	clone IMAGE:5268031, mRNA	BC040578	Hs.287864	7
		/gb=BC040578 /gi=26251832			
-8-	<i>*</i> *	/ug=Hs.287864 /len=3284			
11106	0.029363	BX096783 Soares testis_NHT cDNA	BX096783	Hs.98322	
	4.92000	clone IMAGp998I171794, mRNA	,	110.00022	
•		sequence	٠.		
	*	/clone=IMAGp998I171794_;_IMAGE:731			
		224 /gb=BX096783 /gi=27842978			
		/ug=Hs.98322 /len=730			
11116	0.008722	cDNA FLJ33668 fis, clone	AK090987	Hs.346796	
, , , , , ,	0.000122	BRAMY2028565. /gb=AK090987	/ 11 (000007	113,040700	
		/gi=21749256 /ug=Hs.346796 /len=2294			0.
11126	0.00223	full length insert cDNA clone ZD64C04	AF088052	Hs.384557	-
, , , , ,	0.00220	/gb=AF088052 /gi=3523258	711 000002	113.554557	
	. ,	/ug=Hs.384557 /len=831	•	,	
11142	9 44F-04	cDNA: FLJ22447 fis, clone HRC09479.	AK026100	Hs.344000	<del> </del>
11112	0.112 04	/gb=AK026100 /gi=10438841	741020100	113.514000	
		/ug=Hs.344000 /len=1659	· At		
11163	0.041254	UI-H-DP0-avb-p-04-0-UI.s1	BQ020727	Hs.446656	Talana
	0.0-1204	NCI CGAP Fs1 cDNA clone	DGOZOFZI	113.440000	
	1.	IMAGE:5877363 3', mRNA sequence			
	*	/clone=IMAGE:5877363 /clone_end=3'		_	\$
	8	/gb=BQ020727 /gi=19756005	:		
		/ug=Hs.446656 /len=1208			
11170	0.027604	No significant match (ORF:none)	SEQ.ID.No.23		-
11110	0.02/091	pro significant materi (OKF.none)	0EW.ID.INU.23		<u> </u>

		nding To Differentially Expressed G nes		i iypertension	
Spot	p-value	Description	Gene	Unigene	Protein
		, · · · · · · · · · · · · · · · · · · ·	Accession	Accession	Accession
44400	0.040400	DO4 UT0077 400000 040 407 UT0077	No.	No.	No.
11192	0.013102	RC4-HT0277-160200-013-d07 HT0277	BE151126	Hs.158600	
		cDNA, mRNA sequence /gb=BE151126			
44007	0.000000	/gi=8613847 /ug=Hs.158600 /len=571	14055045		
11207	0.007578	cDNA FLJ31353 fis, clone	AK055915	Hs.352554	
		MESAN2000264. /gb=AK055915			
11011		/gi=16550762 /ug=Hs.352554 /len=2192	* * * * * * * * * * * * * * * * * * *		
11214	7.88E-04	No significant match			
		(ORF:+1:1~147[147], +2:68~193[126])	SEQ.ID.No.25	<u> </u>	
		No significant match, ORF-1(3~442)	SEQ.ID.No.80		
11237	0.014931	vesicle-associated membrane protein 2	NM_014232	Hs.25348	NP_05504
		(synaptobrevin 2) (VAMP2), mRNA	,	0	- 0
÷	•	/cds=(95,445) /gb=NM_014232		-	
		/gi=7657674 /ug=Hs.25348 /len=2159	*	*	/ " =
11241	0.001232	FLJ32072 fis, clone OCBBF1000130	AK056634	Hs.350761	*
	4.	/cds=UNKNOWN /gb=AK056634			*
		/gi=16552092 /ug=Hs.350761 /len=2818		*1	5
11243	0.041254	apoA polymorphism Kringle IV gene,	L14005		* .
		exons 1 and 2			* -
11253	0.013991	hypothetical protein similar to beta-	NM_018096	Hs.85570	NP_06056
		transducin family (FLJ10458), mRNA			
		/cds=(14,1471) /gb=NM_018096			
		/gi=20070287 /ug=Hs.85570 /len=2593			
11258	0.014931	ADP-ribosylation factor GTPase	NM_018209	Hs.25584	NP_78320
		activating protein 1 (ARFGAP1), mRNA		·	
		/cds=(113,1333) /gb=NM_018209		8.	
•		/gi=8922651 /ug=Hs.25584 /len=3248	•	-	
11266	0.015924	B-cell translocation gene 1, anti-	NM 001731	Hs.77054	NP 00172
	·	proliferative (BTG1), mRNA	- <del>-</del>		
		/cds=(309,824) /gb=NM_001731	8.0		
		/gi=4502472 /ug=Hs.77054 /len=1783			
11277	0.016974	ligase I, DNA, ATP-dependent (LIG1),	NM_000234	Hs.1770	NP_00022
		mRNA /cds=(121,2880) /gb=NM_000234	<del>-</del>	. *	_
		/gi=4557718 /ug=Hs.1770 /len=3083			
			•,		_
11278	0.008722	H2A histone family, member X (H2AFX),	NM 002105	Hs.147097	NP_00209
		mRNA /cds=(74,505) /gb=NM 002105			
		/gi=4504252 /ug=Hs.147097 /len=1585			
11279	0.036914	cDNA FLJ11660 fis, clone	AK021722	Hs.281895	
		HEMBA1004610. /gb=AK021722			
		/gi=10432962 /ug=Hs.281895 /len=1769	Ĭ .		
11292	0.012262	DNA sequence from clone RP11-151F5	AL158823	7	
	3.0,2202	on chromosome 9 Contains 2 isoforms	1, 100020	- 54	,
	0.	for part of the AKAP2 gene for A kinase			
		(PRKA) anchor protein 2, a ribosomal			
		protein L21 pseudogene and a CpG			
	I				I . `
		island, complete sequence [Homo			

11293 11308		Description	Gene Accession	Unigene	Protein
	0.049542		LAAAAAAIAM		I A .
	0.049542	·		Accession	Accession
		hypothetical protein (FLJ20485), mRNA	No. NM 019042	No.	No.
11308		• • • • • • • • • • • • • • • • • • • •	NW_019042	Hs.98806	NP_061915
11308		/cds=(112,729) /gb=NM_019042			
11308		/gi=9506680 /ug=Hs.98806 /len=2021	N	11. 470500	140050
	0.018081	hypothetical protein MGC10702	NM_032663	Hs.179520	NP_116052
		(MGC10702), mRNA /cds=(136,1662)			
		/gb=NM_032663 /gi=14249221		/ · *	
11000		/ug=Hs.179520 /len=2126			
11309		mRNA; cDNA DKFZp566C114 (from	AL137442	Hs.286184	
.	•	clone DKFZp566C114), partial cds	÷-		
	•	/cds=(1,951) /gb=AL137442 /gi=6808012		l.	•
		/ug=Hs.286184 /len=3913			<u></u>
11313	0.020482	NADH dehydrogenase (ubiquinone) 1	NM_004541	Hs.74823	NP_004532
		alpha subcomplex, 1, 7.5kDa (NDUFA1),			
	٠	nuclear gene encoding mitochondrial	. *		*
	ı	protein, mRNA /cds=(143,355)			<b>-</b>
		/gb=NM_004541 /gi=13699820			
		/ug=Hs.74823 /len=479			
11316	0.002268	KIAA1721 protein, partial cds	AB051508	Hs.117102	NP_071904
20		/cds=UNKNOWN /gb=AB051508	•.		
		/gi=12697986 /ug=Hs.117102 /len=8047	*		<u> </u>
11319	0.015924	hypothetical protein MGC4276 similar to	NM_030940	Hs.177776	NP_112202
-		CG8198 (MGC4276), mRNA			
		/cds=(70,462) /gb=NM_030940			
	· ,	/gi=24475709 /ug=Hs.177776 /len=1978	.447	1 0	1
11324	0.031117	endoplasmic reticulum stress-inducible,	NM_014685	Hs.146393	NP_055500
		ubiquitin-like domain member 1		4	
		(HERPUD1), mRNA /cds=(96,1271)			-1
·		/gb=NM_014685 /gi=7661869			4
		/ug=Hs.146393 /len=1884			
11343	0.003332	chromosome 1 open reading frame 33	NM_016183	Hs.274201	NP_057267
		(C1orf33), mRNA /cds=(32,751)			
		/gb=NM_016183 /gi=18490986		1	
		/ug=Hs.274201 /len=1185			
11344		secretory carrier membrane protein 4	NM_079834	Hs.306019	NP 524558
	·	(SCAMP-4), mRNA /cds=(82,771)	- ·	X	
	•	/gb=NM_079834 /gi=17738286	,		
		/ug=Hs.306019 /len=2514	٠.		
11348	0.007578	AP1 gamma subunit binding protein 1	NM_007247	Hs.15384	NP_542118
·		(AP1GBP1), transcript variant 1, mRNA	<u> </u>		
		/cds=(44,2113) /gb=NM_007247			
		/gi=18105003 /ug=Hs.15384 /len=5115			,
11349	0.024587	hypothetical nuclear factor SBBI22	NM_020395	Hs.432952	NP_065128
5 , 15	3.52 1007	(LOC57117), mRNA /cds=(207,1595)		1	
		/gb=NM_020395 /gi=21361850		:	
•		/ug=Hs.432952 /len=1716	- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	1	

Cnat	p-value	Description	Gene	Hypertension	Protein
Spot	p-value	Description		Unigen	
			Accession	Accession	Accession
14054	0.000400		No.	No.	No.
11351	0.020482	type V preprocollagen alpha 2 chain	AY016295		
		(COL5A2) gene, exons 34 through 52 and	:		•
		partial cds; and type III preprocollagen	/	*	
		alpha 1 chain (COL3A1) gene, exons 2	-		
		through 52			
11365	0.002084	Rho-specific guanine-nucleotide	NM_014786	Hs.45180	NP_05560
		exchange factor 164 kDa			-
		(P164RHOGEF), mRNA /cds=(16,6207)		`	
	Ì	/gb=NM_014786 /gi=21361457			ľ
		/ug=Hs.45180 /len=7540			
11376	0.041254	a disintegrin-like and metalloprotease	NM_014243	Hs.27916	NP_05505
		(reprolysin type) with thrombospondin			_
		type 1 motif, 3 (ADAMTS3), mRNA			
	·	/cds=(38,3655) /gb=NM_014243	-		
	0-	/gi=21265036 /ug=Hs.27916 /len=5821			
11383	0.006106	DKFZP586G011 protein (LAP1B), mRNA	NM_015602	Hs.234265	NP_05641
	0.000	/cds=(56,1444) /gb=NM_015602	0.0002	110.20 1200	
		/gi=24308098 /ug=Hs.234265 /len=3275		***	. ×
11395	0.048543	LAG1 longevity assurance 2 (S.	NM 013384	Hs.285976	NP 07135
11000	0.040545	cerevisiae) (LASS2), mRNA	14141_0 10004	113.203970	_0, 123
	0		:		
	. *	/cds=(50,742) /gb=NM_013384			·
14440	0.045004	/gi=9937997 /ug=Hs.285976 /len=1646	NINA 000704	11- 77002	ND 07204
11410	0.015924	ring finger protein 38 (RNF38), mRNA	NM_022781	Hs.77823	NP_07361
		/cds=(563,1861) /gb=NM_022781		•	
44404	0.00004	/gi=21918874 /ug=Hs.77823 /len=4694	1111 01015	11 100050	110 0000
11421	0.039034	DKFZp564J157 protein	NM_018457	Hs.426359	NP_06092
		(DKFZP564J157), mRNA /cds=(78,524)	· · · · · · · · · · · · · · · · · · ·		
		/gb=NM_018457 /gi=8922156			
	·	/ug=Hs.426359 /len=1132		-2	
11442	0.006566	cDNA FLJ23640 fis, clone COL00187.	AK074220	Hs.241869	2
		/gb=AK074220 /gi=18676763	6		-
	•	/ug=Hs.241869 /len=2875	4		,
11464	0.01072	hypothetical protein MGC17922	NM_153207	Hs.285833	NP_69493
		(MGC17922), mRNA /cds=(147,1034)	.*		
		/gb=NM_153207 /gi=23397453	4		
	· ·	/ug=Hs.285833 /len=3595		•	
11469	0.046005	hypothetical protein FLJ13920	NM 024558	Hs.13056	NP 07883
		(FLJ13920), mRNA /cds=(28,462)			
		/gb=NM_024558 /gi=13375724	·		
		/ug=Hs.13056 /len=1767			
11471	0.0261	prostaglandin E receptor 2 (subtype EP2),	NM 000956	Hs.2090	NP_00094
, .	0.0201	53kDa (PTGER2), mRNA	11111_000000	113.2000	141 _00004
0.0		/cds=(157,1233) /gb=NM_000956			
		/gi=4506254 /ug=Hs.2090 /len=2372	•.		-2
11170	0.02400		A A L 26700		
11479	0.03489	B lymphocyte activation-related protein	AAL26788		
44405	0.040465	BC-2048	NIA 300444	11. 400 =	ND 11015
11485	0.013102	MADP-1 protein (MADP-1), mRNA	NM_033114	Hs.43847	NP_14910
		/cds=(185,838) /gb=NM_033114	3		
	1	/gi=21314766 /ug=Hs.43847 /len=1834	'	i "	

		nding To Differentially Expressed Genes			
,Spot	p-value	Description	G ne	Unigen	Protein
	•	• 1	Accession	Accession	Accession
			No.	No.	No.
11487	0.01925	hypothetical gene supported by U08191;	XM_050718		
	-	X80878; AL512730; NM_006165	! -		
		(LOC94689), mRNA			. `
11495	0.020482	leukocyte membrane antigen, clone	BC032352	Hs.9688	-100
		MGC:40393 IMAGE:5218501, mRNA,	:	1	
	-	complete cds /cds=(287,1186)	/		
		/gb=BC032352 /gi=21595376	9		
•		/ug=Hs.9688 /len=1876			
11496	0.001232	leucyl-tRNA synthetase (LARS), mRNA	NM_020117	Hs.6762	NP_064502
00	0.00,1202	/cds=(73,3603) /gb=NM_020117		110.0102	
	•	/gi=24496788 /ug=Hs.6762 /len=4248		1	
11498	0.00340	clone MGC:16614 IMAGE:4111344,	BC009313	Hs.193700	
11490	0.009549	mRNA, complete cds /cds=(258,998)	D0003313	113.133700	
	,	/gb=BC009313 /gi=14424569	,		,
	*	/ug=Hs.373515 /len=2052	-		
11522	0.000054		NM 024755	Hs.331328	NP_079031
11533	0.002054	hypothetical protein FLJ13213	NIVI_024755	FIS.331320	NP_0/9031
•		(FLJ13213), mRNA /cds=(234,1670)			* •
	-	/gb=NM_024755 /gi=13376087	•	1	
44500	Ö 004447	/ug=Hs.331328 /len=2617	D00404	2	NID 004000
11536	0.031117	EST(yh89e10.r1 cDNA clone 136938 5')	R38461	* .	NP_001002
<u> </u>		8e-06 match			<u></u>
11551	0.013102	EST(EST64315 Jurkat T-cells VI 5'	AA355853		NP_114107
		ribosomal protein S21)		4	
11552	0.018081	EST(zr43e07.r1 Soares NhHMPu S1	AA233635		
	ľ	clone 666180 5' contains Alu and OFR		•	
		repeat)			
11556	0.001232	hypothetical protein FLJ36812	NM_153260	Hs.194071	NP_694992
	• 50	(FLJ36812), mRNA /cds=(369,1088)		'	2 ×
		/gb=NM_153260 /gi=23397553	• • •		
•		/ug=Hs.194071 /len=2647			
11569	0.006566	hypothetical protein DKFZp434K1421	NM_032141	Hs.374609	NP_115517
		(DKFZP434K1421), mRNA			
		/cds=(29,1705) /gb=NM_032141			
		/gi=14149806 /ug=Hs.374609 /len=2547	0.0		
11585	0.021781	EST (yd08e03.r1 clone 24895 5')	T80443		
11594		unnamed protein product (=IDH gamma	BAA91131		
		gene and TRAP delta gene)			
11600	0.013991	similar to spermatid WD-repeat protein	NM_145241	Hs.133331	NP_660284
,		(LOC114987), mRNA /cds=(238,1338)			
-	64,	/gb=NM 145241 /gi=21687047			,
		/ug=Hs.133331 /len=3121		ļ .	
11604	0.00180	EST(ae50c06.s1 Stratagene lung	AA600135		
	0.00,00	carcinoma 937218 clone IMAGE:950314	1.0.000.00		
		3' contains Alu repeat)	1		
11605	6 02 5 05	hypothetical protein PRO1051	NM 018572	Hs.326548	NP 061042
11000	0.03E-03	1 * '	14141_010372	115.020040	1145_00 1042
		(PRO1051), mRNA /cds=(756,1004)			
		/gb=NM_018572 /gi=8924004		· .	×
		/ug=Hs.326548 /len=1393		1	

		nding To Differ ntially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
	• .	•	Accession	Accession	Accession
11000	0.040.1		No.	No.	No.
11606	0.01047	UI-H-DT1-avz-k-14-0-UI.s1	BQ015886	Hs.22607	
*		NCI_CGAP_DT1 cDNA clone	4	1	
, .		IMAGE:5886469 3', mRNA sequence	40		
*	9	/clone=IMAGE:5886469 /clone_end=3'			1 20 1
,	,	/gb=BQ015886 /gi=19751163			
		/ug=Hs.22607 /len=1207			16.
11608	0.01072	EST(MR0-HT0407-140300-013-h01	BE159552		NP_003751
		HT0407)	·		
11618	0.020482	EST ox12c12.x1	AI034084		
		Soares_fetal_liver_spleen_1NFLS_S1			
	• • • •	IMAGE:1656118 3'	- `		*
11638	0.009349	cDNA FLJ30301 fis, clone	AK054863	Hs.285728	The Property of
		BRACE2003217. /gb=AK054863			
		/gi=16549482 /ug=Hs.285728 /len=2186		* *	
11652	0.009349	EST(nf43h10.s1 NCI_CGAP_Pr2 cDNA	AA573636		
	9.555	clone IMAGE:916579 similar to contains		. 6	
		element MER22 repetitive element)			
	· • •	cignetic individual repetitive elementy.	•	,	
11674	0.010015	EST (qa48c04.x1 Soares_NhHMPu_S1	AI123338		<u>.</u>
11014	0.010013	IMAGE:1689990 3')	A1129330		
11685	0.007056	EST (QV4-NN0039-040500-196-e07	AW895898		
11005	0.007036	NN0039	Avvoapoao	٠.	
14607	0.005674		DE006727		NID 074700
11687	0.005674	EST (601507995F1 NIH_MGC_71 cDNA	BE886737		NP_071769
44000	0.555.04	clone IMAGE:3909695 5')	DAD44570		<u> </u>
		unnamed protein product	BAB14576		
11693	0.003603	cell adhesion molecule-related/down-	NM_016952	Hs.159565	NP_058648
		regulated by oncogenes (CDON), mRNA		•	
		/cds=(1,3723) /gb=NM_016952			* * * * * *
		/gi=8393083 /ug=Hs.159565 /len=3986			
11702	0.01072	eukaryotic translation elongation factor 1	NM_001402	Hs.422118	NP_001393
	] '	alpha 1 (EEF1A1), mRNA /cds=(63,1451)			
		/gb=NM_001402 /gi=25453469			
• 6		/ug=Hs.422118 /len=1837		* •	
11726	0.032959	survival of motor neuron 2, centromeric	NM_017411	Hs.367729	NP 075015
		(SMN2), transcript variant d, mRNA	_	·	
	·	/cds=(164,1048) /gb=NM_017411	· ·		
		/gi=13259525 /ug=Hs.367729 /len=1623		,	
11732	0.015924	hypothetical protein FLJ20699	NM 017931	Hs.15125	NP_060401
	, ,	(FLJ20699), mRNA /cds=(33,1043)	0		
		/gb=NM_017931 /gi=8923627		,	
	}	/ug=Hs.15125 /len=2594		ł	1
11745	4 78E 05	FLJ23172 fis, clone LNG10005	AK026825	Hs.306885	
11/43	7.701-03	/cds=UNKNOWN /gb=AK026825	711020023	113.300003	
14700	0.000500	/gi=10439771 /ug=Hs.306885 /len=1882	A) (704000	115 440444	<del> </del>
11766	0.000000	AV701088 ADA cDNA clone ADAAGB09	AV701088	Hs.419141	
	1	5', mRNA sequence /clone=ADAAGB09		* *	
		/clone_end=5' /gb=AV701088			
		/gi=10717418 /ug=Hs.419141 /len=652			1
-	1			1	

_		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
		00 a	Accession	Accession	Accession
			No.	No.	No.
11769	0.041254	golgi autoantigen, golgin subfamily a, 5	NM_005113	Hs.241572	NP_005104
	·	(GOLGA5), mRNA /cds=(132,2327)	0.00		
••*		/gb=NM_005113 /gi=4826747		*	
		/ug=Hs.241572 /len=2838			
11770	0.013102	FLJ33160 fis, clone UTERU2000485	AK057722	Hs.124733	
		/cds=UNKNOWN /gb=AK057722	•		
		/gi=16553641 /ug=Hs.124733 /len=2328			
11772	0.039034	legumain (LGMN), mRNA	NM_005606	Hs.18069	NP_005597
	· ·	/cds=(142,1443) /gb=NM_005606	•		
		/gi=21914880 /ug=Hs.18069 /len=1981	1.8		· .
11789	0.024587	high mobility group nucleosomal binding	NM_006353	Hs.236774	NP_006344
		domain 4 (HMGN4), mRNA			
		/cds=(239,511) /gb=NM_006353			
	·	/gi=23238232 /ug=Hs.236774 /len=1980		- C - C - C - C - C - C - C - C - C - C	*
11800	0.010015	RAN binding protein 2-like 1	NM_005054	Hs.179825	NP_115636
		(RANBP2L1), transcript variant 1, mRNA			-
		/cds=(78,5375) /gb=NM_005054	*		,
	-	/gi=19718754 /ug=Hs.179825 /len=7164		*	
11807	0.016974	peptidylprolyl isomerase (cyclophilin)-like	NM_016059	Hs.27693	NP_05714
•		1 (PPIL1), mRNA /cds=(222,722)		*	· -
	0.0	/gb=NM_016059 /gi=22035675	•		2
		/ug=Hs.27693 /len=1723			
11808	4.78E-05	Myeloid/lymphoid or mixed-lineage	AW582014	Hs.169986	
		leukemia (trithorax homolog, Drosophila);			
		translocated to, 4, cDNA /gb=AW582014	-		
		/gi=7257063 /ug=Hs 169986 /len=705	. *		
		, g, , , , _ , , , , , , , , , , , ,		*	
11816	0.048543	likely ortholog of rat V-1 protein (V-1),	NM 145808	Hs.21321	NP_66580
		mRNA /cds=(229,585) /gb=NM 145808			
	*	/gi=21956644 /ug=Hs.21321 /len=3770			
11823	0.024587	mRNA for KIAA1614 protein, partial cds.	AB046834	Hs.287381	
11020	0.02.1001	/cds=(1,3628) /gb=AB046834	1,50,000	110.201001	
	;	/gi=10047302 /ug=Hs.287381 /len=4143		•	
11850	0.0261	TGFB inducible early growth response	NM_005655	Hs.82173	NP 005646
11000	0.0201	(TIEG), mRNA /cds=(124,1566)	11111_000000	113.0217.0	
		/gb=NM_005655 /gi=5032176			*
		/ug=Hs.82173 /len=2899	* * * *	- 6	2
11869	0.043576	cDNA FLJ30649 fis, clone	AK055211	Hs.167700	<u> </u>
11009	0.043370	CTONG2006562. /gb=AK055211	ANOUSETT	113. (07700	
		/gi=16549888 /ug=Hs.167700 /len=3061	- ,	÷	
11872	0.03480	FUS interacting protein (serine-arginine	NIM OOGG25		ND 47225
110/2	0.03469		NM_006625		NP_47335
	ŧ	rich) 1 (FUSIP1), transcript variant 1,			
		mRNA (=TLS-associated SR proteins			
		(TASR) gene, complete cds, alternatively			
44070	0.040005	spliced, AY048592.1)	NIA 040400	11. 4.40005	ND 65766
11879	J 0.046005	interleukin-1 receptor-associated kinase 4	NM_016123	Hs.142295	NP_057207
		(IRAK4), mRNA /cds=(50,1432)			*
		/gb=NM_016123 /gi=7705840		y*	
	1	/ug=Hs.142295 /len=2817	l		1

Genes	Correspoi	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	
Spot	p-valu	D scription	Gene	Unigene	Protein
	-		Accession	Accession	Accession
		*	No.	No.	No.
11895	0.043576	development and differentiation	NM_003887	Hs.12802	NP_003878
		enhancing factor 2 (DDEF2), mRNA			
	*	/cds=(341,3361) /gb=NM_003887			
		/gi=4502248 /ug=Hs.12802 /len=5711	*	- X-	·
11906	0.007578	clone IMAGE:5274527, mRNA	BC041375	Hs.11700	
	1,11,11	/gb=BC041375 /gi=27370608	-		
•	-	/ug=Hs.11700 /len=3905	:	*	
11912	0.018081	hypothetical protein MGC40157	NM 152350	Hs.295362	NP 689563
		(MGC40157), mRNA /cds=(106,498)			
		/gb=NM_152350 /gi=22748758			
,		/ug=Hs.295362 /len=1250			
11913	0.006566	mRNA; cDNA DKFZp434H2019 (from	AL137535	Hs.15806	
11010	0.00000	clone DKFZp434H2019) /gb=AL137535	1,15,000	113.10000	
		/gi=6808211 /ug=Hs.15806 /len=1974			
11931	0.000340	signal recognition particle 68kDa	NM_014230	Hs.273307	NP_055045
11331	0.009349	(SRP68), mRNA /cds=(36,1919)	NW_0 14230	118.273307	147_000040
	,				
	-	/gb=NM_014230 /gi=24497619	• '		
44050	0.040000	/ug=Hs.273307 /len=2515	NIM DOOGOA	115 0450	ND 000500
11952	0.012262	SWI/SNF related, matrix associated, actin	   Mini <sup>_</sup> 00390 I	Hs.9456	NP_003592
		dependent regulator of chromatin,			
( )		subfamily a, member 5 (SMARCA5),	* .		1
4	İ	mRNA /cds=(463,3621) /gb=NM_003601	100		
		/gi=21071057 /ug=Hs.9456 /len=3866			,
44050	0.004707	-DNA 51 144420 51	ALCÓDAFOA	11- 007440	4)
11956	0.0017.37	cDNA FLJ11439 fis, clone	AK021501	Hs.287416	
		HEMBA1001299. /gb=AK021501	. (		
14000	0.040000	/gi=10432697 /ug=Hs.287416 /len=1500	NIN 100 4005	11. 00.40.40	ND 004040
11962	0.012262	aquaporin 3 (AQP3), mRNA	NM_004925	Hs.234642	NP_004916
	4	/cds=(63,941) /gb=NM_004925			
		/gi=22165421 /ug=Hs 234642 /len=1835			
11972	0.021781	transmembrane protein 1 (TMEM1),	NM_003274	Hs.94479	NP_003265
		mRNA /cds=(154,3933) /gb=NM_003274	•		
		/gi=19923163 /úg=Hs.94479 /len=6661			
				17 122212	
11975	0.015924	cDNA FLJ37042 fis, clone	AK094361	Hs.432542	
*		BRACE2011947. /gb=AK094361			
<del>,</del>		/gi=21753405 /ug=Hs.432542 /len=2142			
11983	0.046879	RAS-like, estrogen-regulated, growth-	NM_032918	Hs.21594	NP_116307
		inhibitor (RERG), mRNA /cds=(291,890)	, ,		
		/gb=NM_032918 /gi=14249703			
		/ug=Hs.21594 /len=2240			ļ.
12003	0.043576	EST(zi39c11.s1 Soares fetal liver spleen	AA680133		NP_660208
	, .	1NFLS S1 cDNA clone 433172 3')			*
				,	· · ·
12019	0.017681	EST(zv83c02.s1 Soares total fetus	AA425140		
		Nb2HF8 9w clone 760226 3' contains			
		MER14.t2 MER14 repeat)			
12022	3.59E-04	kinesin family protein 3B (KIF3B)	NM 004798		NP 004789

	•	nding To Differentially Expressed Gen s			
Spot	p-value	Description	Gene	Unigene	Protein
		· . *	Accession	Accession	Accession
			No.	No.	No.
12037	0.018081	EST(EST58819 Infant brain 3' contains	AA351153		
ί.		Alu repeat)	•	(8)	
12051	6.55E-04	EST (wn37h08.x1 NCI_CGAP_Gas4	AI888883		
	,	IMAGE:2447679 3')	•	1	
12060	7.18E-04	mRNA for KIAA1387 protein, partial cds.	AB037808	Hs.301434	**
		/cds=(1,2853) /gb=AB037808			**
		/gi=7243154 /ug=Hs.301434 /len=4385			
12061	0.006566	cDNA FLJ36838 fis, clone	AK094157	Hs.407030	
-		ASTRO2011426. /gb=AK094157			
	-	/gi=21753159 /ug=Hs.407030 /len=2646			
12062	0.039034	EST(wc78g04.x1 NCI_CGAP_Pan1 clone	AI701086		
		IMAGE:2324790 3')	•		
12066	0.002844	chromosome 1 open reading frame 19	NM_052965	Hs.32058	NP 443197
	, i	(C1orf19), mRNA /cds=(51,566)	· <del></del>		_
•		/gb=NM_052965 /gi=24308389		100	
٥		/ug=Hs.32058 /len=1943			1
12068	0.008133	cDNA: FLJ22234 fis, clone HRC02022.	AK025887	Hs.56030	
		/gb=AK025887 /gi=10438540			11
		/ug=Hs.56030 /len=2056		*	
12071	0.046879	EST(zs51g05.r1 NCI_CGAP_GCB1 clone	AA287528		, , , , , , , , , , , , , , , , , , ,
		IMAGE:701048 5' contains Alu and THR			
		repeat)	,	•	
12079	0.016974	EST nj89e12.s1 NCI_CGAP_Pr11 cDNA	AA552262	30,13	:
		clone IMAGE:999694	, T		
12098	0.023148	EST(DKFZp566M0246_s1 566 (synonym:	AL038765		
		hfkd2) cDNA clone DKFZp566M0246 3')			
		, , , , , , , , , , , , , , , , , , , ,			
12106	0.027618	autophagy Apg3p/Aut1p-like (APG3),	NM_022488	Hs.26367	NP_071933
		mRNA /cds=(120,1064) /gb=NM_022488			
		/gi=19526772 /ug=Hs.26367 /len=1381			
12112	0.003332	EST(xu58f03.x1 NCI_CGAP_Ut1 clone	AW511419		NP_073572
	7	IMAGE:2805917 3' TR:O35371 O35371			
		PERIPHERIAL BENZODIAZEPINE		==	
		RECEPTOR ASSOCIATED PROTEIN)	•		
12117	0.018081	EST(tj90g04.x1	Al470101	<del> </del>	
	0.010001	Soares_NSF_F8_9W_OT_PA_P_S1	, u.j., o . o .		
		cDNA clone		'	
12140	0.001033	EST nk17g03.s1 NCI_CGAP_Co11 cDNA	AA582722		
	0.00 , 000	clone IMAGE:1013812 3'	7 0 1002722		
12141	0.019069	EST (zc24f10.s1	W43004		
7 1	3.3 , 3003	Soares_senescent_fibroblasts_NbHSF	,1000		
		IMAGE:323275 3')(contains Alu repetitive			
		element)			
12150	0.012402	hypothetical protein FLJ35382	NM 152608	Hs.99210	NP 689821
12150	0.013102	,	102008	115.882 10	1145 003051
		(FLJ35382), mRNA /cds=(165,1235)			
		/gb=NM_152608 /gi=22749244			
	1	/ug=Hs.99210 /len=1349		<u> </u>	

		nding To Differentially Expressed Genes			
Spot	p-valu		Gene	Unigene	Protein
			Accession -	Accession	Accession
:		· · · · · · · · · · · · · · · · · · ·	No.	No.	No.
12151	0.024587	topoisomerase (DNA) II binding protein	NM_007027	Hs.91417	NP_008958
		(TOPBP1), mRNA /cds=(347,4654)	4	*	
	· .	/gb=NM_007027 /gi=20143948			
		/ug=Hs.91417 /len=5261			
12161	0.005674	EST(hh76d05.y1 NCI_CGAP_GU1 cDNA	AW663260	7	
		clone IMAGE:2968713 5' similar to		,	
		contains L1.t1 L1 repetitive element;	*	. *	
12163	0.032959	mRNA; cDNA DKFZp434I2129 (from	AL832450	Hs.376999	·
		clone DKFZp434I2129) /cds=(1,655)			ė e
		/gb=AL832450 /gi=21733015		-	-
		/ug=Hs.376999 /len=2100	• • • • • • • • • • • • • • • • • • • •		
12164	0.027691	cDNA sequence FLJ22790 fis,	AK026443		NP 001675
12178		EST (of53c02.s1 NCI_CGAP_CNS1	AA836671		
	3.5.55	IMAGE:1427906)		***	
12180	0.002054	cDNA FLJ13877 fis, clone	AK023939	Hs.317080	<del></del>
12100	0.002007	THYRO1001403. /gb=AK023939	711702000	113.517000	
		/gi=10436034 /ug=Hs.317080 /len=3065	· )		
12182	0.00340	Williams-Beuren Syndrome critical region	NM 145645	Hs.406306	NP_663620
12102	0.009349	protein 20 copy B (WBSCR20B), mRNA	143043	115.400300	NF_003020
			FT :		*
		/cds=(984,1448) /gb=NM_145645	•		
		/gi=21717802 /ug=Hs.406306 /len=1634			
12184	0.000340	aDNA EL 111096 fin along	AV001049	Un 272240	
12104	0.009349	cDNA FLJ11086 fis, clone	AK001948	Hs.272240	-
		PLACE1005266. /gb=AK001948			
12187	. 0 00000	/gi=7023529 /ug=Hs.272240 /len=1899	NIM 040C00	11- 000000	ND 004450
12167	0.00223	myeloid/lymphoid or mixed-lineage	NM_018682	Hs.333300	NP_061152
		leukemia 5 (trithorax Drosophila) (MLL5);			
		mRNA /cds=(202,5778) /gb=NM_018682	7 -		
		/gi=23503326 /ug=Hs.3333300 /len=6543			
10100	0.040400	507 11/750 100 1150 11	4) (550 (66)		
12189	0.013102	EST AV750486 NPC H.sapiens cDNA	AV750486		-
	×	clone NPCDCF06 5'			<del> </del>
12190	<sub>[.</sub> U.U16974	oxysterol binding protein-like 11	NM_022776	Hs.61260	NP_073613
	9.5	(OSBPL11), mRNA /cds=(306,2549)			, .
	-	/gb=NM_022776 /gi=23111058	• •		
		/ug=Hs.61260 /len=4206			
12193	0.01925	EST (yd68e02.s1 Soares fetal liver spleen	T78464		NP_000436
-		1NFLS IMAGE:113402 3')			٠.
12195	6.55E-04	EST (as58h11.x1 Barstead colon	AI718786		
		HPLRB7 cDNA clone IMAGE:2332965 3'			
		similar to contains Alu repetitive element)			C.
		-			
12197	9.42E-04	DKFZp586E2017_r1 586 (synonym:	AL046885	Hs.413463	
		hute1) cDNA clone DKFZp586E2017 5',			[ · · ·
		mRNA sequence			
	1	/clone=DKFZp586E2017 /clone_end=5'			
•		/gb=AL046885 /gi=5936275		- 1.	Į į
		/ug=Hs.413463 /len=640		1	ļ. '

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gn	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
12207	0.012262	phytoceramidase, alkaline (PHCA),	NM_018367	Hs.23862	NP_060837
		mRNA /cds=(59,862) /gb=NM_018367	-		_
	-	/gi=19923526 /ug=Hs.23862 /len=3404			7-
12213	2.01F-04	repetitive sequence (ALU SUBFAMILY J)	P39188	<del>+ ,</del>	<del></del>
12210	<u> </u>	Continue sequence (ALO SOBI AIVILLE 3)	39100	. '	
12216	0.011460	exon prediction only (aa 2e-15)	CAB90410	,	
12221		hAWMS1 mRNA, complete cds.		11- 445050	
12221	0.0261	• • • • • • • • • • • • • • • • • • •	AB052759	Hs.445652	
		/cds=(232,444) /gb=AB052759			
		/gi=27529922 /ug=Hs.445652 /len=1470			
12227	0.001596	cDNA, 3' end /clone=IMAGE:3038322	BE042649	Hs.275673	
		/clone_end=3' /gb=BE042649			
		/gi=8359628 /ug=Hs.275673 /len=435			
12228	7.88E-04	TSLC1-like 2 (TSLL2), mRNA	NM 145296	Hs.164773	NP 660339
		/cds=(50,1216) /gb=NM_145296	-		
		/gi=21686976 /ug=Hs.164773 /len=2176			
12229	0.043576	clone IMAGE:3924941, mRNA	BC029341	Hs.391380	
احجحب	0.043576	/gb=BC029341 /gi=20379505	00029341	115.351300	
	1 3 -		100		
40000		/ug=Hs.391380 /len=1657			. \.
12236	0.003893	EST (RC2-BN0032-120200-011-h11	AW992887	.0	
		BN0032)		3 No. 7 No. 1	
12239	0.002465	EST(zw57a10.r1	AA429753		*
	Υ	Soares_total_fetus_Nb2HF8_9w cDNA	-		
		clone IMAGE:774138 5')		. *	
12240	0.00189	xq09e02.x1 NCI_CGAP_Ut1 cDNA clone	AW517395	Hs.445194	
*		IMAGE:2750138 3' similar to contains Alu		*	į.
	• •	repetitive element;, mRNA sequence		- 2	
	1	/clone=IMAGE:2750138 /clone_end=3'		-	
		/gb=AW517395 /gi=7155477		X-	i i
			•		
10040	4.005.04	/ug=Hs.445194 /len=519	1140500		
12246	4.93E-04	EST (yo20f05.r1 Soares adult brain	H46503		
		N2b5HB55Y cDNA clone IMAGE:178497		1	
		5')			, ' '
12271	1.63E-04	EST(ne86c04.s1 NCI_CGAP_Kid1 clone	AA480776		
		IMAGE:911142 contains L1.t1 L1 repeat)			
12273	0.009098	EST (RC4-MT0235-061200-011-e04	BF900451		7
		MT0235)			
12284	0.03489	EST384170 MAGE resequences, MAGL	AW971961	Hs.136340	
.2207	0.00400	cDNA, mRNA sequence /gb=AW971961	AVV37 1301	113.130340	
			•		
	8 .	/gi=8161927 /ug=Hs.136340 /len=642			
10000	4 44-44				
12290	0.027691	EST(yd74f02.s1 Soares fetal liver spleen	T79796	, "	
		1NFLS cDNA clone IMAGE:113979 3'			}
		similar to contains Alu repetitive element)			
		-0		*	
12300	0.003603	hypothetical protein MGC32104	NM_144684	Hs.147025	NP_653285
		(MGC32104), mRNA /cds=(101,1651)			
•		/gb=NM_144684 /gi=21389584			-

		nding To Differentially Expressed Genes			
Spot.	p-value	Description	Gene	Unigene	Protein
1			Accession	Accession	Accession
			No.	No.	No.
12311	0.011469	DKFZP566I1024 protein	NM_015411	Hs.279696	NP 056226
		(DKFZP566I1024), mRNA /cds=(48,953)			, -
		/gb=NM_015411 /gi=24308052			
0_0_		/ug=Hs.279696 /len=2005			
12318	0.012262	EST(601434058F1 NIH_MGC_72 cDNA	BE894874		NP_003341
		clone IMAGE:3919071 5')	DEGG (67-1		
12320	0.027691	EST(EST178403 Colon carcinoma (HCC)	AA307521		NP_000980
.2020	0.02,00	cell line cDNA 5' end similar to similar to	701007021	• • • •	_000000
		ribosomal protein L30)			
12322	0.021781	EST(DKFZp547L234_r1 547 (synonym:	AL134310	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·
12022	0.021701	hfbr1) cDNA clone DKFZp547L234 5')	AL 1343 10		·
12222	0.001727	EST (HS_5378_B2_A05_T7A RPCI-11	AQ683118		
12333	0:001737		AQ003110		
	1 - W - 1	Human Male BAC Library genomic clone			
40000	0.040540	Plate=954 Col=10 Row=B)	0.6445404	11 001000	
12336	0.048543	UI-H-ED0-axn-i-09-0-UI.s1	CA445401	Hs.204930	
		NCI_CGAP_ED0 cDNA clone UI-H-ED0-	Ŷ	0.0	**
		axn-i-09-0-UI 3', mRNA sequence	*		
		/clone=UI-H-ED0-axn-i-09-0-UI			
	C-	/clone_end=3' /gb=CA445401			
		/gi=24809821 /ug=Hs.204930 /len=725		•	
12337	0.004677	UI-CF-FN0-aer-f-08-0-UI.s1 UI-CF-FN0	BU609172	Hs 301343	
-		cDNA clone UI-CF-FN0-aer-f-08-0-UI 3',			
		mRNA sequence /clone=UI-CF-FN0-aer-f-		0.8.0	
	(	08-0-UI /clone_end=3' /gb=BU609172			
-	*	/gi=23275387 /ug=Hs.301343 /len=1116			
		EST(cDNA clone IMAGE:5303467 5')	BI597128		
12346	0.039034	selenoprotein H (SELH), mRNA	NM_170746	Hs.290874	NP_734467
		/cds=(243,611) /gb=NM_170746	-		
		/gi=25014108 /ug=Hs.290874 /len=834			
12369	8.63E-04	QV3-BN0047-150400-152-h07 BN0047	AW997115	Hs.274352	
		cDNA, mRNA sequence /gb=AW997115			
. *	ķ.	/gi=8257349 /ug=Hs.274352 /len=686		•	
					-
12373	3.44E-05	602154322F1 NIH_MGC_83 cDNA clone	BF679668	Hs.225723	E 24
	-	IMAGE:4295548 5', mRNA sequence	_, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1.13.225.25	
-	-	/clone=IMAGE:4295548 /clone end=5'		4	0
		/gb=BF679668 /gi=11953563			l ,
		/ug=Hs.225723 /len=845	·		
12375	0.031156	UI-H-DT0-avk-p-22-0-UI.s1	BM996358	Hs.433458	: : :
12010	0.001100	NCI_CGAP_DT0 cDNA clone	סממהפוווים	115.433430	/
		IMAGE:5880837 3', mRNA sequence			
		/clone=IMAGE:5880837 /clone_end=3'			
		/gb=BM996358 /gi=19721259	,		1.
		/ug=Hs.433458 /len=838		A. a	

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
		*	Accession	Accession	Accession
			No.	No.	No.
12376	6.23E-06	ESTs, cDNA, 5' end	BF032850	Hs.5367	
•		/clone=IMAGE:3859365 /clone_end=5"	1		•
		/gb=BF032850 /gi=10740562			
	3	/ug=Hs.5367 (=ESTs, Weakly similar to	8		1
		T02670 probable thromboxane A2	1		
		receptor isoform beta)			
12378	4.95E-05	cDNA FLJ31274 fis, clone	AK055836	Hs.351722	
		KIDNE2006334. /gb=AK055836			
*	. *	/gi=16550665 /ug=Hs.351722 /len=1817	,		
12381	0.001915	FLJ31317 fis, clone LIVER1000421,	AK055879	Hs.350826	
		moderately similar to CYTOCHROME			
		P450 3A5 (EC 1.14.14.1)	**		
-		/cds=UNKNOWN /gb=AK055879	,	ı •	17.
	·	/gi=16550714/ug=Hs.350826 /len=2596	*		
12382	0.007056	clone IMAGE:4151959,	BC011194	Hs.194397	· · · · · · · · · · · · · · · · · · ·
,		mRNA/cds=UNKNOWN /gb=BC011194		1,14,10,140,	
		/gi=15277441 /ug=Hs.194397/len=1842	; ·	•	:
12389	0.003893	UI-HF-BN0-afr-f-07-0-UI.r1 NIH_MGC_50	BU431616	Hs.202538	
		cDNA clone IMAGE:3067908 5', mRNA	20 10 10 10	113.202000	2.0
		sequence /clone=IMAGE:3067908		1	Ÿ
•		/clone_end=5' /gb=BU431616		• 0	
*		/gi=22770103 /ug=Hs.202538 /len=551	,	*	
12398	0.041254	MR2-NT0138-131200-007-h02 NT0138	BF930590	Hs.150059	· · · · · · · · · · · · · · · · · · ·
,,,	9.01.1207	cDNA, mRNA sequence /gb=BF930590	B. 000000	113.70000	
.*		/gi=12348018 /ug=Hs.150059 /len=561			
12399	0.021781	UI-E-CK1-afh-b-14-0-UI.r1 UI-E-CK1	BM702699	Hs.446508	
12000	0.021701	cDNA clone UI-E-CK1-afh-b-14-0-UI 5',	DW1702033	113.44000	1
	7	mRNA sequence /clone=UI-E-CK1-afh-b-			]
~	·	14-0-UI /clone end=5' /gb=BM702699			
		/gi=19015957 /ug=Hs.446508 /len=1088		- "	
12401	0.024587	FLJ25282 fis, clone STM06685, highly	AK058011		NP_003820
12401	0.024307	similar to Rattus norvegicus mRNA for	AK036011		INF_003620
•	Par	_ ·	1 5 7		
12402	5 425 04	multi PDZ domain protein	VC004844	Autority -	
12402		clone 3938P1, complete sequence	AC004814		
12400	0.023146	EST(CM0-HT1297-160201-781-b03	BG995501		
		HT1297 Homo sapiens cDNA, mRNA			
10107	0.007000	sequence)	416004400	11. 050444	
12407	0.007886	cDNA FLJ10258 fis, clone	AK001120	Hs.258111	
		HEMBB1000908. /gb=AK001120		' '	
40400	0.000000	/gi=7022181 /ug=Hs.258111 /len=1490	DE004646	<del> </del> :	ND 0-5
12408	0.029362	cDNA MR1-FN0010-290700-007-g10	BE834948		NP_803133
		FN0010 (=AC099562.1  Homo sapiens	-8:		
	CHC	chromosome 1 clone RP11-213P13,	·		
		WORKING DRAFT SEQUENCE, 3			
		unordered pieces)			

	p-value	nding To Differentially Expressed Genes Description	G ne	Unigene	Protein
Opor	p-value	Description	Accession	Accession	Accession
	•	*	No.	No.	No.
12410	0.016974	BX094545 Soares_NFL_T_GBC_S1	BX094545	Hs.445988	INO.
12-710	0.010014	cDNA clone IMAGp998G143911, mRNA	1001010	113.440000	· ·
	,	sequence		4	
		/clone=IMAGp998G143911_;_IMAGE:15			
		44101 /gb=BX094545 /gi=27842004	· ·		
		/ug=Hs.445988 /len=738	-	1 -	
12423	0.002625	clone IMAGE:4800262, mRNA	BC040182	Hs.235795	1
12720		/gb=BC040182 /gi=25455679	100040102	1113.200730	
		/ug=Hs.235795 /len=3858			
12433		cDNA FLJ14388 fis, clone	AK027294	Hs.9812	
12400	0.007070	HEMBA1002716. /gb=AK027294	711027234	113,3012	-
		/gi=14041878 /ug=Hs.9812 /len=1673	,		
12434		EST(cDNA clone HTFABF07 5')	AV731260		<del> </del>
12434		cDNA FLJ12048 fis, clone	AK022110	Hs.289044	×-
1,2400	0.001002	HEMBB1001990. /gb=AK022110	AR022110	115.205044	] . ·
	•	/gi=10433433 /ug=Hs.289044 /len=1805			
12/52	1 32F-04	EST(cDNA clone IMAGE:784142 5')	AA446766		<del></del>
		EST(cDNA clone IMAGE:75414257)	BF221533	7	NP 714916
12462		FLJ23566 fis, clone LNG10880	AK027219	Hs.306914	114916
12402	0.002020	/cds=UNKNOWN /gb=AK027219	AR027219	113.300314	- 30
-	Ť	/gi=10440298 /ug=Hs.306914 /len=1901	÷,		
12467	0.020319	EST(cDNA clone IMAGE:2728993 3' )	AW292959		<del> </del>
12469		cDNA FLJ10984 fis, clone	AK001846	Hs.8412	<del>                                     </del>
12,400	0.041204	PLACE1001810. /gb=AK001846	121001040	113.0412	,
	•	/gi=7023367 /ug=Hs.8412 /len=2337			•
12473	0.0261	xc09d01.x1 NCI_CGAP_Co21 cDNA	AW083503	Hs.311987	
12773	0.0201	clone IMAGE:2583745 3' similar to	7,44003000	113.311907	
	• •	contains MER14.12 MER14 repetitive	***	,	
		element , mRNA sequence			· .
		/clone=IMAGE:2583745 /clone end=3'	ė	}	·
		/gb=AW083503 /gi=6038579		•	1.
-		/ug=Hs.311987 /len=510		,	
12474	0.002084	clone RP11-350H1 from 7p14-15,	AC006195		<del>                                     </del>
12717	0.002004	complete sequence	AC006195		
12488	6.55E-04	ESTs, cDNA, 3' end	Al356348	Hs.369317	<del>                                     </del>
12400	U.UUL:U4	/clone=IMAGE:2028021 /clone_end=3'	71330340	113.505517	
		/gb=Al356348 /gi=4107969	*		i i
.,		/ug=Hs.369317 /len=512			
12493	0.043576	EST (Soares_fetal_heart_NbHH19W	Al146302	<del> </del>	T
12730	0.0 <del>7</del> 0010	clone IMAGE:1707091 3')	71170302		
12505	0.001465	EST(cDNA clone HTBBSD03 5')	AV722328	<del> </del>	<del>                                     </del>
12506		EST(cDNA clone IMAGE:4724612 5'. )	BG573579		<del> </del>
12508		EST(Embryonic Heart cDNA Library	Al617030	<del> </del>	
12300	0.000000	· · ·	171017030		
	١.	Danio rerio cDNA 5')	1	1	1

Genes	Correspo	nding To Differentially Express d Genes	in Figure 12 -	Hypertension	
	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
12513	0.003332	AGENCOURT_8841454	BQ924341	Hs.442591	1.33.
		Lupski_sciatic_nerve cDNA clone			
		IMAGE:6199422 5', mRNA sequence		<u> </u>	
		/clone=IMAGE:6199422 /clone_end=5'	*.		
		/gb=BQ924341 /gi=22339372	0.0		2
	.00	/ug=Hs.442591 /len=930			
12514	0.020482	DCBCQH10 DCB cDNA, mRNA	BU198777	Hs.50273	
		sequence /gb=BU198777 /gi=22717083		110.002.0	-
		/ug=Hs.50273 /len=867			
12517	0.041254	UI-H-DP0-avt-a-17-0-UI.s1	BQ000272	Hs.371473	
	0.01.1201	NCI_CGAP_Fs1 cDNA clone	DQ000272	110.97 147 9	
		IMAGE:5883928 3', mRNA sequence	0	٠.	8.
_		/clone=IMAGE:5883928 /clone end=3'		1	
		/gb=BQ000272 /gi=19725172		*	
		/ug=Hs.371473 /len=1051			
12519	0.020492	EST(cDNA clone IMAGE:1637714 3'	AI000800	- 10	+
123 13	0.020402	similar to contains Alu repetitive	A1000800	-	
		element;contains L1.t1 L1 repetitive element;)		ł	
12550	0.010001	clone IMAGE:5019705, mRNA	DC024207	11- 404544	<u> </u>
12550	0.010001		BC021287	Hs.184544	
		/gb=BC021287 /gi=18204277	:		+
12566	0.002002	/ug=Hs.184544 /len=2121	DC424047		
12500	0.003893	602507208F1 NIH_MGC_79 cDNA clone	BG434947	Hs.382990	
	ľ	IMAGE:4604760 5', mRNA sequence			
		/clone=IMAGE:4604760 /clone_end=5'	3		-
		/gb=BG434947 /gi=13341453			
40E74	0.000700	/ug=Hs.382990 /len=677	50007700		1
12571		EST, clone IMAGE:4127796, mRNA	BC007799		NP_443107
12573		EST(cDNA clone IMAGE:3125123 3')	BE047402		NP_002700
12574	0.020482	UI-H-ED0-awx-b-15-0-UI.s1	BQ020068	Hs.396278	į.
		NCI_CGAP_ED0 cDNA clone			
		IMAGE:5824814 3', mRNA sequence	(V)	3	
		/clone=IMAGE:5824814 /clone_end=3'		,	
	: 7	/gb=BQ020068 /gi=19755345			
· · · · · · · · · · · · · · · · · · ·	<u> </u>	/ug=Hs.396278 /len=1351			
12577		No significant match, No orf	SEQ.ID.No.3		
12580		No significant match	SEQ.ID.No.34		<u> </u>
12593	0.043544	No significant match,			
	-51	ORF+2(71~409),+1(121~384)	SEQ.ID.No.94		
12604	0.01925	EST(IL3-HT0618-120500-138-D11	BE179957		
		HT0618 cDNA, MRNA sequence)			
12610	0.003603	clone IMAGE:4826196, mRNA, partial	BC030609	Hs.375796	
		cds /cds=UNKNOWN /gb=BC030609	,	*	
		/gi=21040424 /ug=Hs.375796 /len=4340			
12616	0.046005	No significant match	SEQ.ID.No.36		
12618	0.032959	No significant match			м -
		(ORF:+1:52~230[180])	SEQ.ID.No.28		

Spot	p-value	nding To Diff r ntially Expressed Genes Description	G ne	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
12655	0.012262	zt59c06.s1 Soares testis NHT cDNA	AA398215	Hs.290951	110.
		clone IMAGE:726634 3', mRNA	1.		
•		sequence /clone=IMAGE:726634		,	
•		/clone_end=3' /gb=AA398215	•		
*		/gi=2051324 /ug=Hs.290951 /len=427	1.		•*
12657	0.043576	EST (ym54a08.r1 Soares infant brain	H22760		
<u> </u>		1NIB clone IMAGE:52140 5')			
12658	0.015924	guanine nucleotide binding protein (G	NM 002070	Hs.77269	NP_002061
		protein), alpha inhibiting activity			
		polypeptide 2 (GNAI2), mRNA			
		/cds=(124,1191) /gb=NM_002070	-		
•		/gi=4504040 /ug=Hs.77269 /len=1702			
12663	0.036914	GCIP-interacting protein p29 (P29),	NM 015484	Hs.20013	NP_056299
		mRNA /cds=(17,748) /gb=NM 015484			
/		/gi=7661635 /ug=Hs.20013 /len=1344			
12666	0.009349	cDNA sequence FLJ14014 fis, clone	AK024076		NP 699204
		HEMBA1000290			
12667	0.006106	tq86b01.x1 NCI_CGAP_Ov23 cDNA	AI567941	Hs.436171	
7		clone IMAGE:2215657 3' similar to		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
		contains Alu repetitive element;contains		1	X-
		element LTR5 repetitive element ;, mRNA	r		
	-	sequence /clone=IMAGE:2215657			
		/clone_end=3' /gb=Al567941 /gi=4526393		r o	
		/ug=Hs.436171 /len=476			
	1				
12672	0.007578	hypothetical protein FLJ10254	NP 060511		* - *
12679		BX092629 Soares fetal liver spleen	BX092629	Hs.303022	
		1NFLS cDNA clone IMAGp998P06398;			*
		IMAGE:205685, mRNA sequence			
		/clone=IMAGp998P06398_;_IMAGE:2056			
		85 /gb=BX092629 /gi=27822922	365		-
		/ug=Hs.303022 /len=735	*		-
12680	0.018081	EST (CM3-HT0528-010200-086-f04	BE169870	· · · · · · · · ·	
0	9.010001	HT0528)			•
12696	0.03489	cDNA, 3' end /clone=IMAGE:2369618	AI819052	Hs.50918	
		/clone_end=3' /gb=Al819052 /gi=5438216	- m		
		I/ug=Hs 50918 /len=540	, ,		
12712	0.001737	/ug=Hs.50918 /len=540	AW150422		
12712	0.001737	EST(xg51d02.x1 NCI_CGAP_Ut4 cDNA	AW150422		9
12712	0.001737	EST(xg51d02.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2631843 3' similar to	AW150422		
		EST(xg51d02.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2631843 3' similar to contains Alu repetitive element)	*	Hs. 349283	
12712 12715		EST(xg51d02.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2631843 3' similar to contains Alu repetitive element) cDNA FLJ31753 fis, clone	AW150422 AK056315	Hs.349283	
		EST(xg51d02.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2631843 3' similar to contains Alu repetitive element) cDNA FLJ31753 fis, clone NT2RI2007468. /gb=AK056315	*	Hs.349283	*
12715	0.039267	EST(xg51d02.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2631843 3' similar to contains Alu repetitive element) cDNA FLJ31753 fis, clone NT2RI2007468. /gb=AK056315 /gi=16551681 /ug=Hs.349283 /len=2361	AK056315	Hs.349283	NP 38744
	0.039267	EST(xg51d02.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2631843 3' similar to contains Alu repetitive element) cDNA FLJ31753 fis, clone NT2RI2007468. /gb=AK056315	*	Hs.349283	NP_38744

Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
	(		No.	No.	No.
12723	0.001232	qw21c02.x1 NCI_CGAP_Ut4 cDNA clone	AI290157	Hs.387096	
		IMAGE:1991714 3' similar to contains Alu			-
		repetitive element;contains element L1		1 .	
		repetitive element ;, mRNA sequence		=*	*
		/clone=IMAGE:1991714 /clone_end=3'		·	* :-
		/gb=Al290157 /gi=3931823	·		,
		/ug=Hs.387096 /len=571		*	
12726	0.00527	aldehyde dehydrogenase 6 family,	NM_005589	Hs.293970	NP_00558
		member A1 (ALDH6A1), nuclear gene			
	4	encoding mitochondrial protein, mRNA			
	V	/cds=(100,1707) /gb=NM_005589			
		/gi=25777737 /ug=Hs.293970 /len=2183			
12729	0.007056	xg60a08.x1 NCI_CGAP_Ut4 cDNA clone	AW168110	Hs.277648	-
		IMAGE:2632694 3', mRNA sequence			~
		/clone=IMAGE:2632694 /clone_end=3'	*		
		/gb=AW168110 /gi=6399635	170		١.
7 1		/ug=Hs.277648 /len=475			•
12733	0.01072	cDNA, 3' end /clone=IMAGE:2726753	AW293323	Hs.255182	
		/clone_end=3' /gb=AW293323	9		
		/gi=6699885 /ug=Hs.255182 /len=354			
12736	0.002625	EST (zx09d01.r1	AA448588		NP 07506
		Soares_total_fetus_Nb2HF8_9w	-		7
		IMAGE:785953 5')	•		0)0
12743	0.004203	EST (RC3-BN0036-090200-011-h11	AW994082		
		BN0036 cDNA)			• .
12751	7.18E-04	NISC_gj03b10.x1 NCI_CGAP_Pr28	CB048158	Hs.201018	
		cDNA clone IMAGE:3270498 3', mRNA			
	*.	sequence /clone=IMAGE:3270498		-	- (1
		/clone_end=3' /gb=CB048158			
		/gi=27786445 /ug=Hs.201018 /len=384			*
12763	0.001737	UI-H-FG0-bct-g-21-0-UI.s1	BU627064	Hs.85999	
		NCI_CGAP_EN1_2 cDNA clone UI-H-			
		FG0-bct-g-21-0-UI 3', mRNA sequence		- 30	
	• • •	/clone=UI-H-FG0-bct-g-21-0-UI			• 3
		/clone_end=3' /gb=BU627064			
		/gi=23293278 /ug=Hs.85999 /len=1075			
12765	0.013991	EST (RC5-BT0663-050400-012-H04	BE085097		-
		BT0663 cDNA)			
12769	0.036914	ribosomal protein L13a (RPL13A), mRNA	NM_012423	Hs.389335	NP_03655
•		/cds=(23,634) /gb=NM_012423			
		/gi=14591905 /ug=Hs.389335 /len=1142			
12770	0.001344	clone GS1-250N6, complete sequence	AC005158		
12775		acidic (leucine-rich) nuclear	NM 006401	Hs.84264	NP 00639
		phosphoprotein 32 family, member B			
		(ANP32B), mRNA /cds=(211,966)			
	. 8	/gb=NM_006401 /gi=5454087			
	l .	/ug=Hs.84264 /len=1475			

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Genes	Correspon	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	
	p-value	Description	Gene	Unig ne	Prot in
•			Accession	Acc ssion	Acc ssion
			No.	No.	No.
12786	5.42E-04	hr74d11.x1 NCI CGAP Kid11 cDNA	BF115106	Hs.318114	
		clone IMAGE:3134229 3' similar to			00
- 12		contains Alu repetitive element; contains			
		element MER15 repetitive element;,			*
		mRNA sequence /clone=IMAGE:3134229		tin je	
.:		/clone_end=3' /gb=BF115106		,	
0)		/gi=10984582 /ug=Hs.318114 /len=462			
. /		791 1000 1002 749 110.0 10 17 17 1011 102			
12794	0.032959	ribosomal protein L12 (RPL12), mRNA	NM_000976	Hs.405042	NP_000967
12.01	0.002000	/cds=(89,586) /gb=NM_000976		110.400042	
	•	/gi=15431291 /ug=Hs.405042 /len=632			·
12804	0.004677	hypothetical protein FLJ38716	NM 152367	Hs.376194	NP_689580
12004	0.004077	(FLJ38716), mRNA /cds=(266,1354)	102007	113.570154	141 _009500
		/gb=NM_152367 /gi=22748790			7.2
		/ug=Hs.376194 /len=3229		• .	
12806	0.485.05	cDNA FLJ38577 fis, clone	AK095896	Hs.379754	
12000	9.40L-03	HCHON2007650. /gb=AK095896	AVOSOSO	ITS.379734	
		·			
12807	0.002602	/gi=21755247 /ug=Hs.379754 /len=3200 hypothetical protein BC014320	NM_138785	Hs.240767	ND 620440
12007	0.003603	(LOC116254), mRNA /cds=(28,1020)	130700	I S. 240767	NP_620140
		/gb=NM_138785 /gi=20302037	*		
			*	· ·	
12836	0.041254	/ug=Hs.240767 /len=1143 BX090814	BX090814	Un 105157	
12030	0.041234	· · · · · · · · · · · · · · · · · · ·	DAU90014	Hs.125457	v.
*.	,	Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGp998J084249;			
		IMAGE:1673959, mRNA sequence			
	.:	/clone=IMAGp998J084249_;_IMAGE:167			
	-	3959 /gb=BX090814 /gi=27824521			
12837	0.022050	/ug=Hs.125457 /len=471 cDNA, 5' end /clone=IMAGE:5214599	DI044770	115:42270	ND 054700
12031	0.032959		BI911779	Hs.13370	NP_054763
,	Į.	/clone_end=5' /gb=Bl911779			
40000	0.000400	/gi=16175651 /ug=Hs.121740 /len=818	111074047	11 040504	
12839	0.006106	EST383336 MAGE resequences, MAGL	AW971247	Hs.348501	
		cDNA, mRNA sequence /gb=AW971247	, .		
ė		/gi=8161092 /ug=Hs.348501 /len=578	,		:
12042	0.000400	-DNIA -I IMACC: 400700 01 -1	 D04424	0 10	- N
12843	0.006106	cDNA clone IMAGE:123789 3' similar to	R01434		
		contains Alu repetitive element; contains	·		
		THR repetitive element; Soares fetal liver	*		
40046	0.004707	spleen 1NFLS	A1 407000	11: 050445	
12846	0.001737	EST, cDNA, 5' end	AL137968	Hs.256115	
	54	/clone=DKFZp761D0315 /clone_end=5'			,
		/gb=AL137968 /gi=6854648	*		·
40046	0.00000	/ug=Hs.256115 /len=523	11/00/05 : 5		
12848	J 0.002268	cDNA: FLJ23165 fis, clone LNG09846.	AK026818	Hs.279898	
	1	/gb=AK026818 /gi=10439763	-0	1	
12857	0.000707	/ug=Hs.279898 /len=2117 EST(cDNA clone IMAGE:4413411 5' )	BG034856		

	p-value	nding To Diff rentially Expressed Genes Description	Gene	Unigene	Protein.
opot	p value	Scoonpaon	Acc ssion	Accession	Accession
	*	*	No.	No.	No.
2861	0:015924	cDNA FLJ25876 fis, clone CBR02529.	AK098742	Hs.375841	140:
-,-,	*	/gb=AK098742 /gi=21758849		7	•
	· ·	/ug=Hs.375841 /len=1877			00
2862	.0.020482	cDNA MR1-FN0210-301000-002-h09	BF854986	32	
	3.323.32	FN0210		*1. *	
2864	0.032959	FLJ12425 fis, clone MAMMA1003104	AK022487	Hs.9299	
		/cds=UNKNOWN /gb=AK022487		0.00	
		/gi=10433899 /ug=Hs.9299 /len=2742	*		
2873	0.001232	EST53917 Fetal heart II cDNA 3' end	AA347584	Hs.332616	-
		similar to EST containing Alu repeat,			
1		mRNA sequence /clone_end=3'			
		/gb=AA347584 /gi=1999822	4		•
		/ug=Hs.332616 /len=408	-		
2879	0.002625	hypothetical protein FLJ22415	NM 024769	Hs.135121	NP 07904
		(FLJ22415), mRNA /cds=(342,1463)		,	
	-	/gb=NM_024769 /gi=13376114	4.	,	
		/ug=Hs.135121 /len=2627	,		± **
2886	0.001596	EST, 602309245F1 NIH_MGC_88 cDNA	BF981440		
7,554	1.00,000	clone IMAGE:4400362 5'	5. 5511.15	• 5	
2901	8.63E-04	ESTs, cDNA /clone=IMAGE:1203867	AA640737	Hs.336767	· ·
		/gb=AA640737 /gi=2565987	7 10 10 10 1	110.000101	
		/ug=Hs.336767 /len=416	· ·		
2902	0.024587	ESTs, FLJ25251 fis, clone STM03603	AK057980	Hs.256801	
		/cds=UNKNOWN /gb=AK057980			
		/gi=16553972 /ug=Hs.256801 /len=1727			*-
2921	0.00489	BX106452 NCI CGAP Gas4 cDNA clone	BX106452	Hs.200841	* *
		IMAGp998N095583, mRNA sequence		, ,	
•		/clone=IMAGp998N095583_;_IMAGE:225			
		5816 /gb=BX106452 /gi=27834105			
	•	/ug=Hs.200841 /len=458		*	
,					
2926	0.023148	clone IMAGE:4391558, mRNA	BC017743	Hs.41407	
		/gb=BC017743 /gi=17389405		-	
	Y	/ug=Hs.41407 /len=2299	*		
2928	0.048543	UI-1-BB1p-aui-h-09-0-UI.s1	BQ023192	Hs.347924	
• •		NCI_CGAP_PI6 cDNA clone UI-1-BB1p-		•	•
		aui-h-09-0-UI 3', mRNA sequence	10	* * .	ŀ
٠.		/clone=UI-1-BB1p-aui-h-09-0-UI		,	1
:		/clone_end=3' /gb=BQ023192	•		
		/gi=19758471 /ug=Hs.347924 /len=593	*		
2929	0.01072	ESTs, cDNA, 5' end	BE900284	Hs.91216	NP_00576
		/clone=IMAGE:3956086 /clone_end=5'	3 *		
	<u> </u>	/gb=BE900284 /gi=10388502			· .
		/ug=Hs.91216 /len=730			
2930	0.023148	cDNA: FLJ22425 fis, clone HRC08686.	AK026078	Hs.288555	
		/gb=AK026078 /gi=10438812		1	
. 0		/ug=Hs.288555 /len=2132			

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
		0	Accession	Accession	Accession
			No.	No.	No.
12939	0.014931	UI-H-EI0-ayi-a-23-0-UI.s1	BQ007852	Hs.438166	
		NCI_CGAP_EI0 cDNA clone	-	.*	
,		IMAGE:5839006 3', mRNA sequence			1.
		/clone=IMAGE:5839006 /clone_end=3'		1-	
		/gb=BQ007852 /gi=19732752		,	
		/ug=Hs.438166 /len=1071			
12942	0.00527	zr33g12.r1 Soares_NhHMPu_S1 cDNA	AA195350	Hs.270125	,
	•	clone IMAGE:665254 5' similar to	· .		
		contains Alu repetitive element;, mRNA			-
		sequence /clone=IMAGE:665254			÷ ,
	-	/clone_end=5' /gb=AA195350		•	
		/gi=1785041 /ug=Hs.270125 /len=492			
12944	0.024587	QV0-CT0181-041199-048-h11 CT0181	AW752027	Hs.293346	
4377	0.024307	cDNA, mRNA sequence /gb=AW752027	7,02027	113.233340	
٠.		/gi=7667063 /ug=Hs.293346 /len=634			* (71)
		/gi=7007003 /ug=ns.293340 /len=034			
2052	0.015024	cDNA, 3' end /clone=IMAGE:436024	AA699991	Hs.348162	· · · · · · · · · · · · · · · · · · ·
12900	0.015924		AAGaaaa	IDS.340 102	,
	8	/clone_end=3' /gb=AA699991			
0004	0.000705	/gi=2702954 /ug=Hs.348162 /len=614	504050	11 000704	
2961	0.038725	yp92f09.r1 Soares fetal liver spleen	R91059	Hs.330761	
		1NFLS cDNA clone IMAGE:194921 5',	2.4	1	
	7	mRNA sequence /clone=IMAGE:194921			
		/clone_end=5' /gb=R91059 /gi=958599	, ,	1.1	
	9	/ug=Hs.330761 /len=430	χ. •	1 .	ì
				4	
12962	0.011182	UI-H-FH0-bco-e-02-0-UI.s1	CA420130	Hs.365560	•
		NCI_CGAP_FH0 cDNA clone UI-H-FH0-			
•		bco-e-02-0-UI 3', mRNA sequence			
		/clone=UI-H-FH0-bco-e-02-0-UI			
		/clone_end=3' /gb=CA420130	,		4)(4
		/gi=24782785 /ug=Hs.365560 /len=716			
2970	0.020482	EST(yy21h08.s1 Soares melanocyte	N35259		NP_079229
		2NbHM H.sapiens cDNA clone	* .		
		IMAGE:271935 3')	7 *		
2973	0.00242	ESTs, cDNA, 3' end	AW009340	Hs.372482	1
		/clone=IMAGE:2504343 /clone_end=3'			
		/gb=AW009340 /gi=5858118			
		/ug=Hs.372482 /len=490		4	
12977	0.024587	ESTs, cDNA, 5' end	BG027813	Hs.344521	
		/clone=IMAGE:4389132 /clone end=5'			
		/gb=BG027813 /gi=12416651			*
		/ug=Hs.344521 /len=1068			
12980	0.003893	FLJ30434 fis, clone BRACE2009016	AK054996	Hs.367901	
	0.00000	/cds=UNKNOWN /gb=AK054996		1,10.007,001	
		/gi=16549636 /ug=Hs.367901 /len=2738			
12982	0.041547	cDNA FLJ31038 fis, clone	AK055600	Hs.303154	
12302	0.041347	,		113.303134	
		HSYRA2000159 /gb=AK055600			
10000	0.040074	/gi=16550370 /ug=Hs.303154 /len=2981	A14/000010		ND 000000
2983	T 0.0169/4	EST(cDNA clone IMAGE:2771386 3')	AW269219	<u> </u>	NP_689632

Genes	Correspon	nding To Differentially Expr ss d G nes	in Figur 12 -	Hypertension	
Spot	p-value	Description	Gene	Unigen	Protein
			Accession	Accession	Accession
1		V	No.	No.	No.
12990	7.92E-05	BX111054	BX111054	Hs.299415	
		Soares parathyroid tumor NbHPA cDNA			
		clone IMAGp998L124176, mRNA			
		sequence			
		/clone=IMAGp998L124176_;_IMAGE:164	,	ď	
		5979 /gb=BX111054 /gi=27878338			
		/ug=Hs.299415 /len=821	, ,		. *
12996	0.001344	cDNA FLJ11366 fis, clone	AK021428	Hs.189002	
		HEMBA1000282. /gb=AK021428			i
		/gi=10432610 /ug=Hs.189002 /len=2075			
12998	1.63E-04	UI-H-EU0-azv-j-13-0-UI.s1	BQ181732	Hs.442187	
, _ 0 0 0	, ,	NCI_CGAP_Car1 cDNA clone IMAGE:			
	•	5854164 3', mRNA sequence	× **		·
		/clone=IMAGE: 5854164 /clone_end=3'			
		/gb=BQ181732 /gi=20357224			
a •		/ug=Hs.442187 /len=1042	*	*	•
13000	0.001006	EST(cDNA clone B853)	T19901		
		EST(cDNA clone IMAGE:3305814 3')	BE855680		
13002		we13d07.x1 NCI_CGAP_Lu24 cDNA	AI912762	Hs.213389	
1 1 1 1		clone IMAGE:2340973 3', mRNA	,		***
		sequence /clone=IMAGE:2340973	0		<b>,</b>
• •		/clone_end=3' /gb=Al912762 /gi=5632617			'
		/ug=Hs.213389 /len=589	· · · · · · · · · · · · · · · · · · ·		
13005	0.005674	zx55g04.r1	AA203502	Hs.192991	•
•.	7	Soares_fetal_liver_spleen_1NFLS_S1			٠.
*		cDNA clone IMAGE:446454 5', mRNA	*		
•	,	sequence /clone=IMAGE:446454	e		
		/clone_end=5' /gb=AA203502			1
		/gi=1799213 /ug=Hs.192991 /len=952		- (1	
13013	0.010015	EST(cDNA clone IMAGE:2542504 3'	AW057714		
	· ·	similar to contains Alu repetitive element;			
					**
13017	0.031117	BX116697 NCI_CGAP_Co3 cDNA clone	BX116697	Hs.433643	
•		IMAGp998C232238, mRNA sequence			
	~	/clone=IMAGp998C232238_;_IMAGE:901		,	
		582 /gb=BX116697 /gj=27840179	H-1		•
		/ug=Hs.433643 /len=682			
13018	0.012262	EST hv69b07.x1 NCI_CGAP_Lu24	BE220182	. *	NP_060114
		Human cDNA clone IMAGE:3178645 3'			_
13022	0.003079	mRNA; cDNA DKFZp762C074 (from	AL832439	Hs.40527	
		clone DKFZp762C074) /gb=AL832439			
		/gi=21733004 /ug=Hs.40527 /len=3076			
13024	0.005674	cDNA FLJ12317 fis, clone	AK022379	Hs.288464	
		MAMMA1002058. /gb=AK022379		4	
		/gi=10433764 /ug=Hs.288464 /len=2403			
		EST(cDNA clone IMAGE:4455676 5')	BG166249		<del> </del>

Accession   Accession   No.		lyp rtension	in Figure 12 -	nding To Differentially Expr ss d G nes	Correspor	Genes
No.   No.	Protein	Unigene	Gene	Description	p-value	Spot
No.   No.	Accession	Accession	Accession -	*		
13035   2.73E-04   clone MGC:16614 IMAGE:4111344, mRNA, complete cds /cds=(258,998) /gb=BC009313 /gi=14424569 /ug=Hs.373515 /len=2052   dug=Hs.373515 /len=2052   AC113366   AC113366   AC113366   AC113366   AC113366   AC113366   AC113366   AC113366   AC113366   AC113366   AC113365   AC113366   AC113365   AC113366   AC113365   AC113365   AC113366   AC113365   AC113365   AC113365   AC113366   AC113365   A			No.	· ·		
mRNA, complete cds /cds=(258,998)   /gb=BC009313 /gi=14424569   /ug=Hs.373515 /len=2052	10.			clone MGC:16614 IMAGE:4111344	2 73F-04	13035
/gb=BC009313 /gi=14424569 / /ug=Hs.373515 /len=2052	4.15	, , , , , , , , , , , , , , , , , , , ,	*		-1, 7- 7,	, , , , , ,
13045   0.039267   chromosome 5 clone RP11-109F5, WORKING DRAFT SEQUENCE, 4 unordered pieces	*		•		i	
13045   0.039267   chromosome 5 clone RP11-109F5   WORKING DRAFT SEQUENCE; 4   unordered pieces		, 'e				0
WORKING DRAFT SEQUENCE, 4		*** * *	AC113366			13045
Unordered pieces			7.01.10000		0.000201	10010
13051   0.015924   No significant match, ORF+1(277~546)   SEQ.ID.No.52     13052   0.024587   No significant match   SEQ.ID.No.56     13072   0.001476   yr21g01.s1 Soares fetal liver splean   1NFLS cDNA clone IMAGE:205968 3' similar to contains Alu repetitive element; contains MER35 repetitive element; mRNA sequence   /clone=IMAGE:205968 /clone_end=3'   /gb=H58501 /gi=1011333 /ug=Hs.347143   /len=a61     13081   0.01925   Novel   SEQ.ID.No.8     13123   0.046432   BRAF35/HDAC2 complex (80 kDa)   (BHC80), mRNA /cds=(386,2290)   /gb=NM_016621 /gi=19923461   /ug=Hs.106826 /len=3692   /ug=Hs.106826 /len=3692   /ug=Hs.106826 /len=2308   /ug=Hs.101937 /len=2308   /ug=Hs.101937 /len=2308   /ug=Hs.101937 /len=2141			** * ·	·	i	
13052   0.024587   No significant match   SEQ.ID.No.56     13072   0.001476   yr21g01.s1 Soares fetal liver spleen   NFLS cDNA clone IMAGE:205968 3' similar to contains Alu repetitive element; contains MER35 repetitive element; mRNA sequence /clone=IMAGE:205968 /clone_end=3' /gb=H58501 /gi=1011333 /ug=Hs.347143 /len=461   Novel   SEQ.ID.No.8     13123   0.046432   BRAF35/HDAC2 complex (80 kDa) (BHC80), mRNA /cds=(386,2290) /gb=NM_016621 /gi=19923461 / /ug=Hs.106826 /len=3692   NM_016621 / /ug=Hs.106826 /len=3692   NM_016621 / /ug=Hs.346406 /len=2308   NM_016932   FLJ33100 fis, clone TRACH2000873 /cds=UNKNOWN /gb=AK057662 /gi=16553426 /ug=Hs.346406 /len=2308   NM_016932   Hs.101937 /len=2141   NM_016932   NM_016932 /gi=21314676 /ug=Hs.101937 /len=2141   NM_016932 /gi=21314676 /ug=Hs.101937 /len=2141   NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709   NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_004873 /gi=24308092 /ug=Hs.8258 /len=3389   NM_004873 /len=24308092 /lg=Hs.8258 /len=3389   NM_004873 /len=24308092	<del></del>		SEO ID No.52		0.015924	13051
13072   0.001476   yr21g01.s1 Soares fetal liver spleen   1NFLS cDNA clone IMAGE:205968 3' similar to contains Alu repetitive element; contains Alu repetitive element; mRNA sequence /clone=IMAGE:205968 /clone_end=3' /gb=H58501 /gi=1011333 /ug=Hs.347143 /len=461   SEQ.ID.No.8     13081   0.01925   Novel   SEQ.ID.No.8     13123   0.046432   BRAF35/HDAC2 complex (80 kDa) (BHC80), mRNA /cds=(386,2290) /gb=NM_016621 /gi=19923461 / lug=Hs.106826 /len=3692   NM_016621   Hs.181785 /cds=UNKNOWN /gb=AK057662 /gi=16553426 /ug=Hs.346406 /len=2308   NM_016932 /gi=16553426 /ug=Hs.346406 /len=2308   NM_016932   Hs.101937 /len=2141   SIX2), mRNA /cds=(283,1158) /gb=NM_016932 /gi=21314676 /ug=Hs.101937 /len=2141   Chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709   NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP_013247   NP_013247   NP_013247   NP_014536   NP_01453		*				
1NFLS cDNA clone IMAGE:205968 3' similar to contains Alu repetitive element; contains MER35 repetitive element; mRNA sequence /clone=IMAGE:205968 /clone_end=3' /gb=H58501 /gi=1011333 /ug=Hs.347143 /len=461  13081		He 3/171/13				
Similar to contains Alu repetitive element; contains MER35 repetitive element; mRNA sequence //clone=IMAGE:205968 /clone_end=3' //gb=H58501 /gi=1011333 /ug=Hs.347143 /len=461   SEQ.ID.No.8   13123   0.046432   BRAF35/HDAC2 complex (80 kDa) (BHC80), mRNA /cds=(386,2290) //gb=NM_016621 /gi=19923461 //ug=Hs.106826 /len=3692   13133   0.001232   FLJ33100 fis, clone TRACH2000873 //cds=UNKNOWN /gb=AK057662 /gi=16553426 /ug=Hs.346406 /len=2308   13134   0.039034   sine oculis homeobox 2 (Drosophila) (SIX2), mRNA /cds=(283,1158) //gb=NM_016932 /gi=21314676 //ug=Hs.101937 /len=2141   13139   0.00527   chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) //gb=NM_004872 /gi=27545320 //ug=Hs.416495 /len=1709   13142   2.23E-04   DKFZP434D1335 protein (DKFZP434D1335), mRNA /cds=(78,1469) //gb=NM_015578 //gi=24308092 /ug=Hs.8258 /len=3389   13147   0.004536   likely ortholog of mouse gene trap locus 3   NM_013242   Hs.279818   NP		115.547 145	1100001		0.001470	13072
element; mRNA sequence /clone=IMAGE:205968 /clone_end=3' /gb=H58501 /gi=1011333 /ug=Hs.347143 /len=461  13081	8.3		* 0			*
element ; , mRNA sequence /clone=IMAGE:205968 /clone_end=3' /gb=H58501 /gi=1011333 /ug=Hs.347143 /len=461  13081					0.00	
/clone=IMAGE:205968 /clone_end=3' //gb=H58501 /gi=1011333 /ug=Hs.347143 /len=461  3081			. :			
/gb=H58501 /gi=1011333 /ug=Hs.347143 /len=461  13081		·	TV.			
13081   0.01925   Novel   SEQ.ID.No.8     13123   0.046432   BRAF35/HDAC2 complex (80 kDa)   (BHC80), mRNA /cds=(386,2290)   /gb=NM_016621 /gi=19923461   /ug=Hs.106826 /len=3692	<b>.</b>	-				9
13081   0.01925   Novel   SEQ.ID.No.8     13123   0.046432   BRAF35/HDAC2 complex (80 kDa) (BHC80), mRNA /cds=(386,2290) /gb=NM_016621 /gi=19923461 /ug=Hs.106826 /len=3692   Hs.181785     13133   0.001232   FLJ33100 fis, clone TRACH2000873 /cds=UNKNOWN /gb=AK057662 /gi=16553426 /ug=Hs.346406 /len=2308   Hs.181785     13134   0.039034   sine oculis homeobox 2 (Drosophila) (SIX2), mRNA /cds=(283,1158) /gb=NM_016932 /gi=21314676 /ug=Hs.101937 /len=2141     13139   0.00527   chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709   NM_015578   Hs.8258   NP (DKFZP434D1335), mRNA /cds=(278,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389     13147   0.004536   likely ortholog of mouse gene trap locus 3   NM_013242   Hs.279818   NP					1	
13123		,			0.04005	10001
(BHC80), mRNA /cds=(386,2290) /gb=NM_016621 /gi=19923461 //ug=Hs.106826 /len=3692  13133	15 05-705	11 400000				
/gb=NM_016621 /gi=19923461 //ug=Hs.106826 /len=3692  13133     0.001232     FLJ33100 fis, clone TRACH2000873 /cds=UNKNOWN /gb=AK057662 /gi=16553426 /ug=Hs.346406 /len=2308  13134     0.039034	NP_057705	Hs. 106826	NM_016621		0.046432	13123
/ /ug=Hs.106826 /len=3692  13133					1	
13133	•	:				
/cds=UNKNOWN /gb=AK057662 /gi=16553426 /ug=Hs.346406 /len=2308  13134	- 1				× /	
/gi=16553426 /ug=Hs.346406 /len=2308		Hs.181785	AK057662		0.001232	13133
13134 0.039034 sine oculis homeobox 2 (Drosophila) (SIX2), mRNA /cds=(283,1158) /gb=NM_016932 /gi=21314676 /ug=Hs.101937 /len=2141  13139 0.00527 chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709  13142 2.23E-04 DKFZP434D1335 protein (DKFZP434D1335), mRNA /cds=(78,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389  13147 0.004536 likely ortholog of mouse gene trap locus 3 NM_013242 Hs.279818 NP					,	
(SIX2), mRNA /cds=(283,1158) /gb=NM_016932 /gi=21314676 /ug=Hs.101937 /len=2141  13139    0.00527    chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709  13142    2.23E-04    DKFZP434D1335 protein (DKFZP434D1335), mRNA /cds=(78,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389  13147    0.004536 likely ortholog of mouse gene trap locus 3 NM_013242    Hs.279818 NP						
/gb=NM_016932 /gi=21314676 //ug=Hs.101937 /len=2141  13139	NP_058628	Hs.101937	NM_016932		0.039034	13134
/ug=Hs.101937 /len=2141				1.		:
13139   0.00527   chromosome 1 open reading frame 8   NM_004872   Hs.416495   NP   (C1orf8), mRNA /cds=(251,1222)   /gb=NM_004872 /gi=27545320   /ug=Hs.416495 /len=1709   NM_015578   Hs.8258   NP   (DKFZP434D1335), mRNA   /cds=(78,1469) /gb=NM_015578   /gi=24308092 /ug=Hs.8258 /len=3389   NM_013242   Hs.279818   NP   NP   NP   NP   NP   NP   NP   N		••;				
(C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709  13142 2.23E-04 DKFZP434D1335 protein (DKFZP434D1335), mRNA /cds=(78,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389  13147 0.004536 likely ortholog of mouse gene trap locus 3 NM_013242 Hs.279818 NP			•			
/gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709 13142 2.23E-04 DKFZP434D1335 protein (DKFZP434D1335), mRNA /cds=(78,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389 13147 0.004536 likely ortholog of mouse gene trap locus 3 NM_013242 Hs.279818 NP	NP_004863	Hs.416495	NM_004872		0.00527	13139
/ug=Hs.416495 /len=1709  13142 2.23E-04 DKFZP434D1335 protein (DKFZP434D1335), mRNA /cds=(78,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389  13147 0.004536 likely ortholog of mouse gene trap locus 3 NM_013242 Hs.279818 NP				1	. ,	
13142 2.23E-04 DKFZP434D1335 protein	•		7	/gb=NM_004872 /gi=27545320		,
(DKFZP434D1335), mRNA /cds=(78,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389 13147 0.004536 likely ortholog of mouse gene trap locus 3 NM_013242 Hs.279818 NP	-	o (A)				
/cds=(78,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389 13147 0.004536 likely ortholog of mouse gene trap locus 3 NM_013242 Hs.279818 NP	NP_056393	Hs.8258	NM_015578	DKFZP434D1335 protein	2.23E-04	13142
/gi=24308092 /ug=Hs.8258 /len=3389   13147   0.004536   likely ortholog of mouse gene trap locus 3   NM_013242   Hs.279818   NP	L		141	(DKFZP434D1335), mRNA		
13147   0.004536   likely ortholog of mouse gene trap locus 3   NM_013242   Hs.279818   NP		· ·				
				/gi=24308092 /ug=Hs.8258 /len=3389		
	NP_037374	Hs.279818	NM_013242		0.004536	13147
(GTL3), mRNA /cds=(257,838)	-			(GTL3), mRNA /cds=(257,838)		
/gb=NM_013242 /gi=8392874	•	,		/gb=NM_013242 /gi=8392874		
/ug=Hs.279818 /len=1278				/ug=Hs.279818 /len=1278		
	NP_110430	Hs.16390	NM_030803		0.013102	13161
(FLJ10035), mRNA /cds=(251,1132)		*		, · · · · · · · · · · · · · · · · · · ·		
/gb=NM_030803 /gi=24475809		•			. *	
/ug=Hs.16390 /len=2404	,					
	NP 115540	Hs.284168	NM 032164		0.012262	13164
(FLJ12298), mRNA /cds=(205,1890)			=:-:-:	1 • •		
/gb=NM_032164 /gi=14149844		-				·
, , , , , , , , , , , , , , , , , , ,			4,	/ug=Hs.284168 /len=2180		

C4		responding To Differentially Express d Genes			
Spot	p-value	• • •	Gn	Unigen	Protein
		<b>,</b>	Accession	Accession	Accession
			No.	No.	No.
13171	7.18E-04	hypothetical gene supported by	XM_064780		
		XM_064780 (LOC125750), mRNA	,	¢.	
13174	0.0261	AGENCOURT_8342650 NIH_MGC_100	BQ646970	Hs.349092	
		cDNA clone IMAGE:6269019 5', mRNA	*		
	· '	sequence /clone=IMAGE:6269019	yo		
• •	,	/clone_end=5' /gb=BQ646970			
	)	/gi=21771142 /ug=Hs.349092 /len=1081	•		
13175	0.046005	chromosome 1 open reading frame 9	NM 016227	Hs.108636	NP 05731
		(C1orf9), mRNA /cds=(125,4342)			
		/gb=NM_016227 /gi=7705321		·	
•	•	/ug=Hs.108636 /len=5919		:	
13179	0.00527	similar to KH domain RNA binding protein	XM 037438		<del></del>
	0.00027	QKI-5A (H. sapiens) (LOC135473),	7.II007.400		
		mRNA			
13180	0.014031	F-box only protein 7 (FBXO7), mRNA	NM_012179	Hs.5912	NP 03631
10100	0.014331	/cds=(281,1849) /gb=NM_012179	14141_012179	113.5312	INF_03031
	,	/gi=15812192 /ug=Hs.5912 /len=2165			
13181	0.020262	inositol(myo)-1(or 4)-monophosphatase 2	NIM 044047	11- 5753	ND OFFOO
ışıçı	0.029363		NW_014214	Hs.5753	NP_05502
		(IMPA2), mRNA /cds=(215,1081)	÷		
		/gb=NM_014214 /gi=7657235			* *
40400		/ug=Hs.5753 /len=1500			
13188	0.003603	hypothetical protein PRO2013	NM_021243	Hs.238205	-
		(PRO2013), mRNA /cds=(136,381)		*	
:	[	/gb=NM_021243 /gi=24308272			
		/ug=Hs.238205 /len=876			
13190	0.006566	membrane-spanning 4-domains,	NM_152852	Hs.17914	NP_69059
		subfamily A, member 6A (MS4A6A),	÷.		
		transcript variant 1, mRNA			
		/cds=(239,985) /gb=NM_152852	ļ		1
		/gi=23238237 /ug=Hs.17914 /len=1564		• •	
13191	0.011469	hypothetical protein FLJ11151	NM_018340	Hs.14992	NP_06081
		(FLJ11151), mRNA /cds=(95,1039)	_		
		/gb=NM_018340 /gi=8922900	i		
		/ug=Hs.14992 /len=2845		/	* *
13206	0.031117	spinal cord-derived growth factor-B	NM 025208	Hs.112885	NP_14912
		(SCDGF-B), transcript variant 1, mRNA		, , , , , ,	
	. *	/cds=(176,1288) /gb=NM_025208		,	
		/gi=15451919 /ug=Hs.112885 /len=3808	=		
13207	0.023148	ARP8 actin-related protein 8 (yeast)	NM 022899	Hs.124219	NP_07505
. 5201	0.020170	(ACTR8), mRNA /cds=(5,1129)	1111_022000	113.127213	1.1101.000
	,	/gb=NM 022899 /gi=12597636	1		
		/ug=Hs.124219 /len=2797			
13233	0.005674	synovial sarcoma translocation gene on	NIM 01630F	Ho 0774	ND 05700
10233	0.003074		NM_016305	Hs.9774	NP_05738
		chromosome 18-like 2 (SS18L2), mRNA	l e	1	
		/cds=(99,332) /gb=NM_016305			
	l .	/gi=10047103 /ug=Hs.9774 /len=817	1	1	ł –

		nding To Differentially Expressed Genes		Hypertension	
Spot	p-value	Description	Gene	Unigene	Protein
	=		Accession	Accession	Accession
			No.	No.	No.
13236	0.005674	glutamate receptor, metabotropic 6	NM 000843	Hs.248131	NP 000834
		(GRM6), mRNA /cds=(179,2812)			_
		/gb=NM 000843			
		/gi=6006006/ug=Hs.248131 /len=6122	~*.		
13243	0.031117	HSPC163 protein (HSPC163), mRNA	NM_014184	Hs.108854	NP_054903
10210	0.001111	/cds=(34,453) /gb=NM_014184	011101	113.100004	-00 1000
		/gi=7661823 /ug=Hs.108854 /len=652			1.
13247	8 48F-05	phosphoserine phosphatase (PSPH),	NM 004577	Hs.56407	NP 004568
102-11	0.401-03	mRNA /cds=(20,697) /gb=NM_004577	14141_004377	113.50407	_004300
• ."		/gi=21614545 /ug=Hs.56407 /len=1432		161	;
13254	0.00527	FLJ14397 (FLJ14397), mRNA	NM 032779	Un 070094	ND: 116169
132,34	0.00527		NIVI_032779	Hs.270981	NP_116168
		/cds=(14,511) /gb=NM_032779			*
40070	0.00000	/gi=14249437 /ug=Hs.270981 /len=1579	D. 1700000		
13279	0.003603	UI-E-EJ0-ahr-e-11-0-UI.s1 UI-E-EJ0	BU739063	Hs.58668	
-00		cDNA clone UI-E-EJ0-ahr-e-11-0-UI 3',			
		mRNA sequence /clone=UI-E-EJ0-ahr-e-			
		11-0-UI /clone_end=3' /gb=BU739063			
		/gi=23676884 /ug=Hs.58668 /len=1345			
13280	0.006106	cDNA FLJ13792 fis, clone	AK023854	Hs.154751	
		THYRO1000072, weakly similar to			
		MYOSIN LIGHT CHAIN KINASE,		*	1,.
	·	SMOOTH MUSCLE AND NON-MUSCLE		.•(	
		ISOZYMES (EC 2.7,1.117). /cds=(9,1337)	•		
		/gb=AK023854 /gi=10435918			
	,	/ug=Hs.154751 /len=2184	*		
13281	5.96E-04	cDNA FLJ11379 fis, clone	AK021441	Hs.200113	
		HEMBA1000469. /gb=AK021441			
		/gi=10432627 /ug=Hs.200113 /len=1672		`,	
13287	0.020482	mRNA; cDNA DKFZp686B2110 (from	AL832120	Hs.432506	-
	٠.	clone DKFZp686B2110) /gb=AL832120			
•		/gi=21732663 /ug=Hs.432506 /len=4383		s .	
13315	6.03E-05	partial RANBP7 gene for	AJ295844		
		RanBP7/importin7 and partial ZNF143			
	·	gene			
13320	0.023148	cDNA FLJ23879 fis, clone LNG13743.	AK074459	Hs.352648	
10020	0.020110	/gb=AK074459 /gi=18677071	,	110.002010	٠
		/ug=Hs.352648 /len=1514			
13335	5 96E-04	hypothetical protein FLJ12118	NM 024537	Hs.381043	NP_078813
10000	0.002-04	(FLJ12118), mRNA /cds=(24,1718)	024007	113.001040	141 _07 00 13
- w		/gb=NM_024537 /gi=13375694			
	9	/ug=Hs.381043 /len=1843	·	Θ	
13337	3 02 = 04	similar to putative (H.sapiens)	XM_058647		
1000/	3.02E-04	(LOC122704), mRNA (=AL135998.6)	AIVI_030047		
12244	0.022440		NIM 047000		ND 000400
13344	U.ŲZ3148 	hypothetical protein FLJ20085	NM_017660		NP_060130
12255	0.00004.4	(FLJ20085), mRNA	A1 020000	Us 105001	
13355	0.036914	mRNA; cDNA DKFZp313E1815 (from	AL833098	Hs.125031	
		clone DKFZp313E1815) /gb=AL833098	. n		1
		/gi=21733689 /ug=Hs.125031 /len=1937		<u> </u>	

		nding To Diff r ntially Expressed Genes			
spot	p-valu	D scription	Gene	Unigene	Protein
• •			Accession	Accession	Accession
<u> </u>	0.04005	overte not bin din a vertein 0 (OCDD0)	No.	No.	No.
13367	0.01925	oxysterol binding protein 2 (OSBP2)	AF288742	*	
40000	0.007004	gene, complete cds	1		
13386	0.027691	neuron navigator 1 (NAV1), mRNA	NM_020443	Hs.6298	NP_065176
		/cds=(348,5972) /gb=NM_020443			
		/gi=27262621 /ug=Hs.6298 /len=11365			
13405	1.06E-04	qw21c02.x1 NCI_CGAP_Ut4 cDNA clone	Al290157	Hs.387096	
		IMAGE:1991714 3' similar to contains Alu	,		•
		repetitive element;contains element L1			
	· .	repetitive element ;, mRNA sequence		0	
		/clone=IMAGE:1991714 /clone_end=3'		A	
	i	/gb=Al290157 /gi=3931823	0.		
		/ug=Hs.387096 /len=571	*	* /	
13410	0.039034	EST(nz03d07.s1 NCI_CGAP_GCB1	AA740773		
		IMAGE:1286701)			
13419	0.003505	EST(oa56h11.r1 NCI_CGAP_GCB1	AA746385		
		clone IMAGE:1309029 5' contains		*	
		MER10.b3 MER10 MER10 repeat)	***		
13423	0.020482	mRNA; cDNA DKFZp686E1027 (from	AL832759	Hs.269418	
	0.020.02	clone DKFZp686E1027) /gb=AL832759	/ 12002100	113.200-110	· ·
	1.7	/gi=21733340 /ug=Hs.269418 /len=5327			_
13443	0.011469	unknown protein	AAA88036		
13444		EST(ye47c11.r1 clone 120884 5')	T96079		NP 598014
13459		N-ethylmaleimide-sensitive factor (NSF),	<del></del>	Hs.108802	
13433	0.001403		NM_006178	ITS. 100002	NP_006169
•		mRNA /cds=(61,2295) /gb=NM_006178	. #.*	* :	
40467	0.042570	/gi=11079227 /ug=Hs.108802 /len=3960	4 4 6 6 6 6 6 6		NE doctor
13467	0.043576	EST(zt04d06.r1 NCI_CGAP_GCB1 clone	AA280235		NP_005728
10.40.4	0.045.04	IMAGE:712139 5')			
13484	3.34E-04	hypothetical protein FLJ10956	NM_018283	Hs.144407	NP_06075
		(FLJ10956), mRNA /cds=(181,675)		•	
	(1)	/gb=NM_018283 /gi=8922791			
=	1111	/ug=Hs.144407 /len=2022			
13486	0.002054	catenin (cadherin-associated protein),	NM_003798	Hs.58488	NP_00378
	-	alpha-like 1 (CTNNAL1), mRNA	* '		
		/cds=(44,2248) /gb=NM_003798			·
		/gi=4503128 /ug=Hs.58488 /len=2446			
13515	0.012262	EST(hh87d03.x1 NCI_CGAP_GU1 clone	AW627545		
		IMAGE:2969765 3' contains Alu repeat)	1 :		
	, i				
13561	0.004203	EST (yr44h03.s1 Soares fetal liver spleen	H62537		ni.
		1NFLS IMAGE:208181)			٠.
13562	0.046005	AGENCOURT_6653840 NIH_MGC_116	BM924828	Hs.181174	
		cDNA clone IMAGE:5761286 5', mRNA			
:		sequence /clone=IMAGE:5761286			
		/clone_end=5' /gb=BM924828		1	,
					ľ
13565	0.002044	/gi=19375207 /ug=Hs.181174 /len=1422 EST ni39e06.s1 NCI_CGAP_Lu1 cDNA	A A 522700		· · · · ·
13303	0.002044		AA522708		
	·	clone IMAGE:979234 3' similar to			
		contains Alu repetitive element; contains	(X)		
•		MER10.t2 MER10 repetitive element;		I	,

Gen s	Correspo	nding To Differentially Expressed Genes	in Figure 12 -	Hypertension	1
	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
	·	·	No.	No.	No.
13582	0.007578	mRNA; cDNA DKFZp586M1819 (from	AL834255	Hs.355753	NP_848934
		clone DKFZp586M1819) /cds=(1,795)			-
	,	/gb=AL834255 /gi=21739805	*		
		/ug=Hs.355753 /len=1723		* .	*
13592	6.03E-05	hypothetical gene supported by	XM 074528		
		XM_074528 (LOC123829), mRNA			
13604	0.039034	sialyltransferase 6 (N-acetyllacosaminide	NM 174963	Hs.48793	NP 777632
		alpha 2,3-sialyltransferase) (SIAT6),		7	
		transcript variant 1, mRNA	â-		,
		/cds=(178,1512) /gb=NM_174963		,	
		/gi=28373067 /ug=Hs.48793 /len=2478	,		
				7.	
13606	0.002054	phosphoribosylaminoimidazole	NM_006452	Hs.117950	NP_006443
		carboxylase,		,	
		phosphoribosylaminoimidazole	1.		
		succinocarboxamide synthetase (PAICS),		•	
		mRNA /cds=(206,1483) /gb=NM_006452			
·		/gi=17388802 /ug=Hs.117950 /len=3322			
					* .
13628	0.016974	hypothetical protein FLJ22378	NM 025078	Hs.288284	NP 079354
*		(FLJ22378), mRNA /cds=(52,564)			
		/gb=NM_025078 /gi=13376629			
		/ug=Hs.288284 /len=2143	4.7		1
13638	0.036914	protein tyrosine phosphatase, receptor	NM 002844	Hs.79005	NP_002835
	•	type, K (PTPRK), mRNA /cds=(221,4543)	<del></del>	,	
		/gb=NM_002844 /gi=18860901			0
		/ug=Hs.79005 /len=5982			
13639	0.001596		NM 002914	Hs.139226	NP_002905
19	,	(RFC2), mRNA /cds=(208,1272)	_ `		-
		/gb=NM_002914 /gi=4506486			
		/ug=Hs.139226 /len=1709	```		
13644	0.008722		BM544964	Hs.406354	
		cDNA clone IMAGE:5588748 5', mRNA			
		sequence /clone=IMAGE:5588748		,	
*		/clone_end=5' /gb=BM544964			
		/gi=18776658 /ug=Hs.406354 /len=1184			
13647	0.002465	signal transducer and activator of	NM_139276	Hs.321677	NP 644805
	γ.	transcription 3 (acute-phase response			
	4	factor) (STAT3), transcript variant 1,			•
X.		mRNA /cds=(241,2553) /gb=NM_139276	·		
•	,*	/gi=21618339 /ug=Hs.321677 /len=3455		ı	
		1 3 1 2 1 5 1 5 5 5 5 7 4 9 1 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	*		
13659	0.012262	hypothetical protein (HSPC016), mRNA	NM_015933	Hs.397853	NP_057017
		/cds=(39,233) /gb=NM_015933			
		/gi=7705430 /ug=Hs.397853 /len=384			· ·
13661	0.001465	KIAA1198 protein, partial cds	AB033024	Hs.175475	
	3.551,50	/cds=UNKNOWN /gb=AB033024	5000024	1.0.17.0470	
		/gi=6330393 /ug=Hs.175475 /len=6090			
	l	rgi-0000000 rug-1 is. 1 / 04/ 3 /icii-0090	<u> </u>	1	L

		nding To Differentially Expressed Gen			Duckste
Spot	p-value	Description	Gene	Unigene	Protein
	)		Accession	Accession	Accession
			No.	No.	No.
13672	0.032959	six transmembrane epithelial antigen of	NM_012449	Hs.61635	NP_036581
		the prostate (STEAP), mRNA	1.7		·
		/cds=(201,1220) /gb=NM_012449	.*		
		/gi=22027487 /ug=Hs.61635 /len=1330		*	
13677	0.00527	KIAA1377 protein, partial cds	AB037798	Hs.188790	
	(	/cds=UNKNOWN /gb=AB037798	,		*
		/gi=7243134 /ug=Hs.188790 /len=3916	· · · · · · · · · · · · · · · · · · ·	1	
13692	0.036914	cDNA FLJ38575 fis, clone	AK095894	Hs.376206	
		HCHON2007046./gb=AK095894	::		
		/gi=21755244 /ug=Hs.376206 /len=2134			
13704	0.001033	hypothetical protein DKFZp547I224	NM_020221	Hs.240321	
٠. ٠.		(DKFZp547l224), mRNA	_	• .	
		/cds=(3147,3455) /gb=NM_020221			
		/gi=9910201 /ug=Hs 240321 /len=4714		* *	
13735	0.003079	lectin, galactoside-binding, soluble, 8	NM 006499	Hs.4082	NP 006490
,	0.000010	(galectin 8) (LGALS8), mRNA	1111_000 100	1.0.1002	-000 101
	-	/cds=(384,1463) /gb=NM_006499			
		/gi=21361353 /ug=Hs.4082 /len=2593		i i	
13752	0.020363	V-ets erythroblastosis virus E26	AK001630	Hs.18063	NP 005229
10102	0.029303	oncogene homolog 1 (avian), cDNA	AK001030	115.10003	NF_00322
		FLJ10768 fis, clone NT2RP4000150			
	• = 1	I		· ·	
	-	/cds=UNKNOWN /gb=AK001630			
12770	0.000400	/gi=7023001 /ug=Hs.18063 /len=2833	DC020420	U6 40004	
13770	0.020482	Similar to hypothetical protein FLJ22789,	BC029120	Hs.48994	
		clone MGC:34762 IMAGE:5189049,	:	•	
•	* .	mRNA, complete cds /cds=(22,1833)		*	
•		/gb=BC029120 /gi=20810106			
		/ug=Hs.48994 /len=2085			
13782	0.024587	citrate synthase (CS), nuclear gene	NM_004077	Hs.239760	NP_004068
		encoding mitochondrial protein, mRNA	0.0		
		/cds=(1,1401) /gb=NM_004077			
		/gi=4758075 /ug=Hs.239760 /len=1401			
13783	0.002844	centrin, EF-hand protein, 2 (CETN2),	NM_004344	Hs.82794	NP_00433
		mRNA /cds=(48,566) /gb=NM_004344			
·		/gi=4757901 /ug=Hs.82794 /len=1087			
13785	0.041547	Transcriptional co-activator with PDZ-	AK025216	Hs.24341	NP_05628
		binding motif (TAZ), cDNA: FLJ21563 fis,	*		
		clone COL06445 /cds=UNKNOWN			
	100	/gb=AK025216 /gi=10437684			
		/ug=Hs.24341 /len=1750			
13792	1.55E-04	hypothetical protein MGC30052	NM 144721	Hs.143692	NP_653322
		(MGC30052), mRNA /cds=(35,703)			
	,	/gb=NM 144721 /gi=21389506			
•	}	/ug=Hs.143692 /len=2260			
13793	2 08F-05	FLJ12671 Hypothetical protein, mRNA;	AL096734	Hs.301904	NP_11224
		cDNA DKFZp434M011 (from clone	1, 12000704	1.10.00 1007	``` <i>-</i> ' <i>``^</i>
		PODIAN DIVI EPADAMO EL LILOJII CIONO		1 '	ı
				İ	
		DKFZp434M011) /cds=UNKNOWN /gb=AL096734 /gi=5419867	* *		

		nding To Differentially Expressed Genes			
Spot	p-value	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
	-		No.	No.	No.
13794	2.23E-04	myosin VI (MYO6), mRNA	NM_004999	Hs.118483	NP_004990
	,	/cds=(140,3997) /gb=NM_004999			• •
*		/gi=4826845 /ug=Hs.118483 /len=5212			•
13795	8.48E-05	hypothetical protein FLJ21302	NM_022901	Hs.128071	NP_075052
		(FLJ21302), mRNA /cds=(91,1203)			
0.		/gb=NM_022901 /gi=12597640			
		/ug=Hs.128071 /len=3160			·
13814	0.012262	mRNA for KIAA0292 gene, partial cds.	AB006630	Hs.201668	
	*	/cds=(1,5152) /gb=AB006630		1.	
	· ·	/gi=2564331 /ug=Hs.201668 /len=6542			
13816	0.007056	mRNA for FLJ00005 protein, partial cds.	AK000005	Hs.367690	
		/cds=(1,338) /gb=AK000005 /gi=7209310			
- 1		/ug=Hs.367690 /len=4706			<b>)</b> .
13829	2.63E-05	FLJ11463 fis, clone HEMBA1001608	AK021525	Hs.288888	
	1	/cds=UNKNOWN /gb=AK021525		,	
		/gi=10432722 /ug=Hs.288888 /len=1898			
13843	0.016974	ankyrin repeat domain 10 (ANKRD10),	NM 017664	Hs.172572	NP_060134
		mRNA /cds=(136,1398) /gb=NM_017664	_		_
		/gi=8923103 /ug=Hs.172572 /len=2509			
				·	
13857	0.007056	mRNA full length insert cDNA clone	AL109709	Hs.167456	
•		EUROIMAGE 43432. /gb=AL109709			
		/gi=9187596 /ug=Hs.167456 /len=2091		• .	
13887	0.012262	EST (qh80g11.x1	Al249016		NP_115602
	2	Soares_fetal_liver_spleen_1NFLS_S1			
	. ,	IMAGE:1851044 3')			•
13891	0.003893	cDNA FLJ38641 fis, clone.	AK095960	Hs.24831	
		HHDPC2003983. /gb=AK095960			
		/gi=21755328 /ug=Hs.24831 /len=2685			
13895	0.002844	cDNA FLJ23712 fis, clone HEP12427.	AK074292	Hs.44526	
		/gb=AK074292 /gi=18676853			
		/ug=Hs.44526 /len=2170		9	
13896	0.006816	UI-H-FL1-bfx-j-06-0-UI.s1	BU620821	Hs.12420	
		NCI_CGAP_FL1 cDNA clone UI-H-FL1-			· '
		bfx-j-06-0-UI 3', mRNA sequence			**
		/clone=UI-H-FL1-bfx-j-06-0-UI	9.		
		/clone end=3' /gb=BU620821			
		/gi=23287036 /ug=Hs.12420 /len=1123		-0)	*
13910	0.001033	EST(wm16d01.x1 NCI_CGAP_Ut4 cDNA	AI887638		ŗ
		clone IMAGE:2436097 3')			
13923	0.002054	mRNA for KIAA1754 protein, partial cds.	AB051541	Hs.28501	NP_203755
. 5 4 20		/cds=(32,1816) /gb=AB051541			
•		/gi=12698052 /ug=Hs.28501 /len=4088			
13933	5 96F-04	EST(qx14c02.x1 NCI_CGAP_Lym12	Al358712		
	0.002 04	clone IMAGE:2001314 3' contains Alu	1, 110007 12		
			•		1
					ļ
13945	0 024587	and MER4 repeat) EST(tx88e11.x1 NCI_CGAP_Ut4 clone	Al690725		

		nding To Diff r ntially Expressed Genes			
Spot	p-value		Gene	Unigene	Protein
8			Accession	Accession	Accession
		*	No.	No.	No.
13946	0.048543	cDNA FLJ13536 fis, clone	AK023598	Hs.11493	
-		PLACE1006521. /gb=AK023598		·	
		/gi=10435577 /ug=Hs.11493 /len=2132			
13950	0.03489	hypothetical protein FLJ10330	NM_018061	Hs.342307	NP_06053
		(FLJ10330), mRNA /cds=(77,1717)	,		
		/gb=NM_018061 /gi=8922357		9	ē
		/ug=Hs.342307 /len=3239		*	
13952	3.69E-04	cDNA FLJ13342 fis, clone	AK023404	Hs.255890	*
	•	OVARC1001950. /gb=AK023404			0
		/gi=10435328 /ug=Hs.255890 /len=2490		*	- ·
13954	0.039267	EST nw48e08.s1 NCI_CGAP_Ew1	AA730589		
, .		IMAGE:1249862			
13956	9.44E-04	zh79h09.s1	W92715	Hs.59358	, manifest
		Soares_fetal_liver_spleen_1NFLS_S1		,	·
. ,.		cDNA clone IMAGE:418337 3', mRNA	,	.*	. *
		sequence /clone=IMAGE:418337			
٠ ٠٠		/clone_end=3' /gb=W92715 /gi=1421867			
	-	/ug=Hs.59358 /len=397			
13972	0.043576	zo15e02.s1 Stratagene colon (#937204)	AA130992	Hs.426360	
10012	0.040010	cDNA clone IMAGE:586970 3' similar to	7 0 1100002	,	: *
		contains Alu repetitive element; contains			
		element PTR5 repetitive element ;,			' '
•		mRNA sequence /clone=IMAGE:586970			_
	,	•	(	l	Į.
		/clone_end=3' /gb=AA130992			
		/gi=1692483 /ug=Hs.426360 /len=489	12		
13977	0.000722	EST(xo35e05.x1 NCI_CGAP_Ut1 clone	AW591304		
13977	0.008722		AVV591304		
42000	0.005075	IMAGE:2705984 3' contains Alu repeat)	A A 704 500	<del> </del>	
13982	0.005875	EST(nv54h12.r1 NCI_CGAP_Ew1 cDNA	AA721522	1	* -
44005	1 005 04	clone IMAGE:1233671)	4444		
14025	4.06E-04	EST zu07e12.r1 Soares_testis_NHT	AA421543		
		cDNA clone IMAGE:731182 5' similar to		**	-
		contains L1.t3 L1 repetitive element;	25.11		
14033	0.002625	EST yt98a02.r1	H96454		
		Soares_pineal_gland_N3HPG cDNA	<b>\</b>		
		clone IMAGE:232298 5'			. •4
14049	0.024587	ox45b09.s1	AI051746	Hs.374613	
	İ	Soares_total_fetus_Nb2HF8_9w cDNA	•		
		clone IMAGE:1659257 3', mRNA			
		sequence /clone=IMAGE:1659257	*		
	]	/clone_end=3' /gb=Al051746 /gi=3307280			
		/ug=Hs.374613 /len=261			
14051	0.009349	EST(yh44h12.r1 Soares placenta Nb2HP	R26018		
		cDNA clone IMAGE:132647 5')			
14053	0.0261	EST (yg47c12.s1 Soares infant brain	R45369		
		1NIB IMAGE:35771 3') (contains Alu			
		repetitive element)			

	p-value	nding To Diff rentially Expressed Genes Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14061	0.018081	cDNA FLJ14201 fis, clone NT2RP3002955. /gb=AK024263	AK024263	Hs.193063	NO.
14062	0.002625	/gi=10436597 /ug=Hs.193063 /len=4077 P1-Cdc21 mRNA /cds=(1,2774) /gb=X74794 /gi=683749 /ug=Hs.154443 /len=3273	X74794	Hs.154443	
14066	0.043576	cDNA sequence FLJ13663 fis, clone PLACE1011646, highly similar to H.sapiens clone	AK023725		NP_003817
14069	0.001465	EST np77c06.s1 NCI_CGAP_Pr2 cDNA clone IMAGE:1132330 similar to contains Alu repetitive element;	AA622809		
14071	0.037092	EST (xs53a05.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2773328 3')	AW299710		
14074	0.007056	EST tf62g05.x1 NCI_CGAP_Brn23 cDNA clone IMAGE:2103896 3' similar to gb:L21934 STEROL O-ACYLTRANSFERASE (HUMAN);contains L1.t1 L1 repetitive element;			
14075	0.032959	EST (7j51c11.x1 Soares_NSF_F8_9W_OT_PA_P_S1	BF061350		
14084	0.004536	IMAGE:3389972 3') AGENCOURT_8241572 Lupski_dorsal_root_ganglion cDNA clone IMAGE:6180442 5', mRNA sequence /clone=IMAGE:6180442 /clone_end=5' /gb=BQ893048 /gi=22285062	BQ893048	Hs.390713	
14105	0.003603	/ug=Hs.390713 /len=975 Kruppel-like factor 12 (KLF12), transcript variant 1, mRNA /cds=(199,1407) /gb=NM_007249 /gi=21071073 /ug=Hs.23510 /len=10891	NM_007249	Hs.23510	NP_05736
14108	0.007056	EST (381219 MAGE resequences MAGK)	AW969142		
14118	0.039034	EST (EST388185 MAGE resequences, MAGN cDNA)	AW976076		
14121	2.01E-04	spindlin-like protein 2 (SPIN2), mRNA /cds=(494,1192) /gb=NM_019003 /gi=9506850 /ug=Hs.82577 /len=2483	NM_019003	Hs.82577	NP_061870
14133	0.01072	ox08a07.x1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1655700 3', mRNA sequence /clone=IMAGE:1655700 /clone_end=3' /gb=Al023766 /gi=3238810 /ug=Hs.434976 /len=432	AI023766	Hs.434976	

Spot	p-value	Description	Gene	Unigene	Protein
opot	p. value	- Cooribiion	Accession	Accession	Accession
			No.	No.	No.
14149	0.024587	UI-H-DH0-asb-n-04-0-UI.s1	BM989696	Hs.403907	140.
נהו דו	0.02-1001	NCI_CGAP_DH0 cDNA clone	15141303030	1113.405307	
8		IMAGE:5856963 3', mRNA sequence	0	7	*-);-
4 1	2.0.	/clone=IMAGE:5856963 /clone end=3'		•	12.5
		/gb=BM989696 /gi=19709085	. *		
. +		/ug=Hs.403907 /len=1055		8 1	
14156	0.027601	EST(nw90a09.s1 NCI CGAP Pr12 cDNA	ΔΔ037853		-
14 150	0.027091	clone IMAGE:1253848)	MA331033	,	
14160	ก กวกไล้รัว	EST(wd93f02.x1 NCI_CGAP_Lu24 cDNA	A1703393		700
14 100	0.020402	clone IMAGE:2339163 3')	A1703363	-	0.0
14161	0.007579	EST (RC3-HT0600-130400-013-h06	BE178244		
14 10 1	0.007376	HT0600)	DE 170244		
14171	0.016074	nz80g08.s1 NCI_CGAP_GCB1.cDNA	AA767226	Hs.368058	10 N N N 100°
. 14 17 1	0.010974	clone IMAGE:1301822 3', mRNA	<del>                                    </del>	11 18.300036	
		sequence /clone=IMAGE:1301822		0.	· 0
:		/clone_end=3' /gb=AA767226	1.	*	
. '	0 10	/gi=2818241 /ug=Hs.368058 /len=542			:
14172	0.014021	EST (DKFZp586G1121_s1	AL047586		NP_005702
14172	0.014931		MLU47566		INP_005702
		586)(synonym: hute1) clone DKFZp586G1121	. *		
14175	0.043544	ribosomal protein, large, P1 (RPLP1),	NM 001003	Hs.424299	NP_000994
14175	0.043344	mRNA /cds=(130,474) /gb=NM 001003	NIVI_001003	ITIS.424299	INF_000994
	*	, , , , , , , , , , , , , , , , , , , ,			
1/1/02	0 20E 06	/gi=16905511 /ug=Hs.424299 /len=512 EST(cDNA clone IMAGE:3212553 3')	BE467153		NP 059996
14184		EST(clone IMAGE:2509657 3')	Al955713	<del> </del>	NP_059996
14187		EST(RC5-HT0581-210300-021-B05	BE175638	<del>  ·</del>	ļ
14 107	0.00109	HT0581)	DE 173030		
14189	0.021791	NORE1 protein (NORE1), mRNA	NM_031437	Hs.238730	NP_113625
14 109	0.021761	/cds=(64,1236) /gb=NM_031437	NIVI_U3 1437	IUS.530130	INP_113025
14196	0.0064	/gi=13899264 /ug=Hs.238730 /len=3498 EST(yq06d08.s1 Soares fetal liver spleen	R91930		<del></del>
14 190	0.0201	1NFLS cDNA clone IMAGE:196143 3'	1291990	]	-8-
	*2				
**		similar to contains Alu repetitive element)			
14208	0.004536	EST (qh03a05.x1	Al222189		NP_002547
14200	0.004000	Soares NFL_T GBC S1	VIZZZ 109	•	141 _002547
		IMAGE:1843568 3')		-00	
14224	0.004203	af39g09.s1	AA628591	Hs.114288	<del></del>
17224	0.004203	Soares_total_fetus_Nb2HF8_9w cDNA	1,47050391	113.114200	. *
•		clone IMAGE:1034080 3' similar to		1 2 1	
		contains Alu repetitive element;, mRNA		10	-
		sequence /clone=IMAGE:1034080			
			]	*	
		/clone_end=3' /gb=AA628591			
	30.1	/gi=2540978 /ug=Hs.114288 /len=513	L	l	

Cmak		Description	in Figure 12 -		Protein
Spot	p-value	Description	Gene	Unig ne	* .
^	·		Accession	Accession	Accession
. 17. 2. 2			No.	No.	No.
14231	0.00489	wg85c11.x1	AI743032	Hs.310364	
		Soares_NSF_F8_9W_OT_PA_P_S1			
	. **	cDNA clone IMAGE:2371892 3' similar to			1
	a	contains Alu repetitive element;, mRNA		* .	
		sequence /clone=IMAGE:2371892			1
:		/clone_end=3' /gb=Al743032 /gi=5111320	4		
		/ug=Hs.310364 /len=562			
				<u> </u>	*
14240	0.005674	EST(cDNA clone IMAGE:1076536 3'	AA592920	7	-
		similar to TR:G56589 G56589 LONG			
		INTERSPERSED REPETITIVE DNA			1
		CONTAINING 7 ORF'S.; contains L1.t3			·
		L1 repetitive element;)	(¥) ÷		
14244	0.018081	cDNA FLJ11946 fis, clone	AK022008	Hs.323231	1
		HEMBB1000709. /gb=AK022008		10.02020	1
		/gi=10433321 /ug=Hs.323231 /len=3241			
4247	0.003332	clone IMAGE:4836898, mRNA	BC042527	Hs.434231	1
17271	0.000002	/gb=BC042527 /gi=27502923	DC042321	113.404201	
	· .	/ug=Hs.434231 /len=2935	• '		*
14240	0.020262	mitochondrion, complete genome	NC 001807	1277 - 477	<del>, ,</del>
				<del>                                     </del>	
14255	0.01925	EST wt25d05.x1 NCI_CGAP_Ut1 cDNA	AI962961		
	1	clone IMAGE:2508489 3' similar to	ſ····	ì	0
		contains Alu repetitive element; contains			
		L1.t1 L1 repetitive element;	20.732393	1	
14259	0.039034	BX109840	BX109840	Hs.269512	i 1
		Soares_fetal_heart_NbHH19W cDNA	,		
		clone IMAGp998M11793, mRNA			
		sequence		•	
		/clone=IMAGp998M11793_;_IMAGE:346	* .	1	,
	i ·	930 /gb=BX109840 /gi=27877881	•		
		/ug=Hs.269512 /len=749			
14270	0.005674	clone FLC0593 /cds=UNKNOWN	AF113701	Hs.346911	NP_000974
		/gb=AF113701 /gi=6855635	ļ	ľ	
		/ug=Hs.346911 /len=1562	*	-	- *
14276	0.003079	FLJ11984 fis, clone HEMBB1001348	AK022046	Hs.293922	
		/cds=UNKNOWN /gb=AK022046			
	ļ	/gi=10433365 /ug=Hs.293922 /len=3161		İ	}
14283	0.004536	ESTs, cDNA, 5' end /clone=GLCCSC04	AV720392	Hs.293568	
14200	0.004000	/clone_end=5' /gb=AV720392	7.0720002	113.250000	
		/gi=10817544 /ug=Hs.293568 (=ESTs,		4 1	
	1	Weakly similar to AF116721 112	<b>\</b>		
14204	0.047005	PRO2738)	NIM 004742	Ho 405000	ND 004704
14291	0.017885	calmodulin 2 (phosphorylase kinase,	NM_001743	Hs.425808	NP_001734
		delta) (CALM2), mRNA /cds=(69,518)	}	1	1
		/gb=NM_001743 /gi=20428653		1	
	<b></b>	/ug=Hs.425808 /len=1128			
14299	0.032959	cDNA FLJ12106 fis, clone	AK022168	Hs.296699	
	[	HEMBB1002702. /gb=AK022168			1
	1	/gi=10433503 /ug=Hs.296699 /len=2268	4		I .

		nding To Differentially Expressed Genes			
Shot	p-value	Description	Gene	Unigene	Protein
		*	Accession	Accession	Accession
14303	0.00100	CDC26 autumit of anaphaga promoting	No.	No.	No.
14303	0.00189	CDC26 subunit of anaphase promoting	NM_139286	Hs.3991	NP_644815
,	8	complex (CDC26), mRNA /cds=(360,617)			
		/gb=NM_139286 /gi=22027503	·		
4.00.4	0.00400	/ug=Hs.3991 /len=885	446000704	111 - 000001	-
14304	0.03489	cDNA: FLJ23111 fis, clone LNG07835.	AK026764	Hs.268231	
		/gb=AK026764 /gi=10439690		,	
4.4000	0.00400	/ug=Hs.268231 /len=2263	D0047000	·	
14322	0.03489	clone IMAGE:4297077, mRNA	BC017920	Hs.375771	
		/gb=BC017920 /gi=17389820			
1.1005	0.000440	/ug=Hs.375771 /len=1247	7) (-0-10-1		
		EST(clone ADBAOB04 5'.)	AV705982		NP_006633
14339	0.020482	7a19b02.x1 NCI_CGAP_GC6 cDNA	BE503478	Hs.281956	
		clone IMAGE:3219147 3' similar to			
		contains element MER36 repetitive	* -		
-		element ;, mRNA sequence		_	· · ·
/		/clone=IMAGE:3219147 /clone_end=3'			
		/gb=BE503478 /gi=9705875			, i
		/ug=Hs.281956 /len=356			
14341	0.021781	clone IMAGE:4808363, mRNA	BC035933	Hs.127317	,
	•	/gb=BC035933 /gi=23270829	ł		
	* .	/ug=Hs.127317 /len=1784		<u> </u>	<u></u>
14345	0.009349	mRNA; cDNA DKFZp586E1624 (from	AL110152	Hs.94030	
		clone DKFZp586E1624) /gb=AL110152			
		/gi=5817054 /ug=Hs.94030 /len=1341			<u></u>
14346		cDNA clone CBLAPH08 5'	AV739829		
14353	0.00489	cDNA FLJ31303 fis, clone	AK055865	Hs.350200	
		LIVER1000082. /gb=AK055865	-)		<u>,</u>
		/gi=16550700 /ug=Hs.350200 /len=2801		·	
14363	0.03489	ESTs, cDNA, 3' end	Al719659	Hs.372094	Į.
		/clone=IMAGE:2355101 /clone_end=3'		* *	[
		/gb=Al719659 /gi=5036915			<b>\</b> .
		/ug=Hs.372094 /len=528			;
14370	0.002843	EST(cDNA clone IMAGE:4604936 5'.)	BG434732		
14396		cDNA FLJ11437 fis, clone	AK021499	Hs.270791	
		HEMBA1001226 /cds=UNKNOWN			
		/gb=AK021499 /gi=10432694	•		
		/ug=Hs.270791		*	
14401	0.008133	df28a02.w1 Morton Fetal Cochlea cDNA	BI492702	Hs.345492	7
		clone IMAGE:2484387 3', mRNA		. A	
·		sequence /clone=IMAGE:2484387			
		/clone end=3' /gb=BI492702		0	
j		/gi=15332046 /ug=Hs.345492 /len=678			1
14402	0.001611	EST(cDNA clone IMAGE:1854705 3'	Al283553	1	
		similar to contains MER27 t1 MER27			
	1	repetitive element;)	l <sup>·</sup>	1	

Spot	p-value	nding To Differentially Expressed Genes Description	Gene	Unigene	Protein
opot	p raido		Accession .	Accession	Accession
	,	* /	No.	No.	No.
14414	0.039034	AV764634 MDS cDNA clone MDSBZE01	AV764634	Hs.270532	11021
	0.00000	5', mRNA sequence /clone=MDSBZE01			
		/clone end=5' /gb=AV764634			`
	*	/gi=10922482 /ug=Hs.270532 /len=1289			
*	-	791 10022-102749 110.27000271011 1200	.,		
14431	0.03304	cDNA clone e443-f /He443-f Adult heart,	T82627	City of City	<del> </del>
1 1 40 1	0.00001	Clontech	102021	[·	
14451	4.06F-04	No significant match	SEQ.ID.No.13	<del> </del>	7
		No significant match	SEQ.ID.No.48	11	
14455		No significant match, ORF+3(135~404)	SEQ.ID.No.50	·	
14478		EST(Erythroid Cells (LCB:ax library)	BG943485	<del> </del>	NP 714916
17710	0.010013	cDNA clone ax38c12 random)	1	{	1 - 1 - 5 1
14498	0.01925	Novel, ORF+3(144~262)	SEQ.ID.No.86	<del>,, , , , , , , , , , , , , , , , , , ,</del>	
14504		No significant match (ORF:none)	SEQ.ID.No.22	<del> </del>	
14517		xq09e02.x1 NCI_CGAP_Ut1 cDNA clone	AW517395	Hs.445194	
	0.000100	IMAGE:2750138 3' similar to contains Alu	7.000	113.445154	
	0)0	repetitive element;, mRNA sequence	*		
	· .:	/clone=IMAGE:2750138 /clone_end=3'	*		
		/gb=AW517395 /gi=7155477			
		/ug=Hs.445194 /len=519		* '	•
14521	0.03304	HSC15D092 normalized infant brain	Z39248	Hs.27328	- 30
1-021	0.00004	cDNA cDNA clone c-15d09 3', mRNA	200240	113.27020	
		sequence /clone=c-15d09 /clone_end=3'		*	
		/gb=Z39248 /gi=562440 /ug=Hs.27328			
		/len=352		[	l
14528	0.041254	EST (EST34421 Embryo, 6 week I cDNA	AA330691	<del> </del>	<del></del>
14020	0.041204	5' end similar to EST containing L1	7 4 100000 1.		
		repeat)		1	) ·
14539	0.031117	wg09e08.x1	AI744543	Hs.205679	<del> </del>
17000	0.001117	Soares_NSF_F8_9W_OT_PA_P_S1		113.200070	
,.	*	cDNA clone IMAGE:2364614 3', mRNA		1	
		sequence /clone=IMAGE:2364614	9		
1		/clone_end=3' /gb=Al744543 /gi=5112831			Į.
	6	/ug=Hs 205679 /len=521	ĺ		l
14551	0.000763	EST (ng23f02.s1 NCI_CGAP_Ov2 cDNA	AA502813		<del></del>
14001	0.003703	clone IMAGE:930267 similar to contains	7 0 10020 10	,	,
		Alu repetitive element)	,		
14553	0.008473	hypothetical protein H41 (H41), mRNA	NM 017548	Hs.283690	NP_06001
14000	0.000473	/cds=(324,1100) /gb=NM 017548	14101_017540	113.200090	
÷	_	//gi=24475997 /ug=Hs 283690 /len=3346			
14559	0.042472	EST hb88d08.x1 NCI_CGAP_Ut2 cDNA	AW439829	· · · · ·	NP_62012
14338	0.0421/3	clone IMAGE:2890287 3'	VAA-2905à		_02012
	I	TOTOLIC HINTOL: 2030201 3		1 "	<del> </del>
14562	G SEE OA	EST(CR34d06.x1 Jia bone marrow	AI755024	ı	1

		nding To Differentially Express d Genes			
Spot	p-valu	Description	Gene	Unigene	Protein
	=	: 340.	Accession	Accession	Accession
4 4 505	0.000040	, , , , , , , , , , , , , , , , , , ,	No.	No.	No.
14565	0.009349	oq98a10.x1 NCI_CGAP_Co12 cDNA	AI074369	Hs.386367	
		clone IMAGE:1594362 3 similar to			
		contains Alu repetitive element;, mRNA			
		sequence /clone=IMAGE:1594362		-	
	·	/clone_end=3' /gb=Al074369 /gi=3401013			
		/ug=Hs.386367 /len=478			
14568	0.027691	ribosomal protein, large, P0 (RPLP0),	NM_053275	Hs.406511	NP_444505
		transcript variant 2, mRNA			
		/cds=(111,1064) /gb=NM_053275	÷		١.
	<u> </u>	/gi=16933545 /ug=Hs.406511 /len=1148			
14612	0.03489	EST (AL536815 LTI_FL013_FBrn1 clone	AL536815		
		CS0DF020YK05 5')			
14613	0.017885	neuroepithelial cell transforming gene 1	NM_005863	Hs.25155	NP_005854
		(NET1), mRNA /cds=(147,1775)			
		/gb=NM_005863 /gi=19923326			
		/ug=Hs.25155 /len=3236			<u></u>
14614	0.029362		H56096		
	11	1NFLS cDNA clone IMAGE:203498 5'			
		similar to contains Alu repetitive element)			
14638	0.028573	602623674F1 NCI_CGAP_Skn4 cDNA	BG677029	Hs.123445	
		clone IMAGE:4748515 5', mRNA			1
		sequence /clone=IMAGE:4748515	·		
	)	/clone_end=5' /gb=BG677029			
		/gi=13908426 /ug=Hs.123445 /len=882			
14640	0.046005	EST(tz23h03.x1 NCI_CGAP_Ut2 clone	Al823691		
	•	IMAGE:2289461 3' contains L1.t2 L1	-		
-		repeat)			
14648	0.043934	mRNA; cDNA DKFZp667J1615 (from	AL713792	Hs.120388	2 2
		clone DKFZp667J1615) /gb=AL713792			
	,	/gi=19584550 /ug=Hs.120388 /len=4127	, ,		
14650	0.006816	clone IMAGE:4139786, mRNA, partial	BC007901	Hs.433279	
		cds /cds=(1,625) /gb=BC007901			
		/gi=14043927 /ug=Hs.433279 /len=1493			
14653	0.0261	EST (MR0-BT0798-280400-001-d04	BE095198		
		BT0798 cDNA)	1	,	·
14662	0.010015	EST(tt54e09.x1 NCI_CGAP_GC6 cDNA	Al656892	1.0	
		clone IMAGE:2244616 3' similar to		. *	] .
•		contains MER29.b3 MER29 repetitive			<b>\</b>
		element)			
14663	0.00527	EST(zs14a10.r1 NCI_CGAP_GCB1	AA243380		NP_057315
		cDNA clone IMAGE:685146 5')			-34,51
	0.040004	EST (xq76f01.x1 NCI_CGAP_HN11	AW265747	1	1
14672	0.013991	IEST (XQ/QIQT,XTNC) CGAF FINT	1/7/1/200141		

		nding To Differentially Expressed Genes				
Spot	p-value		G ne	Unigene	Protein	
		* .	Accession	Accession	Accession	
		1)1	No.	No.	No.	
14690	0.032959	cDNA FLJ35033 fis, clone	AK092352	Hs.156113		
	-	OCBBF2016590, weakly similar to CELL			· ·	
		SURFACE ANTIGEN 114/A10				
•		PRECURSOR. /cds=(407,934)		,		
•		/gb=AK092352 /gi=21750925	, ,	*		
		/ug=Hs.156113 /len=2884	• .			
4697	0.001465	EST00015 NCI CGAP Lu5 cDNA clone	BF707422	Hs.298289	X X	
		IMAGE:1568018 3', mRNA sequence				
		/clone=IMAGE:1568018 /clone_end=3'	*	4		
	à-	/gb=BF707422 /gi=11999083	•			
	•	/ug=Hs.298289 /len=858		*		
14708	0.039034	FLJ11397 fis, clone HEMBA1000622	AK021459	Hs.169068		
14700	0.00000	/cds=UNKNOWN /gb=AK021459	AIX02 1400	1113.103000	. *	
		/gi=10432651 /ug=Hs.169068 /len=1512	•			
14709	0.00190	Similar to hypothetical protein FLJ20378,	BC035643	Hs.202613		
14 <i>1</i> Ų9	0.00169	clone IMAGE:5547904, mRNA, partial	DC033043	I		
		cds /cds=(1,802) /gb=BC035643				
	000	/gi=23274249 /ug=Hs.202613 /len=1653		*		
4740	0.040040	'DUA DUA DUEZ ES (D. 100 (f.	4104000	11 100=50		
4712	0.012016	mRNA; cDNA DKFZp564D193 (from	AL049252	Hs.406752		
		clone DKFZp564D193) /gb=AL049252		9		
		/gi=4499993 /ug=Hs.406752 /len=3343				
14719	0.01925	EST(cDNA clone IMAGE:2387836 3'	AI760555		NP_65891	
	,	similar to contains Alu repetitive	. 00			
		element;contains element MER22			<b>1</b>	
	,	repetitive element ;)				
14721	0.031156	UI-H-ED0-axn-i-09-0-UI.s1	CA445401	Hs.204930		
		NCI_CGAP_ED0 cDNA clone UI-H-ED0-	* * * * *			
		axn-i-09-0-UI 3', mRNA sequence				
		/clone=UI-H-ED0-axn-i-09-0-UI	.*		**	
	ļ ,	/clone_end=3' /gb=CA445401			•	
•		/gi=24809821 /ug=Hs.204930 /len=725				
14722	0.024491	cDNA FLJ11439 fis, clone	AK021501	Hs.287416	1	
		HEMBA1001299. /gb=AK021501				
	, N.	/gi=10432697 /ug=Hs.287416 /len=1500		,		
14723	0.027656	qm87e02.x1 NCI_CGAP_Lu5 cDNA	Al299478	Hs.303983		
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	clone IMAGE:1895738 3', mRNA	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			
	•	sequence /clone=IMAGE:1895738	*			
		/clone_end=3' /gb=Al299478 /gi=3957519	- 7.			
		/ug=Hs.303983 /len=438				
14727	0.036914	fh01f01.y1 NIH_MGC_17 cDNA clone	AW409578	Hs.279718		
7121	3.000014	IMAGE:2961144 3', mRNA sequence	7.44400070	113.273710		
		/clone=IMAGE:2961144 /clone end=3			]	
		/gb=AW409578 /gi=6935198			,	
1.4720	4 405 04	/ug=Hs.279718 /len=529	ALCOE 7700	11- 404700		
14736	4.48E-04	FLJ33160 fis, clone UTERU2000485	AK057722	Hs.124733		
	."	/cds=UNKNOWN /gb=AK057722	2		·	
	1	/gi=16553641 /ug=Hs.124733 /len=2328		1	,	

		nding To Differentially Expressed Genes			
Spot	p-yalue	Description	Gene	Unigene	Protein
			Accession	Acc ssion	Accession
			No.	No.	No.
14737	0.032959	clone IMAGE:5298326, mRNA	BC036198	Hs.369297	
-	*	/gb=BC036198 /gi=23271941			
•		/ug=Hs.369297 /len=3475			
14746	0.00223	tw36f05.x1 NCI_CGAP_Ut1 cDNA clone	Al889108	Hs.311004	
		IMAGE:2261793 3' similar to contains Alu		1	}
	1	repetitive element;, mRNA sequence			İ
		/clone=IMAGE:2261793 /clone_end=3'	- 8-		
		/gb=Al889108 /gi=5594272			1
		/ug=Hs.311004 /len=489			
14760	0.007334	control			
14766	0.029363	cDNA FLJ30301 fis, clone	AK054863	Hs.285728	
		BRACE2003217. /gb=AK054863			İ
		/gi=16549482 /ug=Hs.285728 /len=2186			
14770	1.46E-04	EST48277 Fetal spleen cDNA 3' end	AA342474	Hs.291585	
		similar to EST containing Alu repeat,			
·	- 18	mRNA sequence /clone end=3"		·	
(6)		/gb=AA342474 /gi=1994946			
		/ug=Hs.291585 /len=430			
14806	0.003893	cDNA FLJ14279 fis, clone	AK024341	Hs.250383	
		PLACE1005574. /gb=AK024341			
		/gi=10436703 /ug=Hs.250383 /len=2005	·	1	
14813	0.023148	ESTs, cDNA /clone=CS0DC008YI07	AL524742	Hs.6616	NP 114032
		/clone_end=5' /gb=AL524742	,,		
- 32		/gi=12788235 /ug=Hs.6616		-	1
14824	0.043934	ribosomal protein L5 (RPL5), mRNA	NM 000969	Hs.180946	NP 000960
		/cds=(63,956) /gb=NM_000969			
		/gi=14591908 /ug=Hs.180946 /len=1033	1		
14850	0.036914	cDNA: FLJ22698 fis, clone HSI12044.	AK026351	Hs.286241	
	0.000,017	/gb=AK026351 /gi=10439190		110.200211	-
•	×	/ug=Hs.286241 /len=1476		4	
14851	0.003079	UI-H-BW1-amm-h-09-0-UI.s1	BF512783	Hs.443691	
	0.0000	NCI_CGAP_Sub7 cDNA clone	DI 012:00	1,10.110001	*
* .	*	IMAGE:3070696 3', mRNA sequence	·		
		/clone=IMAGE:3070696 /clone_end=3'			
		/gb=BF512783 /gi=11597962	*	(A)	
		/ug=Hs.443691 /len=568			
14875	0.039034	RC1-NN0073-090500-012-f02 NN0073	AW898615	Hs.130729	
14,010	0.000004	cDNA, mRNA sequence /gb=AW898615	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	110.100720	· .
•	] ,	/gi=8062820 /ug=Hs.130729 /len=660	·		;
					1.00
14893	0.03480	EST375707 MAGE resequences, MAGH	AW963634	Hs.429581	
ددېد.	0.00708	cDNA, mRNA sequence /gb=AW963634	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1,13.423001	ľ
		/gi=8153470 /ug=Hs.429581 /len=750			1
	1	,,,,, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			1
		3		lí .	
14033	0.021627		SEO ID No 96		-
14933		No significant match, ORF-2(2~412)	SEQ.ID.No.96		
14933 14934		No significant match, ORF-2(2~412) No significant match			
	.0.009098	No significant match, ORF-2(2~412) No significant match (ORF:+1:1~102[102])	SEQ.ID.No.96 SEQ.ID.No.59		

Spot	p-valu	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14962	0.020319	No significant match,			
	*	ORF+3(30~140),+2(131~232)	SEQ.ID.No.72		1.
14964	0.001128	No significant match (ORF:-2:1~144[144])			
	+		SEQ.ID.No.67		

	i	TABLE 3F	Last areas - Last		1.000
Genes	Correspo	nding To Differ ntially Expressed Gene	s in Figure 13 - 0	Obesity	
		Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	0.044044	007	NIA 040000	No.	No.
.1	0.011644	vacuolar protein sorting 28 (yeast)	NM_016208	Hs.339697	NP_057292
	0	(VPS28), mRNA /cds=(62,727)			
	,	/gb=NM_016208 /gi=7705884 /ug=Hs.339697 /len=928	*		
2	0.043827	histone deacetylase 5 (HDAC5),	NM 139205	Hs.9028	NP 631944
. ~	,	transcript variant 2, mRNA	14141_139203	115.9020	NF_031944
		/cds=(305,3418) /gb=NM_139205			. ,
0.0	<b>→</b> .	/gi=21237798 /ug=Hs.9028 /len=5041	,	. 7 .	
18	0.026979	histone H1 (0)	X03473		- a
26		nudix (nucleoside diphosphate linked	NM_019094	Hs.355399	NP_061967
		moiety X)-type motif 4 (NUDT4), mRNA			
		/cds=(191,736) /gb=NM_019094			* * *.
		/gi=24432097 /ug=Hs.355399 /len=3652	. +		٠.
100		* *			
28	0.036211	602184410T1 NIH_MGC_42 cDNA	BF569051	Hs.352114	, , , , , , , , , , , , , , , , , , , ,
*		clone IMAGE:4300347 3', mRNA			
		sequence /clone=IMAGE:4300347	*	*	) <sub>=</sub>
٠	*	/clone_end=3' /gb=BF569051	•		
- 1		/gi=11642431 /ug=Hs.352114 /len=1899			
- 00	0.000004	001110			
38	0.008631	GPAA1P anchor attachment protein 1	NM_003801	Hs.4742	NP_003792
		(yeast) (GPAA1), mRNA /cds=(96,1961) /gb=NM_003801 /gi=6031166			
		/gb=NM_0038017gl=6031166 /ug=Hs.4742 /len=2047	*		*
64	0.010502	B-cell CLL/lymphoma 7B (BCL7B),	NM_001707	Hs.16269	NP_619713
04	0.010332	transcript variant 1, mRNA	14W_001707	115.10209	NF_019713
1.		/cds=(117,725) /gb=NM_001707			
		/gi=20336472 /ug=Hs.16269 /len=1690			
78	0.007994	mRNA, expressed in fibroblasts of	AB019409	7.	
		periodontal ligament, complete cds,			
1		clone:PDL-108			
101	0.011644	conserved gene amplified in	NM_005730	Hs.355816	NP_005721
- "	,	osteosarcoma (OS4), mRNA			
0.1	*	/cds=(306,1157) /gb=NM_005730		- 1	
		/gi=19923329 /ug=Hs.355816 /len=4833			
455					
103	0.00684	supervillin (SVIL), transcript variant 2,	NM_021738	Hs.154567	NP_068506
		mRNA /cds=(754,7398) /gb=NM_021738			- (),
		/gi=11496981 /ug=Hs.154567 /len=8300			
105	0.024072	MADS box transcription enhancer factor	NM_002397	Uc 70005	ND 002200
105	0.024312	2, polypeptide C (myocyte enhancer	VIVI_UU2397    	Hs.78995	NP_002388
		factor 2C) (MEF2C), mRNA			
		/cds=(402,1823) /gb=NM_002397	*		0)0
		/gi=19923214 /ug=Hs.78995 /len=4077	-		

Spot	p-value	Description	Gene	Unigene	Protein
				Accession	Accession
	, .	-	*	No.	No
106	0.023381	brother of CDO (BOC), mRNA	NM_033254	Hs.339352	NP_150279
		/cds=(133,3477) /gb=NM_033254			
		/gi=15147239 /ug=Hs.339352 /len=3534			
					*
. 111	0.046501	casein kinase 2, alpha prime polypeptide	NM_001896	Hs.82201	NP_001887
ļ .	*	(CSNK2A2), mRNA /cds=(164,1216)	•		
	=	/gb=NM_001896 /gi=4503096	,		
	5 12 1 2 1 2 1 2 1 1 2 1 1 2 1 1 2 1 1 2 1 1 1 2 1 1 1 2 1 1 2 1 1 1 2 1 1 1 2 1	/ug=Hs.82201 /len=1677			
131	0.014461	AD-012 protein (LOC55833)		- • .	
180	0.00000	(=AB040924 KIAA1491)	NM_018449		NP_060919.1
132	0.00922	phosphatidylinositol glycan, class C	NM_153747	Hs.433030	NP_714969
		(PIGC), transcript variant 1, mRNA			
		/cds=(312,1205) /gb=NM_153747	9		
		/gi=24430185 /ug=Hs.433030 /len=1514	. •	·	
148	0.046501	wl84f02.x1 NCI_CGAP_Brn25 cDNA	Al884779	Hs.380770	
		clone IMAGE:2431611 3', mRNA			
		sequence /clone=IMAGE:2431611	•		
		/clone_end=3' /gb=AI884779			
		/gi=5589943 /ug=Hs.380770 /len=527	24	,	
177	0.049308	G antigen 1	XP_010196		
208		ubiquitin-like 3 (UBL3), mRNA	NM_007106	Hs.173091	NP_009037
	. *	/cds=(110,463) /gb=NM_007106			
		/gi=6005927 /ug=Hs.173091 /len=3323		•	
210	0.028428	protein tyrosine phosphatase type IVA,	NM_003463	Hs.227777	NP_003454
		member 1 (PTP4A1), mRNA		·	
		/cds=(650,1171) /gb=NM_003463			
17		/gi=17986281 /ug=Hs.227777 /len=4394		ļ	
220	0.004070	staufon DNA hinding protein 2	NIM 014202	110 06970	ND 055209
230	0.024972	staufen, RNA binding protein, 2 (Drosophila) (STAU2), mRNA	NM_014393	Hs.96870	NP_055208
÷		/cds=(202,1641) /gb=NM_014393			
	Ì	/gi=7657624 /ug=Hs.96870 /len=4058		` :	
247	0.025245	G protein-coupled receptor Edg-2	Y09479	· ·	NP_476500
248		hemoglobin, beta (HBB), mRNA	NM 000518	Hs.155376	NP 000509
~ ,,	3.5 , 127 5	/cds=(51,494) /gb=NM_000518	1000010	1.0.100079	
		/gi=28302128 /ug=Hs.155376 /len=626	*		
250	8.95E-04	KIAA1243 protein (KIAA1243), mRNA	NM 014048	Hs.151076	NP_054767
		/cds=(388,801) /gb=NM_014048	<del>-</del> ,		
		/gi=7662513 /ug=Hs 151076 /len=1580			
251	7.33E-04	ATPase, Ca transporting, type 2C,	NM_014382	Hs.106778	NP_055197
	[	member 1 (ATP2C1), mRNA			-
		/cds=(236,2995) /gb=NM_014382			
		/gi=7656909 /ug=Hs.106778 /len=3637	i .		
282	6.62E-04	protein phosphatase 1, regulatory	NM_005398	Hs.303090	NP_005389
		(inhibitor) subunit 3C (PPP1R3C), mRNA			•
*		/cds=(58,1011) /gb=NM_005398			
		/gi=21314622 /ug=Hs.303090 /len=2524			
	L		<u>L</u>		L

Spot	p-value	Description	Gen	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
302	0.036549	origin recognition complex, subunit 2-like	NM_006190	Hs.41694	NP_006181
		(yeast) (ORC2L), mRNA			
		/cds=(215,1948) /gb=NM_006190			[ ,- ]
	w 1	/gi=21359879 /ug=Hs.41694 /len=2815			
318	0.011644	3'-phosphoadenosine 5'-phosphosulfate	NM_005443	Hs.3833	NP_005434
		synthase 1 (PAPSS1), mRNA			
	*	/cds=(27,1901) /gb=NM_005443		*	
:		/gi=20127474 /ug=Hs.3833 /len=2265			
319	2.54E-04	angiopoietin-like 1 (ANGPTL1), mRNA	NM_004673	Hs.241519	NP_004664
		/cds=(434,1909) /gb=NM_004673			
-8		/gi=16905518 /ug=Hs.241519 /len=2066			
1	Topic .				
320	0.013463	hypothetical protein DKFZp564K142	NM_032121	Hs.323562	NP_115497
	` .	similar to implantation-associated protein	*		, j
. 9		(DKFZp564K142), mRNA			
		/cds=(30,1037) /gb=NM_032121	*		
.0	8	/gi=14149774 /ug=Hs.323562 /len=2241	* E		
					No.
356	0.001656	RAB21, member RAS oncogene family	NM_014999	Hs.184627	NP_055814
	*** **	(RAB21), mRNA /cds=(256,933)			
		/gb=NM_014999 /gi=7661921			,
	5 004045	/ug=Hs.184627 /len=2630	ND 00 1500		
359	0.001915	plakophilin 2=X97675 plakophilin 2b	NP_004563		
200	0.047040	(ORF 38%)	V70000		ND OZEGOE
388		MacMarcks	X70326	115 45 40 72	NP_075385
390	0.009313	UDP-galactose transporter related	NM_005827	Hs.154073	NP_005818
	* .	(UGTREL1), mRNA /cds=(88,1056)	0		
	ļ	/gb=NM_005827 /gi=5032212			
202	0.000400	/ug=Hs.154073 /len=1186	AF050447		
393	0.028428		AF253417		
204	0.014464	gene, complete cds	AK024026	Ua 267910	
394	0.014401	FLJ11874 fis, clone HEMBA1007073 /cds=UNKNOWN /gb=AK021936	AK021936	Hs.367819	, !
		I	3 -		
- 78		/gi=10433239 /ug=Hs.367819 /len=2737	* *	*	·
402	0.016640	mRNA for KIAA1250 protein, partial cds.	AB033076	Hs.9873	<del> </del>
402	0.010048	/cds=(140,5473) /gb=AB033076	(Σροσόριο	113.90/3	,
	l · .	//gi=14133246 /ug=Hs.9873 /len=7264			1
415	0.036653	H4 histone family, member G (H4FG),	NM_003542	Hs.46423	NP 003533
415	0.020053	mRNA /cds=(1,312) /gb=NM_003542	TAIVI_003542	113.40423	IAL _003333
		/gi=21071024 /ug=Hs.46423 /len=390	,		
419	0.041270	SYNCRIP	AB035725	<del>                                     </del>	NP 062770
421		eukaryotic translation initiation factor 2-	NM 004836	Hs.102506	NP 004827
741	0.020420	alpha kinase 3 (EIF2AK3), mRNA	114111_004000	1.13.102000	7004027
		/cds=(303,3650) /gb=NM_004836	1.		
	+	/gi=21361154 /ug=Hs.102506 /len=4662			
		/gi-2 130 1 134 /dg-1 15, 102300 /left-4002		(	
423	0.013463	biotinidase (BTD), mRNA /cds=(36,1667)	NM 000060	Hs.78885	NP 000051
72.0	0.010403	/gb=NM_000060 /gi=4557372	1000000		
· ·		/ug=Hs.78885 /len=2016			
L	I	1/49-1 13.1 0000 NEH-ZUTU ,		L.,	<del></del>

Spc	ot	p-value	Description	Gene	Unigene	Protein
	٠,	*		Accession No.	Accession No.	Accession No.
455	5	0.038855	tyrosine 3-monooxygenase/tryptophan 5-	NM 006826	Hs.74405	NP_006817
			monooxygenase activation protein, theta			T
	- 1		polypeptide (YWHAQ), mRNA			
*		٠,	/cds=(120,857) /gb=NM_006826	* .		
<u> </u>			/gi=21464103 /ug=Hs.74405 /len=2166	*		
462	_		erg protein (ets-related gene)	M21535		NP_004440
533	3	0.014461	hemoglobin, gamma G (HBG2), mRNA	NM_000184	Hs.386655	NP_000175
		. :	/cds=(54,497) /gb=NM_000184	* *		7
-	$\dashv$	0.044070	/gi=28302132 /ug=Hs.386655 /len=583		101010	1.5
560	3	0.044072	activating transcription factor 4 (tax-	NM_001675	Hs.181243	NP_001666
8			responsive enhancer element B67)	*- *		* :
			(ATF4), mRNA /cds=(882,1937) /gb=NM_001675 /gi=4502264			
- 1		9	/ug=Hs.181243 /len=2015	*		
570	<u>,                                    </u>	0.00987	cycA gene for cyclin A	X68303		
574	_		mRNA for KIAA1274 protein, partial cds.	AB033100	Hs.300646	
		Ÿ.0202.10	/cds=(265,2850) /gb=AB033100	, ,5000, 100	1.0.0000,10	*
	Ì		/gi=20521819 /ug=Hs.300646 /len=4569			
		,				
596	6	0.02722	tubulin, alpha 3 (TUBA3), mRNA	NM_006009	Hs.433394	NP_006000
	- {		/cds=(100,1455) /gb=NM_006009			*
-			/gi=17986282 /ug=Hs.433394 /len=1677		8	· N
<u> </u>						
602	2	0.004871	helicase with zinc finger domain (HELZ),		Hs.3085	NP_055692
		,	mRNA /cds=(146,5974) /gb=NM_014877	÷ .	*	
×			/gi=7661883 /ug=Hs.3085 /len=6274			
608	ă	0.046805	OTF3 gene	Z11900		•
638	$\rightarrow$		non-SMC (structural maintenance of	NM 145080	Hs.284295	NP 659547
	-	3.525550	chromosomes) element 1 protein	11.10000	. 10.20-1200	
			(NSE1), mRNA /cds=(24,794)			
-	7.		/gb=NM_145080 /gi=21489972			
	-		/ug=Hs.284295 /len=992	*		
64	1	0.046805	mRNA for KIAA1119 protein, partial cds.	AB032945	Hs.172506	
			/cds=(1,3783) /gb=AB032945			
10.2	_	-722	/gi=6329707 /ug=Hs.172506 /len=7438			
643	3	0.003746	glucose regulated protein, 58kDa	NM_005313	Hs.13751	NP_005304
			(GRP58), mRNA /cds=(90,1607)		·	
	Ė		/gb=NM_005313 /gi=21361656			-
67:	3	0.038653	/ug=Hs.13751 /len=2074 fatty-acid-Coenzyme A ligase, long-chain	NM 022077	Hs.81452	NP_075266
] 37.	٦	Ų.UJ00J3	4 (FACL4), transcript variant 2, mRNA	141VI_U428//	115.01402	ME_01:0500
	0.5	*.	/cds=(507,2642) /gb=NM_022977		=	
		,	/gi=12669908 /ug=Hs.81452 /len=5356			
•	- 1	1 -	1.9 .= 1.1.1.1.1.9	I	1	

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
·	•			No.	No.
683	0.008631	serine (or cysteine) proteinase inhibitor,	NM_001085	Hs.234726	NP_001076
		clade A (alpha-1 antiproteinase,		1	-
		antitrypsin), member 3 (SERPINA3),			
		mRNA /cds=(26,1327) /gb=NM_001085			
· .		/gi=9665246 /ug=Hs.234726 /len=1534			9
684	0.038855	tumor necrosis factor receptor	NM_001065	Hs.159	NP_001056
	. : .	superfamily, member 1A (TNFRSF1A),	*		
		mRNA /cds=(282,1649) /gb=NM_001065		]	*
	-	/gi=23312372 /ug=Hs.159 /len=2236			
1989	2 2 2 2 2 2				
689	0.009313	PTK2 protein tyrosine kinase 2 (PTK2),	NM_153831	Hs.740	NP_722560
		transcript variant 1, mRNA		٠,	
		/cds=(231,3389) /gb=NM_153831			
000	0.040400	/gi=27886591 /ug=Hs.740 /len=4453	10044000	11 00700	
690	0.013463		AB011090	Hs.23763	·
- 1		/cds=(1,1953) /gb=AB011090			* • • • •
602	0.040200	/gi=3043559 /ug=Hs.23763 /len=4617	NINA 004070	11- 75404	ND 004007
692	0.049308	chitinase 3-likè 1 (cartilage glycoprotein-	NM_001276	Hs.75184	NP_001267
		39) (CHI3L1), mRNA /cds=(127,1278) /gb=NM_001276 /gi=4557017			
		/ug=Hs.75184 /len=1925	¥.00	99.	
723	0.01911	G protein-coupled receptor kinase 5	NM 005308	Hs.211569	NP 005299
1 123	0.013,1	(GPRK5), mRNA /cds=(221,1993)	000000	115.211509	NF_003299
}		/gb=NM_005308 /gi=4885348			Ç.
- *-		/ug=Hs.211569 /len=2557			
727	0.01004	loss of heterozygosity, 11, chromosomal	NM 014622	Hs.152944	NP_055437
		region 2, gene A (LOH11CR2A), mRNA	<del>-</del>	. *	7
		/cds=(1054,2367) /gb=NM 014622	0.00		
1	,	/gi=7657310 /ug=Hs.152944 /len=3380			
-				}	
730	0.013463	PTD016 protein (LOC51136), mRNA	NM_016125	Hs.30154	NP_057209
		/cds=(183,809) /gb=NM_016125	·.		
		/gi=21361528 /ug=Hs.30154 /len=1917	· ·		<u> </u>
750	0.032277	cDNA FLJ37412 fis, clone	AK094731	Hs.356300	
] .	, "	BRAMY2028796. /gb=AK094731		1	
	<b> </b>	/gi=21753846 /ug=Hs.356300 /len=2442		l l	
<del></del>	0.000=1=		200000	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	<del></del>
757	0.036549	603021120F1 NIH_MGC_114 cDNA	BI488592	Hs.380956	
, ,		clone IMAGE:5191733 5', mRNA			
		sequence /clone=IMAGE:5191733			-
1		/clone_end=5' /gb=BI488592	, i.e.	1	
761	0.00220	/gi=15327820 /ug=Hs.380956 /len=988	NIM 022420	Ha 205474	ND 440047
101	0.00326	caldesmon 1 (CALD1), transcript variant	NM_033138	Hs.325474	NP_149347
		1, mRNA /cds=(230,2611) /gb=NM_033138 /gi=15149460			·
		/ug=Hs.325474 /len=3610		l ·	
771	0.001015	zinc finger protein (ZFD25) (62% aa)	AB027251	<u> </u>	NP_057304
	0.001910	Lenio miger protein (ZFD23) (02 /0 dd)	MUULICUI	L	INF_00/304

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
<u> </u>				No.	No.
779	0.00632	myosin, heavy polypeptide 9, non-	NM_002473	Hs.146550	NP_002464
		muscle (MYH9), mRNA /cds=(1,5883)			
		/gb=NM_002473 /gi=22507396	v.		
		/ug=Hs.146550 /len=7274			
780	0.009313	X-box binding protein 1 (XBP1), mRNA	NM_005080	Hs.149923	NP_005071
		/cds=(49,834) /gb=NM_005080			
		/gi=14110394 /ug=Hs.149923 /len=1836	÷		
	12				
786	0.005382	syntaxin 8 (STX8), mRNA	NM_004853	Hs.380938	NP_004844
	- 1	/cds=(151,861) /gb=NM_004853			•
		/gi=4759187 /ug=Hs.380938 /len=979			
795	0.023381	procollagen C-endopeptidase enhancer	NM_013363	Hs.8944	NP_037495
N.		2 (PCOLCE2), mRNA /cds=(197,1444)	, ,		
		/gb=NM_013363 /gi=16904386			
		/ug=Hs.8944 /len=1988	· · · · · · · · · · · · · · · · · · ·		4
796	0.017843	poly(rC) binding protein 2 (PCBP2),	NM_005016	Hs.63525	NP_114366
↓.		transcript variant 1, mRNA			
		/cds=(89,1189) /gb=NM_005016	•		
		/gi=14141167 /ug=Hs.63525 /len=1362			
797	0.032277	C-type (calcium dependent,	NM_005752	Hs.287364	NP_005743
- [		carbohydrate-recognition domain) lectin,	÷ .		* .
-		superfamily member 1 (cartilage-		120	
1	7 .	derived) (CLECSF1), mRNA	•		
	÷	/cds=(80,673) /gb=NM_005752			
		/gi=5031636 /ug=Hs.287364 /len=673			
811	0.024972	sterol carrier protein 2 (SCP2), mRNA	NM_002979	Hs.75760	NP_002970
		/cds=(22,1665) /gb=NM_002979			·
	<u></u>	/gi=19923232 /ug=Hs.75760 /len=2572			191
815	0,036549	SnRNP assembly defective 1 (SAD1),	NM_006590	Hs.12820	NP_006581
1	ļ	mRNA /cds=(493,1467) /gb=NM_006590			
	. "	/gi=5730024 /ug=Hs.12820 /len=2166	1	. 00	
<b></b>					
824	0.004961	lipoprotein lipase (LPL), mRNA	NM_000237	Hs.180878	NP_000228
	,	/cds=(175,1602) /gb=NM_000237	• •		
A==	2 22 / 2 = =	/gi=4557726 /ug=Hs.180878 /len=3549	<u> </u>	1	×,
833	0.024972	NADH dehydrogenase (ubiquinone) 1	NM_002491	Hs.109760	NP_002482
*2		beta subcomplex, 3, 12kDa (NDUFB3),			*
		mRNA /cds=(253,549) /gb=NM_002491		· .	
		/gi=4505360 /ug=Hs.109760 /len=693	•	ļ	
0.2.4	0.04044	Antrophon 2 (TODANI 2) - DAIA	NIM COSTO 4	11- 400000	ND costá
834	0.01911	tetraspan 3 (TSPAN-3), mRNA	NM_005724	Hs.100090	NP_005715
		/cds=(218,979) /gb=NM_005724	*		
		/gi=21264581 /ug=Hs.100090 /len=1842			*
937	0.024250	novino/orginina nanotitiva nantiivi O	NIM OACOOD	He 407444	ND 057447
837	0.034358	serine/arginine repetitive matrix 2	NM_016333	Hs.197114	NP_057417
10.0	, 8 8	(SRRM2), mRNA /cds=(226,8484)			3 (3)
		/gb=NM_016333 /gi=19923465		ĺ	1
البيال الم	<u> </u>	/ug=Hs.197114 /len=9027			

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Acc ssion	Accession No.
857	0.00632	mitochondrial carrier 1 (MTCH1), nuclear	NM 014341	Hs.279939	NP 055156
		gene encoding mitochondrial protein,	- <del></del>	7	,
		mRNA /cds=(1,1119) /gb=NM_014341	ı		. 1
		/gi=7657344 /ug=Hs.279939 /len=1890			
858	0.011644	calpastatin (CAST), transcript variant 2,	NM 173060	LI'- 250000	ND 775005
000	0.011044	mRNA /cds=(155,2215) /gb=NM 173060		Hs.359682	NP_775085
		/gi=27765084 /ug=Hs.359682 /len=4296			
	·	/gi=2//00004/ug=118.00002/Ne11=4290			
867	0.016648	insulin-like growth factor binding protein	NM_001553	Hs.119206	NP 001544
	i i	7 (IGFBP7), mRNA /cds=(23,871)	7		_
		/gb=NM_001553 /gi=4504618			
		/ug=Hs.119206 /len=1124	*		
887	0.023381		NM_006451	Hs.109643	NP_006442
		protein 1 (PAIP1), mRNA			7: "
	:	/cds=(188,1627) /gb=NM_006451			
	4	/gi=17511254 /ug=Hs.109643 /len=2764			,
890	0.017843	tropomyosin 1 (alpha) (TPM1), mRNA	NM_000366	Hs.77899	NP_000357
		/cds=(151,1005) /gb=NM_000366			- 50
	0 1	/gi=27597084 /ug=Hs.77899 /len=1265			
891	0.00632	ubiquitin-conjugating enzyme E2E 3	NM_006357	Hs.4890	NP_006348
		(UBC4/5 yeast) (UBE2E3), mRNA		1	
		/cds=(120,743) /gb=NM_006357		**	
	0.044070	/gi=5454145 /ug=Hs.4890 /len=1294	1114		N. P. Tanana a .
892	0.041279	transmembrane 4 superfamily member 6	NM_003270 ·	Hs.121068	NP_003261
		(TM4SF6), mRNA /cds=(104,841)			- (3)
		/gb=NM_003270 /gi=21265115		<b>.</b> .	i i
896	0.005383	/ug=Hs 121068 /len=2069 hypothetical protein FLJ32949	NM 173812	Hs.125472	NP 776173
. 030	0.000002	(FLJ32949), mRNA /cds=(1,2277)	1/3012	Ins. 123472	INP_//01/3
١ .	~	/gb=NM_173812 /gi=27883873			ľ
1		/ug=Hs.125472 /len=2277			
899	0.032277	chromosome 21 open reading frame 59	NM 017835	Hs.5811	NP_067077
		(C21orf59), mRNA /cds=(361,777)			
		/gb=NM_017835 /gi=8923436			
	· .	/ug=Hs.5811 /len=1245			
900	0.001319	RAB11A, member RAS oncogene family	NM_004663	Hs.75618	NP_004654
- **		(RAB11A), mRNA /cds=(104,754)			] -
		/gb=NM_004663 /gi=20149549			]
		/ug=Hs.75618 /len=2474			
903	0.016648	S100 calcium binding protein A10	NM_002966	Hs. 400250	NP_002957
,		(annexin II ligand, calpactin I, light	-		1
		polypeptide (p11)) (S100A10), mRNA			
}		/cds=(112,405) /gb=NM_002966	<b>,</b>		
L	L	/gi=4506760 /ug=Hs.400250 /len=649	L <u></u>	<u></u>	I

Spot	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession No.	Accession No.
907	0.028428	splicing factor proline/glutamine rich	NM_005066	Hs.180610	NP_005057
		(polypyrimidine tract binding protein			
	4	associated) (SFPQ), mRNA			
-		/cds=(86,2209) /gb=NM_005066			* (
		/gi=4826997 /ug=Hs.180610 /len=3071	·		
916	0.014461	LIM and senescent cell antigen-like	NM_004987		NP_004978
*		domains 1 (LIMS1) =U09284, PINCH			
		protein			771
919	0.034358	putative protein tyrosine phosphatase	U93051	Hs.356062	NP_000305
		(PTEN) mRNA, complete cds	**	;	
		/cds=(1,1212) /gb=U93051 /gi=1916351			[] <sub>4</sub> *
3	10.00000	/ug=Hs.356062 /len=1212			2
922	0.038855	unc-50 related (DKFZp564G0222),	NM_014044	Hs 13370	NP_054763
	*	mRNA /cds=(1186,1965)		. 1	
		/gb=NM_014044 /gi=24432047			9.0
943	0.014461	/ug=Hs.13370 /len=2189 XIST, coding sequence "a" mRNA (locus	V56400	110 252402	
943	0.014401	DXS399E). /gb=X56199 /gi=37987	V 20 199	Hs.352403	
		/ug=Hs.352403 /len=1614			
952		mRNA; cDNA DKFZp451O194 (from	AL832029	Hs.22559	
902	Q.002.00	clone DKFZp451O194) /gb=AL832029	/\L002020	113.22335	
		/gi=21732569 /ug=Hs.22559 /len=5226			
963	0.003866	nucleoporin 153kDa (NUP153), mRNA	NM 005124	Hs.211608	NP_005115
		/cds=(201,4628) /gb=NM_005124	_	, , , , , , , , , ,	
-	r	/gi=24430145 /ug=Hs.211608 /len=5687			э
	•				-
966	0.01911	CGI-81 protein (DREV1), mRNA	NM_016025	Hs.279583	NP_057109
		/cds=(249,1100) /gb=NM_016025			
	·	/gi=19923448 /ug=Hs.279583 /len=3163			ļ
967	0.007397	hepatoma-derived growth factor (high-	NM_004494	Hs.89525	NP_004485
	ļ	mobility group protein 1-like) (HDGF),			
		mRNA /cds=(316,1038) /gb=NM_004494	,	* 1	
		/gi=4758515 /ug=Hs.89525 /len=2376			
972	0.010816	glioma tumor suppressor candidate	NM_015710	Hs.421907	NP 056525
] "," [	0.010010	region gene 2 (GLTSCR2), mRNA	11111 0 137 10	113.74.1307	_000020
		/cds=(53,1489) /gb=NM_015710	,	Ì	
,		/gi=21359905 /ug=Hs.421907 /len=1610		*	
					, <del>,</del> ,
974	0.046501	putative Rab5 GDP/GTP exchange	NM_014504	Hs.187660	NP_055319
		factor (RABEX5), mRNA /cds=(78,1553)			-
*		/gb=NM_014504 /gi=7657495	*		
		/ug=Hs.187660 /len=3740	*		
1001	4.86E-04	RAD23 B (S. cerevisiae) (RAD23B),	NM_002874	Hs.404283	NP_002865
	· .	mRNA /cds=(352,1581) /gb=NM_002874	. ,		
	,	/gi=19924138 /ug=Hs.404283 /len=2943			. 1
1055	0.000000	LIEO' and DNA and LIEO and DNA	AD047740		7
1055	0.030302	U50' snoRNA and U50 snoRNA	AB017710	يـــــــــــــــــــــــــــــــــــــ	

Spot	p-valu	Description	Gene	Unigene	Prot in
				Accession	Accession
				No.	No.
1090	0.00274	protein phosphatase methylesterase-1	NM_016147	Hs.63304	NP_057231
l .		(PME-1), mRNA /cds=(100,1260)			
1		/gb=NM_016147 /gi=7706644			
		/ug=Hs.63304 /len=2484			
1117	0.044748	CDK5 regulatory subunit associated	NM_025197	Hs.20157	NP_788276
		protein 3 (CDK5RAP3), mRNA			14
		/cds=(994,2253) /gb=NM_025197			
4404	0.000004	/gi=13376787 /ug=Hs.20157 /len=2538		<u> </u>	ND 004540
1181	0.023381	NADH dehydrogenase (ubiquinone) 1,	NM_004549	Hs.193313	NP_004540
	*	subcomplex unknown, 2, 14.5kDa			
		(NDUFC2), mRNA /cds=(151,510)	a ·		*
1		/gb=NM_004549 /gi=19923255	*		*
1101	0.007207	/ug=Hs.193313 /len=2168	NIM OOCCOO	Uo 267629	ND 006600
1184	0.007397		NM_006699	Hs 367638	NP_006690
1		2 (MAN1A2), mRNA /cds=(521,2446)		<u> </u>	
		/gb=NM_006699 /gi=5729912 /ug=Hs.367638 /len=2792		ĺ	
1193	0.038855	CGI-100 protein (CGI-100), mRNA	NM 016040	Hs.348996	NP_057124
1 193	0.030000	/cds=(113,802) /gb=NM_016040	NIVI_0 16040	FIS. 340990	INP_057 124
		/gi=19923441 /ug=Hs.348996 /len=3635			
i i		/g =19925441/dg=118.540990/left=3055	ν'	- 00	
1194	0.016648	proteasome (prosome, macropain)	NM_002790	Hs.76913	NP 002781
	0.010010	subunit, alpha type, 5 (PSMA5), mRNA	002700	11.0.700 10	
		/cds=(86,811) /gb=NM_002790			
1		/gi=23110941 /ug=Hs.76913 /len=1023	: ==	*	
1206	0.043827	ATP synthase, H transporting,	NM 005174	Hs.155433	NP 005165
× 1		mitochondrial F1 complex, gamma	_		
		polypeptide 1 (ATP5C1), mRNA			-
1		/cds=(32,925) /gb=NM_005174			
- 18		/gi=4885078 /ug=Hs.155433 /len=1078	·		
1209	0.016648	membrane protein, palmitoylated 6	NM_016447	Hs.108931	NP_057531
		(MAGUK p55 subfamily member 6)			
1 1		(MPP6), mRNA /cds=(300,1922)			4
45	· · ·	/gb=NM_016447 /gi=21361597			
		/ug=Hs.108931 /len=2201	T.		
1223		KIAA0874	AB020681		NP_056023
1228	0.007994	cDNA FLJ14076 fis, clone	AK024138	Hs.406835	
1		HEMBB1001925. /gb=AK024138	1		
		/gi=10436445 /ug=Hs.406835 /len=2124	1		0
1005	0.040040	PDNA -DNA DICEZ-FO44000 (5-	AL 050207	Un 66700	V 18
1235	U.U10648 	mRNA; cDNA DKFZp564A026 (from	AL050367	Hs.66762	
1	1	clone DKFZp564A026) /gb=AL050367	* ><	-	
1237	0.040300	/gi=4914600 /ug=Hs.66762 /len=3958 similar to rat nuclear ubiquitous casein	NIM 022721	Hs.118064	ND 072560
1231	0.049308	kinase 2 (NUCKS), mRNA /cds=(67,558)	NM_022731	113.110004	NP_073568
1	}	/gb=NM_022731 /gi=12232386			
		/ug=Hs.118064 /len=1811			
		rag- 113. 11000+ /ICH- 1011		*	
<u> </u>	ــــــــــــــــــــــــــــــــــــــ	<u> </u>	<del></del>		

Spot	p-value	Description	Gene	Unigene	Protein
- 1			Accession No.	Accession	Accession
1,000				No.	No.
1250	0.030302	nuclear protein, ataxia-telangiectasia	NM 002519	Hs.89385	NP 002510
		locus (NPAT), mRNA /cds=(35,4318)	4		
		/gb=NM 002519 /gi=4505430			194
		/ug=Hs.89385 /len=5895	;		
1285	0.003866	butyrophilin, subfamily 3, member A1	NM_007048	Hs.284283	NP 008979
		(BTN3A1), mRNA /cds=(360,1901)		. 10.20	
	( ) ·	/gb=NM_007048 /gi=19923378		:	
	(2	/ug=Hs.284283 /len=3452			
1292	0.026653	cellular retinoic acid binding protein 1	NM 004378	Hs.346950	NP_004369
	-1	(CRABP1), mRNA /cds=(75,488)	· · · · · · · ·		
	. * *	/gb=NM_004378 /gi=4758051		1	*
		/ug=Hs.346950 /len=735			
1335	0.042116	hypothetical protein MGC11316	NM 032932	Hs.7985	NP_116321
		(MGC11316), mRNA /cds=(116,226)	552552		
- 1		/gb=NM_032932 /gi=14249729		<b>.</b>	
		/ug=Hs.7985 /len=781			
1336	0.020453	Novel mRNA from chromosome 1, which	AL 096857	Hs.69559	NP_055987
1000	0.020100	has similarities to BAT2 genes	/ LOSGOO	113.03000	_000507
		/cds=(58,8163) /gb=AL096857			*
		/gi=5541862 /ug=Hs.69559 /len=10174			
1363	0.047541	nucleoporin Nup43 (Nup43), mRNA	NM 024647	Hs.53263	NP_078923
1000	0.047.041	/cds=(646,1176) /gb=NM_024647	14141_024047	113.00200	_070323
		/gi=21362033 /ug=Hs.53263 /len=3118			
1375	0.023381	similar to embryonic seven-span	XM_059770		
1373	0.023301	transmembrane protein-like protein (H.	XIM = 0221.10		
1.		sapiens) (LOC135428), mRNA			
1406	0.020453	fibrillin 1 (Marfan syndrome) (FBN1),	NM_000138	Hs.750	NP_000129
1400	0.020400	mRNA /cds=(134,8749) /gb=NM_000138		113.730	_000123
311		/gi=24430140 /ug=Hs.750 /len=9749			] .
			*	) ′	
1424	0.034358	RAP1A, member of RAS oncogene	NM_002884	Hs.865	NP 002875
1727	7.007000	family (RAP1A), mRNA /cds=(313,867)	1.4.4002.004	1.13.555	_002070
н		/gb=NM_002884 /gi=4506412		{	,
		/ug=Hs.865 /len=1579			
1426	0.020453	chemokine (C-C motif) ligand 13	NM_005408	Hs.11383	NP_005399
720	.020400	(CCL13), mRNA /cds=(76,372)	000,400	1.13.11000	
		/gb=NM 005408 /gi=22538799		1	* .
		/ug=Hs.11383 /len=861			100.
1441	0.034358	RE1-silencing transCRiption factor	NM_005612		NP 005603
'''	5.55-556	(REST)	000012	1	
1442	0.041279	amyotrophic lateral sclerosis 2 (juvenile)	NM 015049	Hs.154248	NP_055864
1.72	9.071270	chromosome region, candidate 3	1.4.40.10040	11.13.107270	000004
		(ALS2CR3), mRNA /cds=(382,3126)	-		
1	*	/gb=NM_015049 /gi=13027379			
Į		/ug=Hs.154248 /len=6470		1.	į.
		ray 110. TOTATO NOTITOTIO	+		-2.
	L	<del></del>	<u> </u>		

Snot	p-value	Description	Gene	Unigene	Protein
Opot	p-value	)	Accession No.	Accession	Accession
-			7.000000.0	No.	No.
1443	0.004569	cDNA FLJ13106 fis, clone	AK023168	Hs.12707	
		NT2RP3002455, highly similar to mRNA			
		for KIAA0678 protein. /gb=AK023168			
		/gi=10434970 /ug=Hs.12707 /len=3985	, ,	]	
			N .		
1444	3.17E-04	cDNA: FLJ23165 fis, clone LNG09846.	AK026818	Hs.279898	
		/gb=AK026818 /gi=10439763			1,81
4 4 5 4	0.040000	/ug=Hs.279898 /len=2117	1114 000000	11 11000	ND
1451	0.049308	polymerase (RNA) II (DNA directed)	NM_002696	Hs.14839	NP_002687
		polypeptide G (POLR2G), mRNA			*
200		/cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828			e '
1453	0.01004	methyl-CpG binding domain protein 2	NM 015832	Hs.25674	NP_056647
1400	0.01004	(MBD2), transcript variant testis-specific,	14141_013032	113.23074	141 _000047
		mRNA /cds=(230,1138) /gb=NM_015832	*		<b>!</b>
		/gi=21464120 /ug=Hs.25674 /len=2792		. 5.5	
İ		, g		* -	
1454	0.041279	Dmx-like 1 (DMXL1), mRNA	NM_005509	Hs.181042	NP 005500
	;	/cds=(81,9164) /gb=NM_005509	7		
	3	/gi=21536473 /ug=Hs.181042			
1		/len=11072			
1456	0.009313	CGI-74 protein (CGI-59), mRNA	NM_016019	Hs.7194	NP_057103
,^		/cds=(1,1209) /gb=NM_016019			
1.175	0.01001	/gi=7706309 /ug=Hs.7194 /len=2296			
1473	0.01004	heat shock 70kDa protein 5 (glucose-	NM_005347	Hs.75410	NP_005338
		regulated protein, 78kDa) (HSPA5),			
	1.0	mRNA /cds=(205,2169) /gb=NM_005347 /gi=21361242 /ug=Hs.75410 /len=3925			
		/gi-21361242/ug-ns./5410/leii-3925 	*		
1485	0.016648	SRY (sex determining region Y)-box 5	NM 152989	Hs.87224	NP_821078
1400	0.010040	(SOX5), transcript variant B, mRNA	102000	113.07224	021070
1,0		/cds=(373,2625) /gb=NM_152989	- 35		W.,
	. :	/gi=23308714 /ug=Hs.87224 /len=4492			
1492	0.041279	pleiomorphic adenoma gene-like 1	NM_006718	Hs.75825	NP_006709
		(PLAGL1), transcript variant 2, mRNA	-		
-		/cds=(2242,3633) /gb=NM_006718	-		
		/gi=27894292 /ug=Hs.75825 /len=4816			
1497	0.012483	hypothetical protein MGC45474	NM_152369	Hs.234101	
		(MGC45474), mRNA /cds=(218,2035)	*	1	,
		/gb=NM_152369 /gi=22748794	(		. 1
1507	0.040040	/ug=Hs.234101 /len=2384	NIM O15000	Un 100057	VD 057004
1507	0.048643	ribosomal protein S27-like (RPS27L),	NM_015920	Hs.108957	NP_057004
		mRNA /cds=(73,327) /gb=NM_015920 /gi=18490988 /ug=Hs.108957 /len=523	*	*	
1515	0.026653	ATPase, H transporting, lysosomal	NM_001690	Hs.281866	NP_001681
.5.15	0.920000	70kDa, V1 subunit A, isoform 1	001030	1.10.201000	
	."	(ATP6V1A1), mRNA /cds=(67,1920)		{	
	*	/gb=NM_001690 /gi=19913423	,		
	· ·	/ug=Hs.281866 /len=4567			
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Spot	p-value	Description	Gene	Unigene	Protein
- 10 4 3			Accession No.	Accession	Accession
٤.	*			No.	No.
1526	0.01004	similar to rat myomegalin (LOC64182),	NM 022359	Hs.333512	NP_071754
*		mRNA /cds=(336,1268) /gb=NM_022359		-	-
		/gi=21314705 /ug=Hs.333512 /len=1717		[ ·	
					* *
1528	0.017843	tubulin, alpha, ubiquitous (K-ALPHA-1),	NM_006082	Hs.334842	NP_006073
*		mRNA /cds=(68,1423) /gb=NM_006082			
,		/gi=5174476 /ug=Hs.334842 /len=1596	र्व क	8	
15/5	0.00000				
1540	0.005835	ribosomal protein S4, X-linked (RPS4X),	NM_001007	Hs.389933	NP_000998
		mRNA /cds=(36,827) /gb=NM_001007			
8		/gi=17981705 /ug=Hs.389933 /len=916			
1550	0.004961	proteasome (prosome, macropain)	NM_002788	Hs.346918	NP 687033
1330	0.004301  -	subunit, alpha type, 3 (PSMA3),	14141_002700	113.540,510	141 _007000
<b>.</b> .		transcript variant 1, mRNA /cds=(47,814)			
		/gb=NM_002788 /gi=23110937	*		
		/ug=Hs.346918 /len=949			2.35
1551	0.01004	insulin induced gene 1 (INSIG1)	NM 005542		NP 005533
1557		MR2-CI0186-291100-010-a06 CI0186	BF814502	Hs.446594	
		cDNA, mRNA sequence /gb=BF814502			:
· ·		/gi=12147047 /ug=Hs.446594 /len=530	. *		
L					
1558	0.003552	signal-induced proliferation-associated 1	NM_015556	Hs.172180	NP_056371
		like 1 (KIAA0440), mRNA		}	
]	'	/cds=(349,5763) /gb=NM_015556		× .	M. A.
4550	0.000050	/gi=7662125 /ug=Hs.172180 /len=6028	NINA 040400	11- 200274	ND 050400
1559	0.020053	stromal cell derived factor receptor 1	NM_012428	Hs.389371	NP_059429
		(SDFR1), transcript variant beta, mRNA /cds=(139,1335) /gb=NM_012428			-
	*	/gi=6912645 /ug=Hs.389371 /len=2388			**
		/gi-0912043/ug-Hs.369371/len-2306			* 2 %
1561	0.001592	translocating chain-associating	NM 014294	Hs.4147	NP 055109
1001	0.001002	membrane protein (TRAM), mRNA	1401_014204	110.41-17	
		/cds=(92,1216) /gb=NM_014294			
1		/gi=19923404 /ug=Hs.4147 /len=2722		-	
1562	0.01004	casein kinase 2, alpha 1 polypeptide	NM_001895	Hs.155140	NP_808228
ļ		(CSNK2A1), mRNA /cds=(149,1324)			
İ		/gb=NM_001895 /gi=4503094	1		
<u></u>		/ug=Hs.155140 /len=2195	10		
1567	0.041279	RAD21 (S. pombe) (RAD21), mRNA	NM_006265	Hs.81848	NP_006256
	1	/cds=(185,2080) /gb=NM_006265		<b>,</b> , ,	
	0.00115	/gi=5453993 /ug=Hs.81848 /len=3647	11111015100	10 75050	NE 055055
1569	0.001199	inositol polyphosphate-5-phosphatase,	NM_015160	Hş.75353	NP_055975
}		72kDa (INPP5E), mRNA /cds=(6,1583)			
7, "	1	/gb=NM_015160 /gi=24308012		1	
1570	0.015501	/ug=Hs.75353 /len=2097	NM 002022	Hs.230	ND 000044
1573	0.015521	fibromodulin (FMOD), mRNA	NM_002023	I⊔8.520	NP_002014
1	1	/cds=(21,1151) /gb=NM_002023 /gi=5016093 /ug=Hs.230 /len=2863		1	
Ļ	L	//gi-50 10095 /ug-118.230 /left-2003	<u> </u>	<del></del>	

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Acc ssion
4504	0.000001		1111 004000	No.	No.
1581	0.023381	SH3 domain binding glutamic acid-rich	NM_031286	Hs.109051	NP_112576
}		protein like 3 (SH3BGRL3), mRNA			
		/cds=(72,353) /gb=NM_031286			
1585	0.036540	/gi=13775197 /ug=Hs.109051 /len=764 retinal outer segment membrane protein	NM_000327	Hs.281564	NP 000318
1363	0.030349	1 (ROM1), mRNA /cds=(132,1187)	NIVI_000327	FIS.201004	INP_000316 .
		/gb=NM_000327 /gi=19743809			· ·
[		/ug=Hs.281564 /len=1477	· .	:	
		/ug=113.2010047/cm=1477			
1588	0.012525	cDNA FLJ30869 fis, clone	AK055431	Hs.349611	
		FEBRA2004224. /gb=AK055431			
		/gi=16550154 /ug=Hs.349611 /len=2423			
] .					
1589	0.030302	signal sequence receptor, delta	NM_006280	Hs.102135	NP_006271
		(translocon-associated protein delta)			
11.		(SSR4), mRNA /cds=(50,571)			
		/gb=NM_006280 /gi=5454089		• .	
		/ug=Hs.102135 /len=642		*	
1599		protein XP_037672 (aa, 58%)	XP_037672		
1640	6.62E-04	binder of Arl Two (BART1), mRNA	NM_012106	Hs.9552	NP_036238
	W. C.	/cds=(115,606) /gb=NM_012106	7 70	·	
1001		/gi=17978472 /ug=Hs.9552 /len=1973			
1661	0.014461	cofactor required for Sp1 transcriptional	NM_004830	Hs.29679	NP_057063
		activation, subunit 3, 130kDa (CRSP3),		<b>[</b>	
		mRNA /cds=(120,4226) /gb=NM_004830		l	
		/gi=7019352 /ug=Hs.29679 /len=5176	· .	· .	
1664	0.007994	ng11c09.s1 NCI_CGAP_Thy1 cDNA	AA627170	Hs.404836	
1.004	0.007334	clone IMAGE:1143568 similar to	70.027170	113.404000	
		gb:A18658 INSULIN RECEPTOR	· · · · · · · · · ·		000
1		PRECURSOR mRNA sequence	-	}	
		/clone=IMAGE:1143568 /gb=AA627170			1
		/gi=2540214 /ug=Hs.404836 /len=408			
			<u> </u>		
1702	0.005259	prostatic binding protein (PBP), mRNA	NM_002567	Hs.80423	NP_002558
		/cds=(111,674) /gb=NM_002567	*		
	<b></b>	/gi=4505620 /ug=Hs.80423 /len=1444		<u> </u>	
1720	0.046501	KIAA0971 protein (KIAA0971), mRNA	NM_014929	Hs.84429	NP_055744
1		/cds=(59,2005) /gb=NM_014929			
1700	0.040.455	/gi=7662421 /ug=Hs.84429 /len=4999	14055011	11. 407700	
1733	0.013463	cDNA FLJ30649 fis, clone	AK055211	Hs.167700	
	1	CTONG2006562. /gb=AK055211			
	ļ	/gi=16549888 /ug=Hs.167700 /len=3061			į l
1763	0.042027	zinc finger protein 36, C3H type-like 1	NM 004926	Hs.85155	NP_004917
1/63	0.043027	(ZFP36L1), mRNA /cds=(131,1147)	114141_004920	118.00 100	INF_00491/
		/gb=NM_004926 /gi=15812179			`
		/ug=Hs.85155 /len=3022		<u> </u>	] ]
L	<u> </u>	1/49-119.00 190 /1911-0022	<u> </u>	1	ليحصيا

Snot	p-value	Description	Gene	Unigene	Protein
Spot	p-value	Description	The state of the s	Accession	Accession
		:	Accession No.	No.	No.
1770	0.00326	actin, gamma 1 (ACTG1), mRNA	NM 001614	Hs.14376	NP 001605
.,,,	0.000	/cds=(75,1202) /gb=NM_001614	001011	(1.0.1.10.7	
		/gi=11038618 /ug=Hs.14376 /len=1919		ļ	*
1771	0.034358	melanoma antigen, family D, 2	NM 014599	Hs.4943	NP_803182
		(MAGED2), mRNA /cds=(97,1917)			
		/gb=NM_014599 /gi=21264316	•	*	
		/ug=Hs.4943 /len=2077	31		
1780	0.046501	cDNA FLJ11997 fis, clone	AK022059	Hs.432755	3
		HEMBB1001458. /gb=AK022059			
	* 1	/gi=10433379 /ug=Hs.432755 /len=2393			
1789	0.017843	KIAA1185 protein (KIAA1185), mRNA	NM_020710	Hs.268488	NP_065761
		/cds=(29,1780) /gb=NM_020710			
		/gi=24308206 /ug=Hs.268488 /len=2693			
					- 91
1798	0.004205	NADH dehydrogenase (ubiquinone)	NM_007103	Hs.7744	NP_009034
	- '	flavoprotein 1, 51kDa (NDUFV1), mRNA			
	9	/cds=(70,1464) /gb=NM_007103		χ	
		/gi=20149567 /ug=Hs.7744 /len=1566	,		
4700	0 000001	<u></u>	1114 00000	ļ	100
1799	0.023381	hypothetical protein MGC10911	NM_032302	Hs 85573	NP_115678
		(MGC10911), mRNA /cds=(234,602)			
7.		/gb=NM_032302 /gi=14150059	*	<u> </u>	
1810	0.046501	/ug=Hs.85573 /len=985 hypothetical protein FLJ12716	NM 021942	Hs.5354	NP 068761
1010	.0.0 <del>4</del> 050	(FLJ12716), mRNA /cds=(66,2513)	111111_02 1942	HS.5554	INF_000701
• •		/gb=NM_021942 /gi=21361577	,		
		/ug=Hs.5354 /len=3522			*
1836	0.014461	hypothetical protein FLJ23445	NM 025075	Hs.288151	NP_079351
,,,,,,	0.077101	(FLJ23445), mRNA /cds=(44,658)	11111_020070	113.200101	7070001
,	)	/gb=NM_025075 /gi=13376622	*		*
•		/ug=Hs.288151 /len=963		*	
1840	0.043827		M28031	<del>                                     </del>	
	0.0.00				<b>.</b>
1842	0.043827	Kruppel-like factor 5 (intestinal) (KLF5),	NM_001730	Hs.84728	NP 001721
		mRNA /cds=(312,1685) /gb=NM 001730			
	* ,	/gi=14251214 /ug=Hs.84728 /len=3359			*
1847	3.93E-04	tropomyosin 3 (TPM3), mRNA	NM_153649	Hs.85844	NP_705935
		/cds=(52,798) /gb=NM_153649	<del>-</del>	· .	
		/gi=24119202 /ug=Hs.85844 /len=2089			
1860	0.036549	hypothetical protein FLJ20559	NM_017881	Hs.98135	NP_060351
		(FLJ20559), mRNA /cds=(211,810)			
}		/gb=NM_017881 /gi=8923529	,		,
	<u></u>	/ug=Hs.98135 /len=1172			
1879	0.011644	Rab9 effector p40 (RAB9P40), mRNA	NM_005833	Hs.19012	NP_005824
	]	/cds=(150,1268) /gb=NM_005833		[	
	<u> </u>	/gi=5032014 /ug=Hs.19012 /len=1297	<u> </u>	<u> </u>	<u> </u>

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No
1880	0.016648	ubiquitin carboxyl-terminal esterase L1	NM_004181	Hs.76118	NP_004172
		(ubiquitin thiolesterase) (UCHL1), mRNA	0		
		/cds=(75,746) /gb=NM_004181	9,1		
		/gi=21361090 /ug=Hs.76118 /len=1119	- * * * * * * * * * * * * * * * * * * *		
1932	0.034358	SWI/SNF related, matrix associated,	NM 003077	Hs.250581	NP 003068
		actin dependent regulator of chromatin,			_
		subfamily d, member 2 (SMARCD2),			+
		mRNA /cds=(423,1850) /gb=NM_003077	7		٠,
	4	/gi=21264350 /ug=Hs.250581 /len=2704			
			* 0		
1947	0.041279	transforming, acidic coiled-coil containing	NM 006283	Hs.173159	NP_006274
		protein 1 (TACC1), mRNA	7		_
	• 4	/cds=(321,2738) /gb=NM_006283		1	
		/gi=5454099 /ug=Hs.173159 /len=7758			
1952	0.007397	target of myb1 (chicken) (TOM1), mRNA	NM 005488	Hs.9482	NP_005479
	0.5	/cds=(62,1540) /gb=NM_005488			
-57		/gi=4885636 /ug=Hs.9482 /len=2310	65		
1972	0.009313	mitochondrion, complete genome	NC 001807	<del></del>	1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
1981		SKB1 (S. pombe) (SKB1), mRNA	NM 006109	Hs.12912	NP_006100
	35	/cds=(92,2005) /gb=NM_006109			
		/gi=20070219 /ug=Hs.12912 /len=2413			
1991	0.049308	inner membrane protein, mitochondrial	NM 006839	Hs.78504	NP 006830
		(mitofilin) (IMMT), mRNA /cds=(93,2369)		-	
	1	/gb=NM_006839 /gi=5803114			
		/ug=Hs.78504 /len=2697	•		
2003	0.046501	serine (or cysteine) proteinase inhibitor,	NM 001235	Hs.9930	
		clade H (heat shock protein 47), member	_		
1		2 (SERPINH2), mRNA /cds=(88,1344)		* * * *	
		/gb=NM_001235 /gi=4502596			
		/ug=Hs.9930 /len=2047		·	
2006	0.038855	clathrin, light polypeptide (Lcb) (CLTB),	NM_007097	Hs.380749	NP_009028
1	*	transcript variant brain, mRNA			
	- ()	/cds=(173,862) /gb=NM_007097			
0		/gi=6005994 /ug=Hs.380749 /len=1134		, ,	
2016		HSPC049 protein (HSPC049), mRNA	NM_014149	Hs.172622	NP_054868
	0.0	/cds=(8,2233) /gb=NM_014149	0		
4		/gi=7661753 /ug=Hs.172622 /len=2610			
2039	0.016648	phosphatidyl inositol glycan class T	NM_015937	Hs.84038	NP_057021
	2.7.29.9	(PIGT), mRNA /cds=(20,1756)		1.5.5.000	
} '	*	/gb=NM_015937 /gi=23397652	* .	- 2 -	
		/ug=Hs.84038 /len=2171			
2045	0.036549	T-cell-activation protein (PGR1), mRNA	NM_033296	Hs.406590	NP_150638
-3.5	3.0000-70	/cds=(146,529) /gb=NM_033296	000200		
		/gi=15193293 /ug=Hs.406590 /len=1534			
	÷	10 100200 /ug=115.400000 /left= 1004			1.4
2046	0.005382	legumain (LGMN), mRNA	NM 005606	Hs.18069	NP_005597
2070	3.000002	/cds=(142,1443) /gb=NM_005606		113,10003	141 _000091
		/gi=21914880 /ug=Hs.18069 /len=1981			* * * * * * * * * * * * * * * * * * * *
L		rgi-2 13 14000 rug-113, 10003 rieli- 130 l	Ļ	L	<u> </u>

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
2072	0.000077	transportation factor D4 mitaglion defail	NIM 040000	<b>No.</b> Hs.279908	No.
2073	0.032277	transcription factor B1, mitochondrial	NM_016020	H\$.279908	NP_057104
	,	(TFB1M), mRNA /cds=(73,1113)		•	. :
	8	/gb=NM_016020 /gi=7705784			
2400	0.044070	/ug=Hs.279908 /len=1290	NIM 004040	He 70014	NP 001203
2100	0.041279	complement component 1, q	NM_001212	Hs.78614	NP_001203
		subcomponent binding protein (C1QBP),			
		nuclear gene encoding mitochondrial protein, mRNA /cds=(79,927)		H	
			* .		
	,	/gb=NM_001212 /gi=11038669 /ug=Hs.78614 /len=1332			*
2141	0.024072	transcription factor 12 (HTF4, helix-loop-	NM_003205	Hs.21704	NP_003196
2141	0.024972	helix transcription factors 4) (TCF12),	11 11  _003203	П5.21704	145_003.190
-	,	mRNA /cds=(214,2262) /gb=NM_003205	*		*
		/gi=4585865 /ug=Hs.21704 /len=4202	- 32-		
		/gi=43000007ug=H5.217047lef1=4202			*
2155	0.030302	clone alpha_est218/52C1 mRNA	AF001542	Hs.356442	
		sequence /gb=AF001542 /gi=2529714		57.	
		/ug=Hs.356442 /len=2992		, a	*
2179	0.017843	nuclear antigen Sp100 (SP100), mRNA	NM_003113	Hs.77617	NP_003104
	*	/cds=(32,2671) /gb=NM_003113	-	*	
•	-	/gi=19923235 /ug=Hs.77617 /len=3579			
2190	0.049308	Deleted in split-hand/split-foot 1 region	NM_006304	Hs.333495	NP_006295
		(DSS1), mRNA /cds=(129,341)	, P		
		/gb=NM_006304 /gi=5453639	* · · ·	+	
		/ug=Hs.333495 /len=509			
2205	0.024972	apoptosis-related protein TFAR15	AF022385		NP_665859
		(TFAR15)			110 000100
2212	0.001089	chromosome 21 open reading frame 4	NM_006134	Hs.284142	NP_006125
		(C21orf4), mRNA /cds=(159,635)			
-		/gb=NM_006134 /gi=8659558			0
0044	0.004045	/ug=Hs.284142 /len=750	A1047200	11-00445	
2214	0.001915	ts79a05.x1 NCI_CGAP_GC6 cDNA	AI917390	Hs.99415	
	1	clone IMAGE:2237456 3', mRNA sequence /clone=IMAGE:2237456	1)		
			· · ·	-00	
		/clone_end=3' /gb=Al917390			
2230	D OOBS 4	/gi=5637245 /ug=Hs.99415 /len=462 PMS1 postmeiotic segregation increased	NM 000534	Hs.111749	NP 000525
2230	0.00004	1 (S. cerevisiae) (PMS1), mRNA	Liam_00000#	113.11.1743	LAF_000323
		/cds=(81,2879) /gb=NM_000534		8	
		/gi=11496979 /ug=Hs.111749 /len=3121			
		/gi=114909797dg=113.1117497leti=0121	-	* .	
2235	0.036549	tight junction protein 2 (zona occludens	NM_004817	Hs.75608	NP_004808
		2) (TJP2), mRNA /cds=(80,3430)			
		/gb=NM_004817 /gi=4759341			
	1	/ug=Hs.75608 /len=4484			
2253	0.021876	small EDRK-rich factor 2 (SERF2),	NM_005770	Hs.380718	NP_005761
	]	mRNA /cds=(1023,1319)	-8		1-
1		/gb=NM_005770 /gi=21361286		÷	
		/ug=Hs.380718 /len=1408		<u> </u> -	

Spot	p-value	Description	Gene	Unigene	Protein
				Accession	Accession
			*	No.	No.
2255	0.023381	cadherin 5, type 2, VE-cadherin	NM 001795	Hs.76206	NP_001786
	0.02.00	(vascular epithelium) (CDH5), mRNA			
·	, ·	/cds=(121,2475) /gb=NM_001795	,		* * -
		/gi=14589894 /ug=Hs.76206 /len=4098			
2256	0.028428	splicing factor 3a, subunit 3, 60kDa	NM 006802	Hs.77897	NP_006793
	0.020 .20	(SF3A3), mRNA /cds=(9,1514)	, , , , , , , , , , , , , , , , , , ,		
		/gb=NM_ 006802 /gi=5803166			
	, ,	/ug=Hs.77897 /len=2733			
2264	0.021876	genomic protocadherin gamma cluster	NG_000012		
,		(PCDHG@) on chromosome 5			- 000
2271	0.036549	transcription factor IGHM enhancer 3,	AF196779	<del> </del>	
0.0	0.0000	JM11 protein, JM4 protein, JM5 protein,			
		T54 protein, JM10 protein, A4			*,
	,	differentiation-dependent protein, triple			
	1 .	LIM domain protein 6, and synaptophysin	,	· '	
	χ. Ι	genes, complete cds; and L-type calcium		4	3
	7 7	channel a>			
2273	0.005835	Pirin (PIR), mRNA /cds=(231,1103)	NM_003662	Hs.424966	NP_003653
22.0	0.00000	/gb=NM 003662 /gi=4505822	000002	1.10.12.1000	
		/ug=Hs.424966 /len=1318	*		
2285	0.011644	cDNA FLJ40438 fis, clone	AK097757	Hs.429537	i. <del></del>
	0.0	TESTI2039776, highly similar to	1		
		POTENTIAL PHOSPHOLIPID-			4
		TRANSPORTING ATPASE IIB (EC		' .	
<b>]</b> .		3.6.1). /gb=AK097757 /gi=21757625			
ļ ·		/ug=Hs.429537 /len=1923			
2296	0.01004	serine/threonine kinase 38 like	NM_015000	Hs.184523	NP 055815
		(STK38L), mRNA /cds=(174,1568)	_		] * =
r .		/gb=NM_015000 /gi=24307970	• 17		100
		/ug=Hs.184523 /len=4725			
2304	0.028428	hypothetical gene supported by	XM 072157		
r.		AK026099 (LOC128680), mRNA			7
2314	0.023381	specificity protein 3 (SP3) mRNA,	AY070137	Hs.154295	
' '	2 * 1 - ×	complete cds /cds=(385,2526)	e		1)
ĺ		/gb=AY070137 /gi=18091786			140,
	*	/ug=Hs.154295 /len=3979			<u> </u>
2340	0.046501	mRNA; cDNA DKFZp434F2311 (from	AL137603	Hs.233890	
		clone DKFZp434F2311) /gb=AL137603	· · · · · · · · · · · · · · · · · · ·		1
		/gi=6808349 /ug=Hs.233890 /len=842	<u> </u>		
2395	0.038855	Purkinje cell protein 4 (PCP4), mRNA	NM_006198	Hs.80296	NP_006189
ł	4	/cds=(59,247) /gb=NM_006198		`	
	,	/gi=5453857 /ug=Hs.80296 /len=540		<u>'</u>	<u> </u>
2396	0.004569	nonmuscle myosin heavy chain-B	M69181	Hs.296842	
` .	٠,	(MYH10) mRNA, partial cds.			<b>∤</b> .
'		/cds=(80,6007) /gb=M69181 /gi=641957	*(-		
L		/ug=Hs.296842 /len=7596	·		
2399	0.030302	mitochondrion, complete genome	NC_001807		

	Spot	p-value	Description	Gene	Unigene	Protein
	٠,			Accession No.	Accession No.	Accession No.
ŀ	2434	0.016648	small nuclear ribonucleoprotein D3	NM_004175	Hs.1575	NP 004166
	2.0.	0.010010	polypeptide 18kDa (SNRPD3), mRNA	.,	1.10, 1070	
]	-		/cds=(88,468) /gb=NM_004175		:	. **
l		*	/gi=4759159 /ug=Hs 1575 /len=626		*	· · · · · · · · · · · · · · · · · · ·
t	2466	0.01911	likely ortholog of mouse gene trap locus	NM 013242	Hs.279818	NP_037374
			3 (GTL3), mRNA /cds=(257,838)			_
			/gb=NM_013242 /gi=8392874	* *		
			/ug=Hs.279818 /len=1278			
	2477		of human GTP-binding protein G25K	AL121737		NP_426359
ſ	2497	0.023381	YEA4 protein (YEA), mRNA	NM_032826	Hs.292566	NP_116215
		•	/cds=(301,1296) /gb=NM_032826		. `	5
			/gi=21314760 /ug=Hs.292566 /len=2334			
L						
l	2506	0,001199	bHLH-PAS transcription factor MOP9	AF231338	Hs.222024	NP_064568
١			(MOP9) mRNA, long form, complete		4	
		. ×	cds, alternatively spliced /cds=(58,1815)			
			/gb=AF231338 /gi=7963663	- 1	)	
	0.505	0.040040	/ug=Hs.222024 /len=2008	NIM 004400	LI <sub>0</sub> 400440	NP 001393
	2525	0.010048	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA	111111_001402	Hs.422118	INP_001393
1	-		/cds=(63,1451) /gb=NM_001402	· · · · · · · · · · · · · · · · · · ·	719 711	* * *
			/gi=25453469 /ug=Hs.422118 /len=1837			
١			/gi=23433409 /ug=113.4221 10 /ieii=1037 	*		
	2534	0.020453	dendritic cell protein (GA17), mRNA	NM 006360	Hs.406648	NP 006351
			/cds=(53,1177) /gb=NM_006360			
٠٠		. ,	/gi=23397428 /ug=Hs.406648 /len=1268		-	
				*	, ÷	
Ī	2545	0.028428	chromosome 8 open reading frame 1	NM_004337	Hs.40539	NP_004328
٠.			(C8orf1), mRNA /cds=(346,1863)		•	
			/gb=NM_004337 /gi=4757889			,
1	* -		/ug=Hs.40539 /len=4199			
	2564		mitochondrion, complete genome	NC_001807	====	
	2588	0.049308	apolipoprotein D (APOD), mRNA	NM_001647	Hs.75736	NP_001638
1			/cds=(62,631) /gb=NM_001647			. "
	2646	0.042525	/gi=4502162 /ug=Hs.75736 /len=809	NM 016252	Hs.250646	NP_057336
1	2616	0.012525 	baculoviral IAP repeat-containing 6	NIVI_U 10252 /	IDS.20040	NP_05/330
.]		,	(apollon) (BIRC6), mRNA /cds=(1,14490) /gb=NM_016252			
1			/gi=10442821 /ug=Hs.250646		1	
	•,		/gi=104426217ug=11s.230040  /len=14490	*		*
	2649	0.023381	zizimin1 (zizimin1), mRNA	NM_015296	Hş.8021	NP_056111
	,	5.525551	/cds=(56,6265) /gb=NM_015296	1 9 . 5 _ 5 _ 5	1.0.002	-555,17
		-	/gi=24308028 /ug=Hs.8021 /len=7522		,	
ı	2666	0.00274	yeast Sec31p (KIAA0905), mRNA	NM 014933	Hs.70266	NP_057295
			/cds=(54,3716) /gb=NM_014933			-
			/gi=7662369 /ug=Hs.70266 /len=4129			- 4

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession No.	Accession No.
2680	0.003866	SEC63, endoplasmic reticulum	NM_007214	Hs.31575	NP_009145
		translocon component (S. cerevisiae			_
		(SEC63L), mRNA /cds=(133,2415)		1	- 30
		/gb=NM_007214 /gi=14591934		}	
0000	0.000034	/ug=Hs.31575 /len=3368	NIA 004007	11- 450040	ND 004050
2698	0.008031	topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA /cds≈(127,4722)	NM_001067	Hs.156346	NP_001058
		/gb=NM_001067 /gi=19913405	*		
	, `	/ug=Hs.156346 /len=5698			*
2716	0.021876	general transcription factor IIIC,	NM_012086	Hs.90847	NP_036218
		polypeptide 3, 102kDa (GTF3C3), mRNA	_	1	
	-	/cds=(94,2754) /gb=NM_012086		1	
	1	/gi=6912397 /ug=Hs.90847 /len=2961			"
0740	0.040040	47 had had	AE40EE44	U- 200000	ND 057455
2718	0.016648	17-beta-hydroxysteroid dehydrogenase type VII isoform mRNA, complete cds.	AF165514	Hs.380900	NP_057455
		/cds=(79,414) /gb=AF165514			V
		/gi=9294734 /ug=Hs.380900 /len=1272		<b>1</b>	5
2720	0.002294	mitogen-activated protein kinase kinase	NM_006575	Hs.246970	NP 006566
		kinase kinase 5 (MAP4K5), mRNA	_		
		/cds=(321,2861) /gb=NM_006575			
	, "	/gi=14589908 /ug=Hs.246970 /len=3000			-
2730	0.007994	small membrane protein 1 (SMP1),	NM_014313	Hs.107979	NP_055128
		mRNA /cds=(151,624) /gb=NM_014313	,		
		/gi=20357549 /ug=Hs.107979 /len=2284	·	1	8
2732	0.016648	Similar to RIKEN cDNA 4921510P06	BC009053	<del> </del>	NP_055494
	,	gene, clone MGC:9752 IMAGE:3855177,	·		
		mRNA, complete cds			
2741	0.00632		NM_004871	Hs.8868	NP_004862
	,	(GOSR1), mRNA /cds=(13,765) /gb=NM_004871 /gi=4758455			
	1	/gg=Hs.8868 /len=999			i .
2743	0.021876	clone MGC:9947 IMAGE:3876105,	BC013590	Hs.2437	- 0
		mRNA, complete cds /cds=(51,2216)			1
:		/gb=BC013590 /gi=15488925		}	, ,
		/ug=Hs.2437 /len=2651			<u>                                     </u>
2773	0.034358	nucleosome assembly protein 1-like 1	NM_139207	Hs.302649	NP_631946
		(NAP1L1), transcript variant 1, mRNA /cds=(125,1300) /gb=NM_139207	,		*
		/gi=21327707 /ug=Hs.302649 /len=3582			
		13. 2.02770774g 113.002043716H=0502			
2779	0.001747	nuclear factor (erythroid-derived 2)-like 2	NM_006164	Hs.155396	NP_006155
		(NFE2L2), mRNA /cds=(114,1931)			
		/gb=NM_006164 /gi=20149575			}
	L	/ug=Hs.155396 /len=2439	<u> </u>	<u>L</u>	<u> </u>

Spot	p-value	Description	Gene	Unig ne	Protein
4,114			* -	Accession	Accession
		<u> </u>		No.	No.
2791		hypothetical protein FLJ10283	NM_018046	Hs.284216	NP_060516
·		(FLJ10283), mRNA /cds=(218,1039)		ļ <sup>*</sup>	-31
	+	/gb=NM_018046 /gi=8922325			
		/ug=Hs.284216 /len=1876			
2811	0.003552	DnaJ (Hsp40) subfamily C, member 3	NM_006260	Hs.9683	NP_006251
		(DNAJC3), mRNA /cds=(28,1542)	•	<i>:</i>	1
,		/gb=NM_006260 /gi=24234721	* 1	,	
2829	9 05E 04	/ug=Hs.9683 /len=1542 mitochondrion, complete genome	NC 001807	= +	<del>,</del>
2851		allograft inflammatory factor 1 (AIF1),	NM 004847	Hs.76364	NP 116573
2031	0.02 1070	transcript variant 2, mRNA	[VIVI_004047	113.70304	141-110212
		/cds=(454,852) /gb=NM 004847	-		
		/gi=6680470 /ug=Hs.76364 /len=1363			
2865	0.023381	nudix (nucleoside diphosphate linked	NM 019094	Hs:355399	NP_061967
	0.000	moiety X)-type motif 4 (NUDT4), mRNA		,	
		/cds=(191,736) /gb=NM 019094			
		/gi=24432097 /ug=Hs.355399 /len=3652			
				·	
2892	0.01004	t-complex 1 (TCP1), mRNA	NM_030752	Hs.4112	NP_110379
	1	/cds=(22,1692) /gb=NM_030752			
		/gi=13540472 /ug=Hs.4112 /len=2019			
2964	0.023381		NM_001656	Hs.792	NP_150231
		64kDa (ARFD1), transcript variant alpha,			
ļ		mRNA /cds=(23,1747) /gb=NM_001656		ļ	
		/gi=15208639 /ug=Hs.792 /len=3565			] -
3000	0.043827	clone IMAGE:5590200, mRNA	BC035781	Hs.12862	<del>                                     </del>
	0.0.00	/gb=BC035781./gi=23272860			1
1		/ug=Hs.12862 /len=2951			
3008	0.012525	nuclear receptor subfamily 2, group F,	NM_021005	Hs.347991	NP_066285
		member 2 (NR2F2), mRNA			
,		/cds=(343,1587) /gb=NM_021005			
\ \ \\		/gi=14149745 /ug=Hs.347991 /len=1740			1
3009	0.043827	Hypothetical protein(cDNA: FLJ23391	AK027044		NP_006708
2045	0.0000	fis, clone HEP17320)	NO 004007		
3015		mitochondrion, complete genome	NC_001807	Hs.301206	NP_004789
3046	0.017043	kinesin family member 3B (KIF3B), mRNA /cds=(168,2411) /gb=NM_004798	NM_004798	115.301200	INF_004709
· ·	].	/gi=4758645 /ug=Hs.301206 /len=4724	,		
	1	191 -17000-10 ray-113.00 1200 /1611-47.24			
3051	0.010816	clone MGC:45564 IMAGE:4384472,	BC036746	Hs.132230	12.
		mRNA, complete cds /cds=(188,1123)			
		/gb=BC036746 /gi=22477830			}
		/ug=Hs.132230 /len=3767	-		
3073	0.043827		NM_014761	Hs.75824	NP_055576
1	1	mRNA /cds=(64,1158) /gb=NM_014761			
		/gi=7661971 /ug=Hs.75824 /len=2348		====	3
	<u></u>		<u> </u>		

Snot	p-value	Description	Gene	Unigene	Protein
Spor	p-value	Description	Accession No.	Accession	Accession
	1		Accession No.	No.	No.
3081	0.049308	transmembrane 4 superfamily member 6	NM 003270	Hs.121068	NP 003261
7001	Q.Q-1300Q	(TM4SF6), mRNA /cds=(104,841)	WW_000270	113.121000	141 _000201
		/gb=NM_003270 /gi=21265115	*	* * *	1
, ,		/ug=Hs.121068 /len=2069			
3084	0.028811	nucleobindin 2 (NUCB2), mRNA	NM 005013	Hs.3164	NP_005004
3004	0.020011	/cds=(220,1482) /gb=NM_005013		113.5104	141 _000004
		/gi=4826869 /ug=Hs.3164 /len=1586			* .
3093	0.041279	cDNA FLJ38472 fis, clone	AK095791	Hs.50150	
3033	0.041213	FEBRA2022148. /gb=AK095791	A1090791	113.30130	
		/gi=21755125 /ug=Hs.50150 /len=2454		* *	
3170		chromosome 20 open reading frame 64	NM 033550	Hs.282990	NP 291028
3170	0.017043	(C20orf64), mRNA /cds=(246,1007)	NN_055550	115.202990	NF_291020
		/gb=NM_033550 /gi=19923655			
	( )	/ug=Hs.282990 /len=2207	7. (4)		
3171	0.041270	transforming, acidic coiled-coil containing	NIM ODGOOD	Hs.173159	NP 006274
317.1	0.041279		14101_000203	IUS. 11.9 198	NP_006214
		protein 1 (TACC1), mRNA	100.	E.,	
		/cds=(321,2738) /gb=NM_006283			
2480	0.000052	/gi=5454099 /ug=Hs.173159 /len=7758 melanoma adhesion molecule (MCAM),	NM 006500	110 244570	ND 000404
3189	0.020003		NNI_000000	Hs.211579	NP_006491
		mRNA /cds=(27,1967) /gb=NM_006500		- %-	
	. ·	/gi=5729917 /ug=Hs.211579 /len=3583			
2010	0.040200		NC 004007		
3218		mitochondrion, complete genome	NC_001807	115 404507	
3247	0.002294	602410168F1 NIH_MGC_92 cDNA	BG394022	Hs.421597	
		clone IMAGE:4538560 5', mRNA			
1		sequence /clone=IMAGE:4538560		·	,
		/clone_end=5' /gb=BG394022		i	* * * * *
	. * :	/gi=13287470 /ug=Hs.421597 /len=1059			
1 2000	F 00F 04	DETROVIDUO DEI ATER DOI	D44000		
3280	5.98⊑-04	RETROVIRUS-RELATED POL	P11369		
2202	0.000540	POLYPROTEIN	A F000430		ND 054750
3283	0.036549		AF092136	11- 407040	NP_054759
3289		likely ortholog of mouse hepatoma-	NM_016073	Hs.127842	NP_057157
		derived growth factor, related protein 3	:	· ·	
1.		(HDGFRP3), mRNA /cds=(156,767)			
		/gb=NM_016073 /gi=21359902	×-		
2200	0.000050	/ug=Hs.127842 /len=1973	A F0 F0 C0 O	<u> </u>	
3298		monocyte/neutrophil elastase inhibitor	AF053630	110 450000	ND 444000
3333	0.028428	SH3-domain kinase binding protein 1	NM_031892	Hs.153260	NP_114098
}		(SH3KBP1), mRNA /cds=(292,2289)			
1 .		/gb=NM_031892 /gi=13994241 ,	2	*	*101
3334	0.020055	/ug=Hs.153260 /len=3348	VKU36060	Ho 99044	
3334	0.030000	cDNA: FLJ23307 fis, clone HEP11549,	AK026960	Hs.88044	
		highly similar to AF041037 novel			<u>}</u>
1		antagonist of FGF signaling (sprouty-1)			<b>i</b> -
		mRNA. /gb=AK026960 /gi=10439945 /ug=Hs.88044 /len=2520	-	,	
3349	0.049642		AJ005458		
0348	0.040043	protein phosphatase 2C beta	177002420		<u> </u>

Si	not I	p-value	Description	Gene	Unigene	Protein
"	,,,	p. yaide	Description	Accession No.	Accession	Accession
-	ł	,		Agocosion No.	No.	No.
33	372	0.009313	solute carrier family 11 (proton-coupled	NM 014585	Hs.5944	NP_055400
			divalent metal ion transporters), member			
	- 1		3 (SLC11A3), mRNA /cds=(315,2030)	*	*	
١			/gb=NM_014585 /gi=19923794	· . • • • • • • • • • • • • • • • • • • •		*
			/ug=Hs.5944 /len=3333			
33	86	0.038855	Yes-associated protein 1, 65kDa (YAP1),	NM 006106	Hs.84520	NP 006097
	· [		mRNA /cds=(250,1614) /gb=NM_006106	•		· -
	1		/gi=20986484 /ug=Hs.84520 /len=5128			
	`					
34	43	0.046501	guanylate kinase 1 (GUK1), mRNA	NM_000858	Hs.3764	NP_000849
			/cds=(225,818) /gb=NM_000858			
		- 2	/gi=20127414 /ug=Hs.3764 /len=1082			
34	145	0.049308	mRNA; cDNA DKFZp434A1520 (from	AL137544	Hs.406722	
	1		clone DKFZp434A1520); partial cds			
	Į	***	/cds=(1,551) /gb=AL137544 /gi=6808224			[* *
			/ug=Hs.406722 /len=2775			. 3 1
34	182	0.00684	proteasome (prosome, macropain) 26S	NM_002805	Hs.79387	NP_002796
			subunit, ATPase, 5 (PSMC5), mRNA		, ,	
	.		/cds=(42,1262) /gb=NM_002805			
<u>.</u>			/gi=24497434 /ug=Hs.79387 /len=1332			
35	510	0.016648	adenylate kinase 3 like 1 (AK3L1),	NM_016282	Hs.43436	NP_057366
			mRNA /cds=(141,824) /gb=NM_016282		\$-	
		. :	/gi=19923436 /ug=Hs.43436 /len=2642		*	
· .				* * * * * * * * * * * * * * * * * * * *		3
35	518	0.022757	hypothetical protein FLJ23548	NM_024590	Hs.22895	NP_078866
"		* * *	(FLJ23548), mRNA /cds=(204,713)	*	1	
		*	/gb=NM_024590 /gi=13375780		-	
- 31	-04	0.004004	/ug=Hs.22895 /len=1871	NIM 450000	115 240000	ND COOCC
35	521	0:004961		NM_152306	Hs.348602	NP_690856
			finger domains 2 (URF2), transcript	,		
l			variant 1, mRNA /cds=(341,1852) /gb=NM 152306 /gi=23312361			
			/ug=Hs.348602 /len=3720			` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` `
			/ug=H5.540002 /leH=3720	,		· m
31	532	0.020453	enabled (Drosophila) (ENAH), mRNA	NM 018212	Hs.14838	NP 060682
"	JUZ	0.020400	/cds=(77,646) /gb=NM_018212	14141-0 102 12	11.13.14000	111 _000002
	-		/gi=8922657 /ug=Hs.14838 /len=2943		1	
3'	534	0.004205	hypothetical protein FLJ22875	NM 032231	Hs.406548	NP_115607
ľ		0.00-200	(FLJ22875), mRNA /cds=(152,634)	1002201	1.5.155545	1 10007
			/gb=NM 032231 /gi=15638951	·	1	
1		, .	/ug=Hs.406548 /len=1019	-		
3!	536	0.038855	mRNA for KIAA1367 protein, partial cds.	AB037788	Hs.224961	
``			/cds=(1,1741) /gb=AB037788			
			/gi=7243114 /ug=Hs.224961 /len=4196			3
3!	548	0.030302	eukaryotic translation initiation factor 3,	NM_001568	Hs.106673	NP 001559
			subunit 6 48kDa (EIF3S6), mRNA			
	:	100	/cds=(23,1360) /gb=NM_001568			
		Y	/gi=4503520 /ug=Hs.106673 /len=1510			
1		0.000450	<del>                                     </del>	AF143314		7 · · · · · · · · · · · · · · · · · · ·
35	570	0.020453	PTEN (PTEN) gene, exons 3 through 5	/\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		

Spot	p-value	Description	Gene (	Unigene	Protein
		£	Accession No.	Accession	Accession
				No.	No
3580	0.020453	te65d01.x1 Soares_NFL_T_GBC_S1	Al377292	Hs.410753	
		cDNA clone IMAGE:2091553 3', mRNA			,
		sequence /clone=IMAGE:2091553	\$ -	į į	
		/clone_end=3' /gb=Al377292	- 0	. 1	· ·
		/gi=4187145 /ug=Hs.410753 /len=238	8		
3597		hypothetical protein FLJ20152	NM 019000	Hs.82273	NP_061873
		(FLJ20152), mRNA /cds=(217,1287)	₹ :	, .	
		/gb=NM 019000 /gi=21361616	- 22		
		/ug=Hs.82273 /len=2989	£		
3602	0.032277	thioredoxin-like 2 (TXNL2), mRNA	NM 006541	Hs.42644	NP 006532
¢		/cds=(5,1012) /gb=NM_006541	17		_
		/gi=5730103 /ug=Hs 42644 /len=1942	Y-1	. 5	Ce .
3609	0.012525	mortality factor 4 like 1 (MORF4L1),	NM 006791	Hs.6353	NP_006782
	7	mRNA /cds=(132,1103) /gb=NM_006791			
		/gi=5803101 /ug=Hs.6353 /len=1766			
		9			•
3617	0.032277	microtubule associated testis specific	NM 015112	Hs.101474	NP 055927
	1-	serine/threonine protein kinase	-		
	1	(MAST205), mRNA /cds=(284,5488)			
* 1		/gb=NM_015112 /gi=14149670			
		/ug=Hs.101474 /len=5737			
3623	0.014461	cDNA FLJ14089 fis, clone	AK024151	Hs.306668	
		MAMMA1000257. /gb=AK024151			
		/gi=10436462 /ug=Hs.306668 /len=1730			
			, i		
3727	0.01911	Sec7p-like protein mRNA, partial cds.	U59752	Hs.8517	
		/cds=(1,801) /gb=U59752 /gi=1465756			
	-	/ug=Hs.8517 /len=997	· ,	*	
3740	0.010816	5,10-methenyltetrahydrofolate	NM_006441	Hs.118131	NP_006432
		synthetase (5-formyltetrahydrofolate	- V	* ,	
6	0	cyclo-ligase) (MTHFS), mRNA			,00
		/cds=(14,625) /gb=NM_006441	* 1 **		4
		/gi=5453745 /ug=Hs.118131 /len=857			
3761	0.020453	peroxisomal acyl-coenzyme A oxidase	S69189		NP_009223
3777	0.017843	galactosidase, alpha (GLA), mRNA	NM_000169	Hs.69089	NP_000160
		/cds=(61,1350) /gb=NM_000169			k J
٠.		/gi=4504008 /ug=Hs.69089 /len=1350	*		
3787	0.034358	secretory leukocyte protease inhibitor	NM_003064	Hs.251754	NP_003055
	•	(antileukoproteinase) (SLPI), mRNA			
•		/cds=(23,421) /gb=NM_003064		-	
		/gi=15834622 /ug=Hs 251754 /len=598			
3793	0.043827	myosin, light polypeptide 5, regulatory	NM_002477	Hs.170482	NP_002468
		(MYL5), mRNA /cds=(106,627)	_	·	
	:	/gb=NM_002477 /gi=4505304		} :	j .
		/ug=Hs.170482 /len=661			
3794	0.041279	coatomer protein complex, subunit alpha	NM 004371	Hs.75887	NP_004362
		(COPA), mRNA /cds=(467,4141)	- ·		
		/gb=NM_004371 /gi=6996002			
		/ug=Hs.75887 /len=5064		1 7	1

Spot	p-value	Description	Gene	Unigene	Protein
100	-		Accession No.	Accession	Accession
				No.	No.
3804	0.008631	thymidine kinase 1, soluble (TK1),	NM_003258	Hs.105097	NP_003249
		mRNA /cds=(58,762) /gb=NM_003258	9		
		/gi=4507518 /ug=Hs.105097 /len=1421	E		-
3806	0.032277	period 1 (Drosophila) (PER1), mRNA	NM_002616	Hs.68398	NP_002607
		/cds=(188,4060) /gb=NM_002616		*	
		/gi=4505712 /ug=Hs.68398 /len=4656			
3830	0.012525	eukaryotic translation elongation factor 1	NM_001959	Hs.421608	NP_066944
		beta 2 (EEF1B2), transcript variant 1,	*		
		mRNA /cds=(236,913) /gb=NM_001959			
	(C)	/gi=16519564 /ug=Hs.421608 /len=961			
2025	Ë 00E 04	NECTO A COLOR DATE	1114 000450	7000	ND 600450
3835	5.98E-04	NEL-like 2 (chicken) (NELL2), mRNA	NM_006159	Hs.79389	NP_006150
		/cds=(97,2547) /gb=NM_006159	*		
3844	0.000453	/gi=5453765 /ug=Hs.79389 /len=3198 CGI-101 protein (F-LAN-1), mRNA	NM_016041	110 200121	ND 057405
3044		/cds=(7,636) /gb=NM_016041	NIVI_U 1604 1	Hs.286131	NP_057125
	í · · · · · ·	/gi=7705603 /ug=Hs.286131 /len=1123	(Y)	*	
3846	0.032788	myosin light chain 1 slow a (MLC1SA),	NM 002475	Hs.90318	NP_002466
2040	0.032700	mRNA /cds=(48,674) /gb=NM_002475	14141_00247.5	1115.50510	INF_002400
10		/gi=17986280 /ug=Hs.90318 /len=778			
3882		zinc finger protein 207 (ZNF207), mRNA	NM 003457	Hs.62112	NP 003448
		/cds=(203,1639) /gb=NM 003457		1.0.02.172	
		/gi=4508016 /ug=Hs.62112 /len=2347	*		
	1				
3883	0.028428	Meis1, myeloid ecotropic viral integration	NM 002398	Hs.170177	NP 002389
		site 1 (mouse) (MEIS1), mRNA	1.3		_
1		/cds=(66,1238) /gb=NM_002398			٠.
1		/gi=4505150 /ug=Hs.170177 /len=2511			
3907	0.030302	Ig superfamily protein (Z39IG), mRNA	NM_007268	Hs.8904	NP_009199
	- ·	/cds=(46,1245) /gb=NM_007268			
	12 2 2 2	/gi=6005957 /ug=Hs.8904 /len=1787			
3911	0.017843	mitochondrion, complete genome	NC_001807	11. 400405	ND' 040700
3921	0.003552	ALFY (ALFY), mRNA /cds=(231,10811)	NM_014991	Hs.198135	NP_848700
		/gb=NM_014991 /gi=25014113			
		/ug=Hs.198135 /len=10811		<u> </u>	
3923	0.01011	prepro insulin-like growth factor-I (IGF-I)	M59812		
3923	0.01911	gene, exon 1	10103012		
3958	0.016648	CGI-150 protein (CGI-150), mRNA	NM 016080	Hs.279061	NP 057164
5500	3.0,0040	/cds=(202,1716) /gb=NM_016080	1.440.10000	11.13.27.300 (	
		/gi=7705645 /ug=Hs.279061 /len=2580		1	
4000	0.00145	KIAA1156	AB032982		NP_055665
4014		mRNA; cDNA DKFZp667O1616 (from	AL713722	Hs.365655	
		clone DKFZp667O1616) /gb=AL713722			
	<b>1</b>	/gi=19584452 /ug=Hs.365655 /len=1773	. 8	·	
		Ţ	l		1

Spot	p-value	Description	Gene	Unigene	Protein
				Accession	Accession
				No.	No.
4017	0.015521	Ras association (RalGDS/AF-6) domain	NM_014737	Hs.80905	NP_739580
	1 1	family 2 (RASSF2), transcript variant 1,		· · · · · · · · · · · · · · · · · · ·	
		mRNA /cds=(197,1177) /gb=NM_014737		1-	1
1. 1		/gi=7661963 /ug=Hs.80905 /len=5426	• ,		
4036	0.041279	IDN3 protein (IDN3), transcript variant A,		Hs.225767	NP_597677
		mRNA /cds=(363,7160) /gb=NM_133433	0.0		
		/gi=19718748 /ug=Hs.225767 /len=8124	,	. ***	
1001	0.00004	1: W 17 - 6 (1015) - DAIA	NINA 20 4000	11. 40000	ND 077000
4064	0.00684	ubiquitin-like 5 (UBL5), mRNA	NM_024292	Hs.13836	NP_077268
		/cds=(66,287) /gb=NM_024292	*.		
4068	0.00604	/gi=13236509 /ug=Hs.13836 /len=413 hypothetical protein PRO2013	NM_021243	Un 02005	
4000	0.00004	(PRO2013), mRNA /cds=(136,381)	NIVI_UZ 1243	Hs.238205	
	-	/gb=NM_021243 /gi=24308272		* *	).
(		/ug=Hs.238205 /len=876			
4103	0.013463	protein kinase C, nu (PRKCN), mRNA	NM_005813	Hs.143460	NP_005804
1 1100	0.010400	/cds=(556,3228) /gb=NM_005813	14141_000015	1113.149400	1111 _000004
		/gi=6563384 /ug=Hs.143460 /len=5792	•.		
4106	0.030302	pre-B-cell colony-enhancing factor	NM_005746	Hs.239138	NP_005737
		(PBEF), mRNA /cds=(28,1503)			
	2.0	/gb=NM_005746 /gi=5031976			
		/ug=Hs.239138 /len=2376			
4115	0.011644	WNT1 inducible signaling pathway	NM_003880	Hs.194678	NP_569080
		protein 3 (WISP3), transcript variant 1,	· .	3	
		mRNA /cds=(111,1175) /gb=NM_003880		i	
-		/gi=18491002 /ug=Hs.194678 /len=1307			
-					
4121	0.010816	natural killer cell enhancing factor	L19184		NP_002565
1100		(NKEFA)			115 005000
4122	0.030302	serologically defined colon cancer	NM_005869	Hs.23557	NP_005860
١.		antigen 10 (SDCCAG10), mRNA	0		0.5
		/cds=(482,1600) /gb=NM_005869 /gi=5031958 /ug=Hs.23557 /len=1857			**
4129	0.036549	UI-H-DT0-aue-f-11-0-UI.s1	BQ030407	Hs.374637	100
4129	0.030549	NCI_CGAP_DT0 cDNA clone	BQ030407	113.374037	
		IMAGE:5868298 3', mRNA sequence	*		3
		/clone=IMAGE:5868298 /clone_end=3'			
* -		/gb=BQ030407 /gi=19765686	*		· ·
		/ug=Hs.374637 /len=991		1	*
4145	0.014461	RAB10, member RAS oncogene family	NM_016131	Hs.236494	NP_057215
		(RAB10), mRNA /cds=(91,693)	-		
		/gb=NM_016131 /gi=7705848	*		
		/ug=Hs.236494 /len=3164			<u></u>
4161	0.032277	sarcolemmal associated protein (SLAP1)	U21155		
		mRNA, complete cds			
4206	0.021876	ring finger protein 4 (RNF4), mRNA	NM_002938	Hs.66394	NP_002929
		/cds=(271,843) /gb=NM_002938	<b>_</b>		~
L		/gi=4506560 /ug=Hs.66394 /len=2918	<u>L</u>		

Spot	p-valu	Description	Gene	Unigene	Protein
	-		Acc ssion No.	Accession	Accession
				No.	No.
4217	0.032277	eukaryotic translation elongation factor 1	NM_032378	Hs.334798	NP_115754
		delta (guanine nucleotide exchange			
•	*	protein) (EEF1D), transcript variant 1,			
	. *	mRNA /cds=(198,2141) /gb=NM_032378	**		
,		/gi=25453473 /ug=Hs 334798 /len=2216	<i>y</i> -		
4246	0.037211	hypothetical protein MGC10471	NM_030818	Hs.24998	NP_110445
•		(MGC10471), mRNA /cds=(227,1417)		}	
		/gb=NM_030818 /gi=13540613			
4057	0.000450	/ug=Hs.24998 /len=1688	NINA COCCES	11. 40444	115 07/75/
4257	0.020453	leucine proline-enriched proteoglycan	NM_022356	Hs.10114	NP_071751
		(leprecan) 1 (LEPRE1), mRNA		*	0
		/cds=(42,2456) /gb=NM_022356			
4286	0.024072	/gi=21361917 /ug=Hs.10114 /len=2993 cartilage specific proteoglycan	X17406		NP 037359
4294		hypothetical protein FLJ20729	NM_017953	Hs.5111	NP_060423
74,04	0.071213	(FLJ20729), mRNA /cds=(135,1547)	     4  v  _0   1   902	113.0111	141:_000423
		/gb=NM_017953 /gi=20149642	,		- 00
•	•	/ug=Hs.5111 /len=2821	:		
4307	0.038855	HT015 protein (HT015)	AF223466		NP 061049
4315		polymerase (RNA) II (DNA directed)	NM_021128	Hs.441072	NP_066951
		polypeptide L, 7.6kDa (POLR2L), mRNA			
*		/cds=(22,225) /gb=NM_021128		-	*
		/gi=14589956 /ug=Hs.441072 /len=392	,		
4353	0.046501	splicing factor, arginine/serine-rich 7,	NM_006276	Hs.184167	NP 006267
		35kDa (SFRS7), mRNA /cds=(54,467)		'	-
		/gb=NM_006276 /gi=24415993			
		/ug=Hs.184167 /len=2754			· (T)
4357	0.032277	hypothetical protein PRO1580	NM_018502	Hs.270863	NP_060972
	.,,	(PRO1580), mRNA /cds=(763,1524)			
0		/gb=NM_018502 /gi=23346636		· · ·	
		/ug=Hs.270863 /len=1859		-	
4364	0.026653	oxysterol binding protein-like 8	NM_020841	Hs.109694	NP_065892
		(OSBPL8), mRNA /cds=(481,3150)			
		/gb=NM_020841 /gi=22035617			
1205	0.046504	/ug=Hs.109694 /len=7239	NIM 000007	Up 4050	ND 004700
4385	U.U405U1	cyclin L ania-6a (LOC57018), mRNA	NM_020307	Hs.4859	NP_064703
-		/cds=(55,1635) /gb=NM_020307	,	*	
4389	0.00200	/gi=9945319 /ug=Hs.4859 /len=2076 ADP-ribosylation factor 3 (ARF3)	NM 001659		NP 001650
4395		hypothetical protein LOC51255	NM 016494	Hs.11156	NP 057578
4000	0.004000	(LOC51255), mRNA /cds=(31,492)	14141_0 10484	113.11100	_03/3/6
		/gb=NM_016494 /gi=24475978	*		
( · ·	,	/ug=Hs.11156 /len=601			**
4407	0.015521	15 kDa selenoprotein (SEP15), mRNA	NM_004261	Hs.90606	NP 004252
		/cds=(5,493) /gb=NM_004261			
		/gi=20127464 /ug=Hs.90606 /len=1519			8.
4419	0.011644	KIAA0742	AB018285		NP 060903

Spot	p-value	D scription	Gene	Unigene	Protein
			Accession No.	Accession	Accession
4421	0.041270	sel-1 suppressor of lin-12-like (C.	NM_005065	<b>No.</b> Hs.181300	<b>No.</b> NP 005056
4421	0.041279	elegans) (SEL1L), mRNA	NIVI_003003	ns. 161300	
		/cds=(46,2430) /gb=NM_005065			
		/gi=19923668 /ug=Hs.181300 /len=7885		i	
		3			· · · ·
4440	0.007397	alcohol dehydrogenase 5 (class III), chi	NM_000671	Hs.78989	NP_000662
		polypeptide (ADH5), mRNA			
		/cds=(163,1287) /gb=NM_000671		• .	
4440	0.005000	/gi=11496890 /ug=Hs.78989 /len=2496	NIN 4 004044		
4443	0.005382	APEX nuclease (multifunctional DNA	NM_001641	Hs.73722	NP_542380
	0	repair enzyme) 1 (APEX1), transcript variant 1, mRNA /cds=(333,1289)	;		
		/gb=NM_001641 /gi=18375500	* *	<u> </u>	
	,	/ug=Hs.73722 /len=1574			
4448	0.030302	exostoses (multiple)-like 2 (EXTL2),	NM_001439	Hs.61152	NP 001430
		mRNA /cds=(288,1280) /gb=NM_001439			
1. 1	. 0	/gi=14149608 /ug=Hs.61152 /len=2833			
ļ					
4475		RNA binding motif protein 8B (RBM8B)	AF231512		
4476	0.021876	adaptor-related protein complex 3, beta	NM_003664	Hs.155172	NP_003655
5		1 subunit (AP3B1), mRNA /cds=(138,3422) /gb=NM_003664	-		~
1	*	/gi=24638436 /ug=Hs.155172 /len=4021	*		
		19		۰.	
4500		X2 box repressor	U22680		
4509	0.032277	likely ortholog of mouse deleted in	NM_005669	Hs.178112	NP_005660
		polyposis 1 (DP1), mRNA /cds=(38,595)			
		/gb=NM_005669 /gi=24307896			·
		/ug=Hs.178112 /len=3000			
4516	0.043827	putative cyclin G1 interacting protein	NM 006349	Hs.10028	NP_006340
		(CG1I), mRNA /cds=(31,495)			
		/gb=NM_006349 /gi=5453616	- %		·
		/ug=Hs.10028 /len=725			
4524	0.049308	ribosomal protein S23 (RPS23), mRNA	NM_001025	Hs.3463	NP_001016
		/cds=(32,463) /gb=NM_001025			
1551	7 225 04	/gi=14790142 /ug=Hs.3463 /len=506	NC 001807		
4551 4552		mitochondrion, complete genome TAF5-like RNA polymerase II, p300/CBP-	NC_001807	Hs.26782	NP_055224
1 7002	0.002211	associated factor (PCAF)-associated	VIVI_U 144US	113.20702	
		factor, 65kDa (TAF5L), mRNA	1		*
1		/cds=(98,1867) /gb=NM_014409	• •		
		/gi=21269865 /ug=Hs.26782 /len=3065	0(-		1
4556	0.008631	phosphorylase, glycogen; liver (Hers	NM_002863	Hs.771	NP_002854
	· · ·	disease, glycogen storage disease type			
		VI) (PYGL), mRNA /cds=(52,2595) /gb=NM_002863 /gi=4506352			
		/ug=Hs.771 /len=2643			
	<u>'</u>	rug=na.rr i ricii=2040	1100	L	L

Spot	p-value	Description	Gene	Unigene	Protein
				Accession	Accession
				No.	No.
4570	0.016648	hypothetical protein KIAA0758 protein,	AB018301		NP_056049
		partial cds		:	·
4571	0.003866	chromosome 1 open reading frame 13	NM_030769	Hs.23756	NP_110396
- '		(C1orf13), mRNA /cds=(45,1007)			
		/gb=NM_030769 /gi=13540532			
		/ug=Hs.23756 /len=1552		,	,
4580	0.036549	zinc finger protein 208 (ZNF208), mRNA	NM_007153	Hs.55452	NP_009084
		/cds=(1,3504) /gb=NM_007153			· -
:	·	/gi=6005975 /ug=Hs.55452 /len=3504		•	
4583	0.028428	restin (Reed-Steinberg cell-expressed	NM_002956	Hs.31638	NP_002947
0.		intermediate filament-associated protein)	*		_
		(RSN), mRNA /cds=(133,4416)			
		/gb=NM_002956 /gi=4506750			
		/ug=Hs.31638 /len=5857			5 · · ·
4584	8.10E-04	Rho-associated, coiled-coil containing	NM_005406	Hs.17820	NP_005397
		protein kinase 1 (ROCK1), mRNA			
	• •	/cds=(1,4065) /gb=NM_005406	•	• •	
	:	/gi=4885582 /ug=Hs.17820 /len=4065		I I	,
4601	0.043827	cDNA: FLJ21869 fis, clone HEP02442.	AK025522	Hs.28465	
		/gb=AK025522 /gi=10438064		2	
	,	/ug=Hs.28465 /len=2287			
4614	9.88E-04	sperm antigen-36	AF187554		
4620	0.00145	hypothetical protein MGC3196	NM_024084	Hs.309161	
		(MGC3196), mRNA /cds=(178,291)	·		10
	* *	/gb=NM_024084 /gi=13129079	*		1.0
		/ug=Hs.309161 /len=603			
4690	0.030302	enthoprotin (ENTH), mRNA	NM_014666	Hs.132853	NP_055481
		/cds=(102,1979) /gb=NM_014666			÷-
		/gi=7661967 /ug=Hs.132853 /len=3336			*
4701	0.024972	ubiquitin-like 5 (UBL5), mRNA	NM_024292	Hs.13836	NP_077268
)		/cds=(66,287) /gb=NM_024292			
-		/gi=13236509 /ug=Hs.13836 /len=413			
4710	0.020453	vinculin (VCL), transcript variant meta-	NM_014000	Hs.75350	NP_054706
<b>.</b>		VCL, mRNA /cds=(86,3490)		. 9	
		/gb=NM_014000 /gi=7669549			e e
		/ug=Hs.75350 /len=5341			
4737	0.002294	deoxyribonuclease II, lysosomal	NM_001375	Hs.118243	NP_001366
-		(DNASE2), mRNA /cds=(94,1176)	× ×		
<u> </u>		/gb=NM_001375 /gi=4503348		-x 1 ()	
=171	   a.e	/ug=Hs 118243 /len=1975	·	<u> </u>	
4738		hypothetical protein (KIAA1439)	AB037860		NP_005586
4747	0.046501	leucine zipper transcription factor-like 1	NM_020347	Hs.30824	NP_065080
, -		(LZTFL1), mRNA /cds=(125,1024)	X-	* .	
		/gb=NM_020347 /gi=9966792			
		/ug=Hs.30824 /len=3384			
4834	0.016648	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gene	Unigene	Protein
	,		Accession No.	Accession	Accession
				No.	N
4837	0.049308	UI-H-BW1-amj-g-07-0-UI.s1	BF513214	Hs.445888	
		NCI_CGAP_Sub7 cDNA clone	***		
		IMAGE:3070261 3', mRNA sequence		· ."	
	- 1	/clone=IMAGE:3070261 /clone_end=3'		*	
		/gb=BF513214 /gi=11598393		- W W	0.
	* * *	/ug=Hs.445888 /len=620			*
4866	0.020453	FLJ31373 fis, clone NB9N42000342	AK055935	Hs.281434	
		/cds=UNKNOWN /gb=AK055935		ж	
		/gi=16550787 /ug=Hs.281434 /len=2472	12	. *	e er te e
4885	0.046501	clone alpha_est218/52C1 mRNA	AF001542	Hs.356442	
		sequence /gb=AF001542 /gi=2529714			*
	1	/ug=Hs.356442 /len=2992			
4887	0.002882	mRNA; cDNA DKFZp434N079 (from	AL133591	Hs.141480	
		clone DKFZp434N079) /gb=AL133591			
	*	/gi=6599179 /ug=Hs.141480 /len=1965			
4915	0.036549	hypothetical protein FLJ13149	NM_021826	Hs.112188	NP_068598
	, '	(FLJ13149), mRNA /cds=(291,2585)			
		/gb=NM_021826 /gi=11141902			
	,	/ug=Hs.112188 /len=2836	• • •		
4926	0.043827	nuclear receptor coactivator 1 (NCOA1),	NM_147223	Hs.74002	NP_671766
		transcript variant 2, mRNA	1		
	¥	/cds=(202,4401) /gb=NM_147223	· ·		
	112	/gi=22538456 /ug=Hs.74002 /len=4721			
4932	0.001915	alpha-subunit of prolyl 4-hydroxylase	U14616		
		gene, exon 12			· · · · · · · · · · · · · · · · · · ·
4950	0.01004	mRNA for KIAA1865 protein, partial cds.	AB058768	Hs.179260	-
		/cds=(622,2793) /gb=AB058768			
,		/gi=14017946 /ug=Hs.179260 /len=3641		78	
4960	0.032277	hypothetical protein FLJ20958	NM 022102	Hs.261023	NP_071385
		(FLJ20958), mRNA /cds=(141,914)			
		/gb=NM_022102 /gi=13430855		*	
		/ug=Hs.261023 /len=1842			
4964	0.041279	hypothetical protein FLJ22643	NM_024635	Hs.43579	NP_078911
		(FLJ22643), mRNA /cds=(15,650)			
: .	2	/gb=NM_024635 /gi=13375865			
		/ug=Hs.43579 /len=997	*		
5000	0.008631	diphtheria toxin receptor (heparin-binding	NM_001945	Hs.799	NP_001936
	*	epidermal growth factor-like growth		-	/ -
		factor) (DTR), mRNA /cds=(262,888)			
		/gb=NM_001945 /gi=4503412	<u> </u>		
	<u></u>	/ug=Hs.799 /len=2360			
5005	0.032277	ankyrin repeat and SOCS box-containing	NM_016114	Hs.153489	NP_057198
		1 (ASB1), mRNA /cds=(87,1094)	• 0		·
		/gb=NM_016114 /gi=22208961	,		
	ļ. ·	/ug=Hs.153489 /len=6798	· ,	·	
L	<u> </u>			L	<u> </u>

Spot	p-value	Description	Gene	Unigene	Protein
		*	Accession No.	Accession No.	Accession No.
5006	0.020453	cDNA FLJ33181 fis, clone	AK090500	Hs.379218	NO.
	3,323,137,	ADRGL2003684, highly similar to HLA		1	
		CLASS I HISTOCOMPATIBILITY	+	ļ	
		ANTIGEN, ALPHA CHAIN H	• 0	*	
		PRECURSOR. /gb=AK090500		,	
.ā		/gi=21748675 /ug=Hs.379218 /len=2290		*	
5018	0.034358	mRNA; cDNA DKFZp762B195 (from	AL359585	Hs.356766	
		clone DKFZp762B195) /gb=AL359585	*		
,		/gi=8655645 /ug=Hs.356766 /len=2183			
5046		topoisomerase II alpha-4 (AF285159)	AAG13405		
5048	0.016648	single-stranded DNA binding protein	NM_003143	Hs.923	NP_003134
ŀ		(SSBP1), mRNA /cds=(79,525)			
-	γ.	/gb=NM_003143 /gi=4507230		<b>1</b>	*
		/ug=Hs.923 /len=628			
5061	0.015521	wc09c01.x1 NCI_CGAP_Pr28 cDNA	Al674177	Hs.200089	
9	· .	clone IMAGE:2314656 3' similar to	8		· ·
	'	gb:J05016 PROTEIN DISULFIDE		· ·	
,	14.0	ISOMERASE-RELATED PROTEIN			2.5
* .		PRECURSOR mRNA sequence		9	
		/clone=IMAGE:2314656 /clone_end=3'			
		/gb=Al674177 /gi=4874657			
5005	0.040040	/ug=Hs.200089 /len=526	NA 450740	11- 0077	ND 744044
5095	0.016648	nucleoporin 62kDa (NUP62), transcript	NM_153719	Hs.9877	NP_714941
		variant 1, mRNA /cds=(408,1976)			
		/gb=NM_153719 /gi=24497608	'		•
5400	2.025.04	/ug=Hs.9877 /len=3403	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	·	
5103	3.93E-04	signal transducer and activator of	ÄF417842		
		transcription 6, interleukin-4 induced (STAT6) gene, complete cds			
5141	0.012525	ubiquitin carrier protein (E2-EPF), mRNA	NIM 014501	Hs.174070	NP_055316
3141	0.012323	/cds=(60,737) /gb=NM_014501	14101_014301	113.174070	147_000010
		/gi=7657045 /ug=Hs.174070 /len=890		-	
5153	0.021876	ATPase, H transporting, lysosomal	NM 004888	Hs.90336	NP 004879
3133	0.021070	13kDa, V1 subunit G isoform 1	11111_004000	113.30330	100-07-0
	*	(ATP6V1G1), mRNA /cds=(94,450)			*
		/gb=NM 004888 /gi=20357534	* -		
		/ug=Hs 90336 /len=1110		10	
5169	0.049308		X56160		NP 002151
5204		stathmin-like 3 (STMN3), mRNA	NM_015894	Hs.285753	NP .056978
		/cds=(83,625) /gb=NM_015894			
1		/gi=14670374 /ug=Hs.285753 /len=2255		*	•
	***		3	,	
5205	8.95E-04	mRNA for KIAA1458 protein, partial cds.	AB040891	Hs.27263	
		/cds=(22,1860) /gb=AB040891	*		
		/gi=7959176 /ug=Hs.27263 /len=5843			1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Spot	p-value	Description	Gene Accession No.	Unigene Acc ssion No.	Protein Accession No.
5233	·	ATP synthase, H transporting, mitochondrial F0 complex, subunit e (ATP5I), mRNA /cds=(64,273) /gb=NM_007100 /gi=6005716 /ug=Hs.85539 /len=336	NM_007100	Hs.85539	NP_009031
5234	n.	deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424 /len=6735		Hs.154424	NP_054644
5252		stromal cell protein (LOC55974), mRNA /cds=(61,726) /gb=NM_018845 /gi=10047123 /ug=Hs.292154 /len=1316	NM_018845	Hs 292154	NP_061333
5281	0.021876	ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=NM_000970 /gi=16753226 /ug=Hs.409045 /len=950	NM_000970	Hs.409045	NP_000961
5308	0.020453	hypothetical protein FLJ10305 (FLJ10305), mRNA /cds=(155,1729) /gb=NM_018052 /gi=20070298 /ug=Hs.5894 /len=2235	NM_018052	Hs.5894	NP_060522
5310	0.038855	cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1), mRNA /cds=(210,1097) /gb=NM_053056 /gi=16950654 /ug=Hs.82932 /len=4306	NM_053056	Hs.82932	NP_444284
5359	0.026653	RAP1A, member of RAS oncogene family (RAP1A), mRNA /cds=(313,867) /gb=NM_002884 /gi=4506412 /ug=Hs.865 /len=1579	NM_002884	Hs.865	NP_002875
5388	0.013463	peroxiredoxin 1 (PRDX1), mRNA /cds=(61,660) /gb=NM_002574 /gi=4505590 /ug=Hs.180909 /len=937	NM_002574	Hs.180909	NP_002565
5395	0.046501	vesicle amine transport protein 1 (T californica) (VAT1), mRNA /cds=(57,1238) /gb=NM_006373 /gi=18379348 /ug=Hs.157236 /len=2738	NM_006373	Hs.157236	NP_006364
5407	0.046501	mRNA for exportin (tRNA) /cds=(59,2947) /gb=Y16414 /gi=2924334 /ug=Hs.380785 /len=3497	Y16414	Hs.380785	NP_009166
5408	0.030302	mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (MAP3K7IP2), transcript variant 2, mRNA /cds=(176,1786) /gb=NM_145342 /gi=21735558 /ug=Hs.109727 /len=4359	NM_145342	Hs.109727	NP_663317
5432	0.00299	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446

Spot	p-value	D scription	Gene	Unigene	Protein
,			Accession No.	Accession	Accession
5515	0.017843	cell cycle progression 8 protein (CPR8),	NM 004748	No. Hs.82506	<b>No.</b> NP 004739
70.0		mRNA /cds=(13,1140) /gb=NM_004748		1.0.42004	56 165
		/gi=4758047 /ug=Hs.82506 /len=1856	<b>.</b>		
5541	0.043827	DKFZP434C245 protein	NM_015426	Hs.59461	NP_056241
		(DKFZP434C245), mRNA			
	·	/cds=(107,1201) /gb=NM_015426			,y- #-
<u> </u>		/gi=14149683 /ug=Hs.59461 /len=1359			
5577	0.049308	kangai 1 (suppression of tumorigenicity	NM_002231	Hs.323949	NP_002222
		6, prostate; CD82 antigen (R2 leukocyte	0	* * *	
		antigen, antigen detected by monoclonal			
		and antibody IA4)) (KAI1), mRNA			
		/cds=(182,985) /gb=NM_002231 /gi=13259537 /ug=Hs.323949 /len=1623			
;	. *	/gi=13259537 /ug=HS.323949 /iefi=1623			
5592	0.021876	hypothetical protein MGC12904	NM 031219	Hs.7739	NP_112496
3332	0.02 1070	(MGC12904), mRNA /cds=(196,951)	14141_001219	113.7733	1112430
		/gb=NM_031219 /gi=13654293			
		/ug=Hs.7739 /len=1143		:	
5609	0.046501	peroxisomal proliferator-activated	NM_033405	Hs.151714	NP_208384
		receptor A interacting complex 285			_
	1,4	(PRIC285), mRNA /cds=(425,6667)			
	,	/gb=NM_033405 /gi=21703357	***	*	¥ -
		/ug=Hs.151714 /len=7804			
5614	0.012525	mRNA; cDNA DKFZp761J0720 (from	AL833252	Hs.349845	
		clone DKFZp761J0720) /gb=AL833252			· ·
		/gi=21733885 /ug=Hs.349845 /len=3602	*	1.	÷
				**	1115 00 10 1
5622	0.004569	eukaryotic translation initiation factor 4	NM_004953	Hs.433750	NP_004944
. ' .		gamma, 1 (EIF4G1), mRNA	·		
		/cds=(369,4559) /gb=NM_004953			
5671	0.024250	/gi=4826709 /ug=Hs.433750 /len=5018 EPC-1 (=M76979	U57446		
30/1		PEDF;U29953;M90493)	007440		
5672		clone IMAGE:5265581, mRNA	BC035165	Hs.400548	*
33,2	0.0-0001	/gb=BC035165 /gi=23272508		1.0.11000,10	÷.
<u> </u>		/ug=Hs.400548 /len=2237	*	-	
5698	0.041279	serine (or cysteine) proteinase inhibitor,	NM_000295	Hs.297681	NP_000286
		clade A (alpha-1 antiproteinase,		,	<del>-</del>
	. "	antitrypsin), member 1 (SERPINA1),			
		mRNA /cds=(233,1489) /gb=NM_000295			*
1		/gi=21361197 /ug=Hs.297681 /len=1584		1	
5699	0.036549	laminin receptor 1 (ribosomal protein SA,	NM_002295	Hs.181357	NP_002286
		67kDa) (LAMR1), mRNA /cds=(86,973)			
1		/gb=NM_002295 /gi=9845501		i .	
<u> </u>		/ug=Hs.181357 /len=1039	I	<u> </u>	1

S	pot	p-value	Description	Gene	Unigene	Protein
-	12.5			Accession No.	Acc ssion	Accession
				, 10000010111 1101	No.	No.
5	702	0.013463	adaptor-related protein complex 3, delta	NM 003938	Hs.75056	NP_003929
1		· ,	1 subunit (AP3D1), mRNA			
			/cds=(312,3773) /gb=NM 003938		<u>'</u>	
		w '.	/gi=20127437 /ug=Hs.75056 /len=4950			
5	707	0.004569	nucleolar autoantigen (55kD) similar to	NM 006455	Hs.446459	NP_006446
	н		rat synaptonemal complex protein			_
'			(SC65), mRNA /cds=(12,1325)		•	
		0	/gb=NM_006455 /gi=5454037		- ×3	
	·		/ug=Hs.446459 /len=2347			
5	708	0.041279	NDRG family member 4 (NDRG4),	NM_020465	Hs.322430	NP 075061
		•	mRNA /cds=(77,1192) /gb=NM_020465	1.4.T		_
			/gi=14165263 /ug=Hs.322430 /len=3241			
5	720	0.036549	carbonic anhydrase II (CA2), mRNA	NM_000067"	Hs.155097	NP_000058
		•	/cds=(66,848) /gb=NM_000067		7	
L			/gi=4557394 /ug=Hs.155097 /len=1551			
5	745	0.017843	clone IMAGE:5299888, mRNA	BC039397	Hs.112237	
			/gb=BC039397 /gi=24659826			
L			/ug=Hs.112237 /len=1338	(-)		
5	757	0.016648	ribosomal protein S3 (RPS3), mRNA	NM_001005	Hs.414990	NP_000996
			/cds=(19,750) /gb=NM_001005	`		
			/gi=15718686 /ug=Hs.414990 /len=843		4	
5	806	0.024972	5'-nucleotidase, cytosolic II (NT5C2),	NM_012229	Hs.138593	NP_036361
ľ		٠.	mRNA /cds=(145,1830) /gb=NM_012229	* *		
1		. *	/gi=20149601 /ug=Hs.138593 /len=3364		* :	*
Ļ	005	2 2 2 2 2 2				
5	865	0.041279	protein tyrosine phosphatase, receptor	NM_002838	Hs.170121	NP_563580
			type, C (PTPRC), transcript variant 1,			
-		,	mRNA /cds=(93,4007) /gb=NM_002838	*	0	
'			/gi=18641346 /ug=Hs.170121 /len=5026			
<u> </u>	966	0.000000	manalaid differentiation advantage	NIM 000 400	11- 00440	ND 000450
0	866	0.030302	myeloid differentiation primary response	NM_002468	Hs.82116	NP_002459
		4	gene (88) (MYD88), mRNA		1	
			/cds=(40,930) /gb=NM_002468			· · ·
5	869	0.046501	/gi=19923143 /ug=Hs.82116 /len=2678 ATPase, Class I, type 8B, member 1	NM_005603	Hs.406187	NP_005594
1 "	503	0.040001	(ATP8B1), mRNA /cds=(1,3756)	14W_000000	113.400107	-00008 <del>4</del>
		- 8	/gb=NM_005603 /gi=5031696			
		s•	/ug=Hs.406187 /len=3756	* -		
5	880	0.043827	amyloid beta precursor protein	NM_006380	Hs.84084	NP_006371
]		0.00.0027	(cytoplasmic tail) binding protein 2		1.0.0 1004	555571
}	. •	i.	(APPBP2), mRNA /cds=(289,2046)			ļ
			/gb=NM_006380 /gi=18104961		*	
			/ug=Hs.84084 /len=6468			'
5	897	0.021876	destrin (actin depolymerizing factor)	NM_006870	Hs.408576	NP_006861
10			(DSTN), mRNA /cds=(73,570)			_= + ,
	9	0 1 0	/gb=NM_006870 /gi=6466447		0.0	
			/ug=Hs.408576 /len=1439			
			21	<b>-</b>	<del></del>	<u> </u>

١ ١	Spot	p-value	Description	Gene	Unigene	Protein
	-		•	Accession No.	Acc ssion	Accession
Ŀ	·			1	No.	No.
{	5917		RED CELL ACID PHOSPHATASE 1,	P24666		
,		100	ISOZYME F (ACP1) (LOW			
1			MOLECULAR WEIGHT		61	
l		1	PHOSPHOTYROSINE PROTEIN			
ŀ			PHOSPHATASE) (ADIPOCYTE ACID	Car.		.: 9
		*	PHOSPHATASE, ISOZYME ALPHA)			
Ŀ		m 21 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	(62% aa)			
_	5920		mitochondrion, complete genome	NC_001807		
۱ :	5934		enthoprotin (ENTH), mRNA	NM_014666	Hs.132853	NP_055481
			/cds=(102,1979) /gb=NM_014666	W		•
Ŀ	5005		/gi=7661967 /ug=Hs.132853 /len=3336	BE044500		
۱ :	5935	8.95E-04	MR2-CI0186-291100-010-a06 CI0186	BF814502	Hs.446594	
l			cDNA, mRNA sequence /gb=BF814502			
			/gi=12147047 /ug=Hs.446594 /len=530	,		
100		0.000000		NINA 000704	11-400044	ND 000705
;	5936	0.003866	amine oxidase, copper containing 3	NM_003734	Hs.198241	NP_003725
			(vascular adhesion protein 1) (AOC3),			
ŀ			mRNA /cds=(161,2452) /gb=NM_003734	* * *		
l			/gi=6806883 /ug=Hs 198241 /len=4040		1.	• •
H	5020	0.004747	DTAEA DAIA salusassas II D TEIID	NINA 002070	LI- 400000	ND 000000
:	5939	0.001747	BTAF1 RNA polymerase II, B-TFIID	NM_003972	Hs.180930	NP_003963
			transcription factor-associated, 170kDa			-32
	-	. 4	(Mot1 S. cerevisiae) (BTAF1), mRNA			
			/cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345			*
ì		*	19 -21411009149-AS. 1609301 e  -6343			
Н	5945	1.005.04	dermatopontin (DPT), mRNA	NM_001937	Hs.80552	NP 001928
Ι΄	0940	1.00L-04	/cds=(7,612) /gb=NM_001937	NIVI_00 1937	115.00552	NF_001920
			/gi=4755134 /ug=Hs.80552 /len=717		.60	*
<u> </u>	5946	0.010816	son of sevenless 1	Z11574		NP_033257
_	5971		UI-E-CI1-abg-f-09-0-UI r1 UI-E-CI1	BM691540	Hs.172047	141 _000207
	00, 1	0.011011	cDNA clone UI-E-CI1-abg-f-09-0-UI 5',	DIVIOU 10-10	110.172047	
	19		mRNA sequence /clone=UI-E-CI1-abg-f-			
1			09-0-UI /clone_end=5' /gb=BM691540	194		
l			/gi=19004798 /ug=Hs.172047 /len=1039		. :	• •
l			The state of the		-2-	
L	5974	0.032277	KIAA0266 gene product (KIAA0266)	NM_021645	Hs.127376	NP 067677
Ľ			mRNA /cds=(734,3034) /gb=NM_021645			
			/gi=11063982 /ug=Hs.127376 /len=5585			
			3			
Г	5975	7.33E-04	cell-line RPMI 8226 chloride ion current	AF232225		
-			inducer protein I(Cln) gene,	0		
Г	5976	1.81E-04	ox06a01.s1	AI033469	Hs.386279	
			Soares_fetal_liver_spleen_1NFLS_S1	=		
			cDNA clone IMAGE:1655496 3' similar		. *	
			to gb:M86849 GAP JUNCTION BETA-2			*
L			PROTEIN mRNA sequence		l	
			/clone=IMAGE:1655496 /clone_end=3'	-	. *	] ,
		***	/gb=Al033469 /gi=3254422			
		· ·	/ug=Hs.386279 /len=551	1	1	6.

Snot	p-value	Description	Gene	Unig n	Protein	
Opor	p-value	Description	Accession No.	Accession	Accession	
0000	0.000077	100 (001000)	1111 000001	No.	No.	
6006	0.032277	ribosomal protein L23a (RPL23A),	NM_000984	Hs.419463	NP_000975	
		mRNA /cds=(22,492) /gb=NM_000984	*	*	* 15 .	
		/gi=17105393 /ug=Hs.419463 /len=546		<u></u>		
6007	0.01911	similar to 3-HYDROXYISOBUTYRATE	XM_059866	. ,		
		DEHYDROGENASE, MITOCHONDRIAL				
		PRECURSOR (HIBADH) (H. sapiens)	X			
	-	(LOC136773), mRNA				
			-	-		
6020	0.00274	cDNA FLJ37774 fis, clone	AK095093	Hs.119533		
>- A 1		BRHIP2026021, highly similar to Mus		,		
		musculus formin binding protein 30			- · · · · · · · · · · · · · · · · · · ·	
, 1		mRNA. /gb=AK095093 /gi=21754285				
		/ug=Hs.119533 /len=2767				
6031	0.036540	ER-resident protein ERdj5 (ERdj5),	NM_018981	Hs.1098	NP 061854	
0031	0.030349	mRNA /cds=(416,2797) /gb=NM_018981		113, 1030	147_001034	
		/gi=24308126 /ug=Hs.1098 /len=4193				
10000	2 22255		15412-2			
6032		NOD1 protein (NOD1) gene	AF149773			
6078	0.030302	toll-like receptor 4 (TLR4), transcript	NM_003266	Hs.159239	NP_612567	
		variant 3, mRNA /cds=(408,2807)		. ".		
		/gb=NM_003266 /gi=19924147	*			
		/ug=Hs.159239 /len=3934				
6079	0.036549	extracellular matrix protein 2, female	NM_001393	Hs.35094	NP_001384	
• • • • • • • • • • • • • • • • • • • •		organ and adipocyte specific (ECM2),				
		mRNA /cds=(74,2173) /gb=NM_001393				
	ac.	/gi=4557542 /ug=Hs 35094 /len=3171				
6084	0.009313	SR rich protein (DKFZp564B0769),	NM_032870	Hs.18368	NP_116259	
		mRNA /cds=(33,2450) /gb=NM_032870				
-		/gi=18699723 /ug=Hs.18368 /len=2663	0			
,		1000072074g   110.1000071611 2000			*	
6133	0.020596	core promoter element binding protein	NM_001300	Hs.285313	NP_001291	
0133	0.020590	(COPEB), mRNA /cds=(118,969)	14141_00 1300	118.200010	141 _001291	
* .		/gb=NM 001300/gi=9961346	· .			
				· .		
0407	0.000050	/ug=Hs.285313 /len=1470	NNA 040000	11- 20400	ND 02C220	
6187	0.026653	beta-1,3-glucuronyltransferase 3	NM_012200	Hs.26492	NP_036332	
		(glucuronosyltransferase I) (B3GAT3),	V	٠.		
	× .	mRNA /cds=(30,1037) /gb=NM_012200	· ·		1	
"		/gi=12408653 /ug=Hs.26492 /len=1456		. *		
	•					
6188	0.016648	phosphodiesterase 10A(PDE10A) mRNA	NM_006661		NP_006652	
6205	0.028428	jumping translocation breakpoint (JTB),	NM_006694	Hs.6396	NP_006685	
		mRNA /cds=(433,873) /gb=NM_006694				
1	1.	/gi=5729888 /ug=Hs.6396 /len=1040		300		
					· .	
6221	0.034358	adenylate kinase 1 (AK1), mRNA	NM_000476	Hs.76240	NP_000467	
]	3.30,000	/cds=(75,659) /gb=NM_000476		]		
		/gi=4502010 /ug=Hs.76240 /len=2271				
<u> </u>		1191 -10020 TO 109-113.1 02-10 /1011-221 1		J	1.9	

Spot	p-value	Description	Gene	Unigene	Protein
	. 2		Accession No.	Accession	Accession
6230	0.022248	nudix (nucleoside diphosphate linked	NM 019094	<b>No.</b> Hs.355399	No. NP_061967
0200	0.022210	moiety X)-type motif 4 (NUDT4), mRNA	1414_010004	113.00000	1111 _00 1007
		/cds=(191,736) /gb=NM_019094		*	
		/gi=24432097 /ug=Hs.355399 /len=3652			
-		3,			
6258	0.026653	deleted in liver cancer 1 (DLC1), mRNA	NM_006094	Hs.8700	NP_006085
	_ * * *	/cds=(296,3571) /gb=NM_006094	- · · · · · · · · · · · · · · · · · · ·		
= /		/gi=6633799 /ug=Hs 8700 /len=3821			
6287	0.030302	uncharacterized hypothalamus protein	NM_018480	Hs.24371	NP_060950
· ·	4	HT007 (HT007), mRNA /cds=(228,887)			
., .		/gb=NM_018480 /gi=8923801			
		/ug=Hs.24371 /len=1172			
6297	0.041279	5'-nucleotidase, cytosolic II (NT5C2),	NM_012229	Hs.138593	NP_036361
		mRNA /cds=(145,1830) /gb=NM_012229			
		/gi=20149601 /ug=Hs.138593 /len=3364			
6007	0.00000	-DNA 51 107000 61	11004045	11 1000	
6307	0.006602	cDNA FLJ37296 fis, clone	AK094615	Hs:4983	•
4	90	BRAMY2015420. /gb=AK094615		·X- * .	
6310	0.036549	/gi=21753707 /ug=Hs.4983 /len=3181 eukaryotic translation initiation factor 2,	NM 004094	110 454777	ND 004005
0310	0.030349	subunit 1 alpha, 35kDa (EIF2S1), mRNA	14141_004094	Hs.151777	NP_004085
	*	/cds=(100,1047) /gb=NM 004094			
-50-	0.0	/gi=19923248 /ug=Hs.151777 /len=2992	-		
٠.		1302024074g=113.13177771611=2332			
6311	0.002508	peptidylprolyl isomerase A (cyclophilin A)	NM 021130	Hs.401787	NP 066953
*		(PPIA), mRNA /cds=(45,542)			
	1	/gb=NM_021130 /gi=10863926			
		/ug=Hs.401787 /len=753	*	. "	, , ,
6334	0.008631	pilin-like transCRiption factor	AF122004		NP_036360
6347		mitochondrion, complete genome	NC_001807		
6368	0.032277	gamma-aminobutyric acid (GABA) A	NM_000809	Hs.248112	NP_000800
	a se	receptor, alpha 4 (GABRA4), mRNA		*	
		/cds=(39,1703) /gb=NM_000809			
		/gi=4557604 /ug=Hs 248112 /len=1703			
6386		mitochondrion, complete genome	NC_001807	17 48-55	ND OFFICE
6387	0.028428	epithelial protein lost in neoplasm beta	NM_016357	Hs.10706	NP_057441
		(EPLIN), mRNA /cds=(102,2381)	¥		
	8 4	/gb=NM_016357 /gi=7705372		:	
6392	0.017005	/ug=Hs.10706 /len=3655 clock (mouse) (CLOCK), mRNA	NM_004898	Hs.150602	NP 004889
0092	0.017990	/cds=(339,2879) /gb=NM_004898	14141_004696	113.130002	141 _004009
ľ	÷	/gi=25777594 /ug=Hs.150602 /len=5801			<u></u>
	:	20///004/ug=118.100002/lef140001			÷
6396	0.041279	ADP-ribosyltransferase (NAD ; poly(ADP-	NM 005484	Hs.24284	NP_005475
	1	ribose) polymerase)-like 2 (ADPRTL2),			-555
1	;	mRNA /cds=(150,1754) /gb=NM_005484			*
		/gi=11496991 /ug=Hs.24284 /len=1887			
1				· ·	

Spot	p-value	Description	Gene	Unigene	Protein
<b>V</b>			Accession No.	Accession	Accession
0.100	0.010505		****	No.	No.
6403	0.012525	glyceronephosphate O-acyltransferase	NM_014236	Hs.12482	NP_055051
		(GNPAT), mRNA /cds=(158,2200)	÷		
,		/gb=NM_014236 /gi=7657133			
6407	0.002552	/ug=Hs 12482 /len=2470 hypothetical protein LOC51244	NM 016474	Uo 15900C	ND 057550
0407	0.003552	(LOC51244), mRNA /cds=(340,1233)	NIVI_010474	Hs.158006	NP_057558
		/gb=NM_016474 /gi=24475969	* * *		
	0	/ug=Hs.158006 /len=1614			·
6412	1.61E-04	KIAA0716 gene product (KIAA0716),	NM 014705	Hs.118140	NP_055520
		mRNA /cds=(192,2489) /gb=NM_014705	_		
	*.	/gi=7662263 /ug=Hs.118140 /len=4652		五	·
* -					
6414	0.026653	eukaryotic translation initiation factor 4	NM_001418	Hs.183684	NP_001409
-	7	gamma, 2 (EIF4G2), mRNA			
•	,	/cds=(307,3030) /gb=NM_001418			
·		/gi=4503538 /ug=Hs.183684 /len=3820			- 1
6424		intersectin short form	AF064243		NP_003015
6426	0.036549	microtubule-associated protein 1B	NM_005909	Hs.103042	NP_114399
	,	(MAP1B), transcript variant 1, mRNA		1	,
•		/cds=(223,7629) /gb=NM_005909	(-		
		/gi=14165457 /ug=Hs.103042 /len=9416	. ••		***
6428	0.036540	serologically defined colon cancer	NM_004713	Hs.388584	NP 004704
0420	0.030349	antigen 1 (SDCCAG1), mRNA	14141_004713	115.300304	NF_004704
• . •		/cds=(183,1271) /gb=NM_004713			
		/gi=4759077 /ug=Hs.388584 /len=2078	,		
6432		protein kinase, cAMP-dependent,	NM 002736	Hs.77439	NP_002727
		regulatory, type II, beta (PRKAR2B),	_		_
		mRNA /cds=(167,1423) /gb=NM_002736			
		/gi=4506064 /ug=Hs.77439 /len=3259			
	-0			•	
6439	0.038855	protein phosphatase 1, catalytic subunit,	NM_002709	Hs.21537	NP_002700
		beta isoform (PPP1CB), mRNA		*	-
	4	/cds=(259,1242) /gb=NM_002709	(j)		
	110	/gi=4506004 /ug=Hs.21537 /len=3590	1.0		
6442	0.002066	Mile internator (MONIDOA), mDNA	NIM 014029	Hs.52081	NP 055753
6443	0.003866	Mlx interactor (MONDOA), mRNA /cds=(153,1733) /gb=NM_014938	NM_014938	HS.52061	INP_055753
.*		/gi=7662347 /ug=Hs.52081 /len=4339		9	
6444	0.034358	protein phosphatase 3 (formerly 2B),	NM 021132	Hs.151531	NP 066955
A Lin	3.004000	catalytic subunit, beta isoform		1.5.101001	
		(calcineurin A beta) (PPP3CB), mRNA	+	<b>\</b>	<b>\</b>
		/cds=(117,1691) /gb=NM_021132		. (	
		/gi=11036639 /ug=Hs.151531 /len=3079		*	
6475	0.003866	ubiquitin-conjugating enzyme (PUBC1)	AF317220		NP_003330
		mRNA, complete cds			
6476	0.026653	ELK3, ETS-domain protein (SRF	AK026078	Hs.288555	
		accessory protein 2), FLJ22425 fis, clone			
	L	HRC08686 (AK026078.1)	<u> </u>		

ាសា	p-value	Description	Gene	Unigene	Protein
y pot	p value		Accession No.	Accession	Accession
			/ 100000 ion 110.	No.	No.
6496	0.028428	TATA element modulatory factor 1	NM 007114	Hs.267632	NP_009045
		(TMF1), mRNA /cds=(1,3282)		1	*
	P	/gb=NM_007114 /gi=6005903	,		
	. *	/ug=Hs.267632 /len=3282	·		
6529	1.61E-04	nuclear factor of kappa light polypeptide	NM_020529	Hs.81328	NP_065390
		gene enhancer in B-cells inhibitor, alpha			
• •		(NFKBIA), mRNA /cds=(95,1048)		6	
		/gb=NM_020529 /gi=10092618		ļ	(i) v
		/ug=Hs.81328 /len=1550			•
6530	0.036549	pleckstrin domain containing, family A	NM_020904	Hs.9469	NP_065955
		(phosphoinositide binding specific)	"	*	
		member 4 (PLEKHA4), mRNA			
		/cds=(526,2865) /gb=NM_020904	*	. ** 12	
0507	0.000004	/gi=10190743 /ug=Hs.9469 /len=3056	1114 005440		ND 005 (0)
6537	0.008631	selenoprotein P, plasma, 1 (SEPP1),	NM_005410	Hs.275775	NP_005401
		mRNA /cds=(37,1182) /gb=NM_005410			* .
	0	/gi=4885590 /ug=Hs.275775 /len=2038	*		0
6550	0.020453	t-complex-associated-testis-expressed 1-	NIM OOGEAO	Hs.266940	ND 006540
<del>0</del> 550	0.020455	like 1 (TCTEL1), mRNA /cds=(1,342)	     14  14  14  15  15  15	IDS.200940	NP_006510
0		/gb=NM_006519 /gi=5730084			· · ·
		/ug=Hs.266940 /len=713	*	•	
6551	0.034358	URB mRNA, complete cds	AF506819	Hs.356289	
	4.90.000	/cds=(146,2998) /gb=AF506819	, 555575		
,		/gi=21039408 /ug=Hs.356289 /len=3320.			•
					*
6554	0.043827	mitochondrial ribosomal protein L13	NM_014078	Hs.333823	NP_054797
		(MRPL13), nuclear gene encoding			
	.	mitochondrial protein, mRNA			
		/cds=(287,823) /gb=NM_014078			·
		/gi=21265072 /ug=Hs.333823 /len=1086			
"					
6565	0.036549	PTK9 protein tyrosine kinase 9 (PTK9),	NM_002822	Hs.82643	NP_002813
	İ	mRNA /cds=(61,1113) /gb=NM_002822			-
		/gi=4506274 /ug=Hs.82643 /len=3000	*		•
6571	0.020452	KIAAAA22 protoin (KIAAA422) mBNA	NIM O1EO16	He 26470	NID OFCOOL
00/1	0.020453	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM 015216	NM_015216	Hs.26179	NP_056031
		/gi=7662117 /ug=Hs.26179 /len=5814	÷ .		
6574	0.01004		D00591		
6592		methylene tetrahydrofolate	NM_006636	Hs.154672	NP_006627
ا ا	0.020720	dehydrogenase (NAD_dependent),	000000	1.0.104072	
		methenyltetrahydrofolate cyclohydrolase		,	
		(MTHFD2), nuclear gene encoding	*	-x-	
		mitochondrial protein, mRNA	· .		
		/cds=(77,1111) /gb=NM_006636			
		/gi=13699869 /ug=Hs.154672 /len=2154		Į.	
i	1		I	1	

	Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
				,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	No.	No.
ľ	6594	0.034358	lactate dehydrogenase A (LDHA), mRNA	NM 005566	Hs.2795	NP_005557
١			/cds=(98,1096) /gb=NM_005566	_		
1		·- !	/gi=5031856 /ug=Hs.2795 /len=1661		÷	
						*
	6609	0.012525	fibroblast growth factor 2 (basic) (FGF2),	NM_002006	Hs.284244	NP_001997
1			mRNA /cds=(302,934) /gb=NM_002006	,		
_	, .	* 1	/gi=15451897 /ug=Hs.284244 /len=6802	Δ.		· ·
Į						
ı	6610	0.005835	Similar to RIKEN cDNA 3830613O22	BC035645	Hs.356876	
١			gene, clone IMAGE:5551209, mRNA,			** ** ** ** ** ** ** ** ** ** ** ** **
ı			partial cds /cds=(282,4079)			
١		. •	/gb=BC035645 /gi=23272851		9	
ļ			/ug=Hs.356876 /len=4079			
1	6651	0.001915	tumor necrosis factor (ligand)	NM_003810	Hs.83429	NP_003801
			superfamily, member 10 (TNFSF10),	-		
	į.		mRNA /cds=(96,941) /gb=NM_003810			•
ļ			/gi=23510439 /ug=Hs.83429 /len=1776	3 .	100	
	6656	0.046501	protein phosphatase 1, regulatory	NM_006241	Hs.267819	NP_006232
ļ			(inhibitor) subunit 2 (PPP1R2), mRNA			
			/cds=(235,852) /gb=NM_006241		*	200
	ŧ	*	/gi=19923357 /ug=Hs.267819 /len=3355	8		
ŀ		0.040000	AMB	NIM 000000	11- 007004	ND 0000F0
	6673	0.049308	cAMP responsive element binding	NM_006368	Hs.287921	NP_006359
	. :		protein 3 (luman) (CREB3), mRNA			
Ì			/cds=(439,1554) /gb=NM_006368 /gi=22219461 /ug=Hs.287921 /len=1837			
1	*	٠.	igi–222 1946 i 7ug–ns.20792 i 7ieii– 1037	,	•	
ł	6692	3 035-04	mitochondrial ribosomal protein S18B	NM_014046	Hs.274417	NP 054765
1	0032	Ģ.50L°0∓	(MRPS18B), nuclear gene encoding	14141_014040	113.27 4717	-05-705
		- 1	mitochondrial protein, mRNA		. ~	
١			/cds=(38,814) /gb=NM_014046			*
	44 ==		/gi=16554601 /ug=Hs.274417 /len=1439	***		
						*
1	6727	0.036549	ribosomal protein L13 (RPL13),	NM_033251	Hs.431392	NP_150254
		11.0	transcript variant 2, mRNA			
l		,	/cds=(238,873) /gb=NM_033251			
١		- 4	/gi=15431294 /ug=Hs.431392 /len=1296	100 0		
١		1.	-			
İ	6759	0.036549	signal recognition particle 19kDa	NM_003135	Hs.2943	NP_003126
			(SRP19), mRNA /cds=(82,516)			
		*	/gb=NM_003135 /gi=4507212		*	
١	-	•	/ug=Hs.2943 /len=894		4 3 4	
1	6773	0.041279	hypothetical protein FLJ14834	NM_032849	Hs.62905	NP_116238
			(FLJ14834), mRNA /cds=(326,1237)	*		
	•		/gb=NM_032849 /gi=21361885	· .		
		*	/ug=Hs.62905 /len=2342		·	

Snot	p-value	Description	Gene	Unigene	Protein	
Opor	b-saine	Description		Accession	Accession	
		* *	Accession No.			
6793	0.036549	transforming growth factor, beta receptor	NM 003243	<b>No.</b> Hs.342874	<b>No.</b> NP_003234	
0,35	0.000040	III (betaglycan, 300kDa) (TGFBR3),	NIVI_003243	115.342074	ME_003534	
19	1	mRNA /cds=(349,2898) /gb=NM_003243	*			
		/gi=4507470 /ug=Hs.342874 /len=4208	*			
	*	/gi=+00/+/0/ug=113:0420/+/1c1i=4200				
6813	0.034358	constitutive photomorphogenic protein	NM 022457	Hs.105737	NP 071902	
	0.00 1000	(COP1), mRNA /cds=(1,2196)	024 107	110.100707	141 _07 1002	
, ,		/gb=NM_022457 /gi=21359962			* * * * * * * * * * * * * * * * * * * *	
Ì '		/ug=Hs.105737 /len=2196	•			
6822	0.023381	MSTP031 protein (MSTP031), mRNA	NM_032035	Hs.105689	NP_114424	
		/cds=(663,1091) /gb=NM_032035	-			
		/gi=14042961 /ug=Hs.105689 /len=1284				
		3				
6825	0.043827	hypothetical protein MGC4400	NM 032679	Hs.130891	NP 116068	
, i	,	(MGC4400), mRNA /cds=(381,1817)	_		, <del></del> -	
		/gb=NM_032679 /gi=14249251	***			
		/ug=Hs.130891 /len=3067		*	dec	
6846	0.049308	mitogen-activated protein kinase kinase	NM_003188	Hs.7510	NP_663306	
		kinase 7 (MAP3K7), transcript variant A,	- · ·			
	-500	mRNA /cds=(306,2045) /gb=NM_003188				
		/gi=21735560 /ug=Hs.7510 /len=2912		ere e e		
			*		1	
6943	0.007397	hypothetical protein FLJ10849	NM_018243	Hs.8768	NP_060713	
* 1		(FLJ10849), mRNA /cds=(94,1383)	31			
		/gb=NM_018243 /gi=8922711		·		
, ×		/ug=Hs.8768 /len=2845			*	
6970	0.043827	neuroplastoma apoptosis-related RNA-	AF295068			
		binding protein (CUGBP2) gene, exons		1 .		
		10, 11a, 11b, 12, 13a, 13b, 14, and				
		complete cds, alternatively spliced				
6989	0.036549	transmembrane 9 superfamily member 1	NM_006405	Hs.91586	NP_006396	
		(TM9SF1), mRNA /cds=(35,1855)	*	**		
*		/gb=NM_006405 /gi=21361314	× .			
		/ug=Hs.91586 /len=2138				
6998	0.049308	DKFZp434P0235 (from clone	AL117519	Hs.34348	NP_849157	
.]	ł	DKFZp434P0235) /cds=UNKNOWN	٠,			
		/gb=AL117519 /gi=5912035	=			
6000	0.040504	/ug=Hs.34348 /len=1124	NIM 040500	110 460005	ND 000500	
6999	U.U465U1	ring finger protein 20 (RNF20), mRNA	NM_019592	Hs.168095	NP_062538	
		/cds=(91,3018) /gb=NM_019592				
		/gi=16554452 /ug=Hs.168095 /len=3936	*			
7045	0.00684	mothioning adenacyltronafarasa II. bat-	NIM 042202	Ho 54640	ND 027445	
/045	0.00084	methionine adenosyltransferase II, beta	NM_013283	Hs.54642	NP_037415	
	0.0	(MAT2B), mRNA /cds=(73,1077)		,		
		/gb=NM_013283 /gi=20127525				
7051	0.014461	/ug=Hs.54642 /len=2054	NM 004126	Hs.83381	NP_004117	
1001	0.014401	guanine nucleotide binding protein 11 (GNG11), mRNA /cds=(352,573)	NM_004126	115.03301		
	<b>,</b> .	/gb=NM_004126 /gi=20127455				
14.	<b>'</b>	/ур=NM_0041267gl=20127455  /ug=Hs.83381/len=884	540			
		/ug=113.00001 /IE11=004	<u> </u>		L	

Spot	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Accession	Acc ssion
٠.	9 1		, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	No.	No.
7052	0.043827	SUMO-1-specific protease (SUSP1),	NM_015571	Hs.27197	NP_056386
	*	mRNA /cds=(1,3339) /gb=NM_015571	=		_
		/gi=7662311 /ug=Hs.27197 /len=4210		* * * * * * * * * * * * * * * * * * * *	·
7068	0.020453	KIAA1128 protein (KIAA1128), mRNA	NM 018999	Hs.81897	NP 061872
	.*	/cds=(553,2253) /gb=NM_018999	-		
		/gi=24308130 /ug=Hs.81897 /len=7248			
7069		adenosine monophosphate deaminase	NM 000480	Hs.83918	NP_000471
		(isoform E) (AMPD3), mRNA	<u>-</u>		-
		/cds=(345,2675) /gb=NM 000480	*	,	
		/gi=4502078 /ug=Hs.83918 /len=3915			
7077	0.00299	mitochondrion, complete genome	NC 001807		3
7078		KIAA0438 gene product (KIAA0438),	NM_014819	Hs.279849	NP 055634
		mRNA /cds=(118,2244) /gb=NM_014819			_
		/gi=7662123 /ug=Hs.279849 /len=4765			
					(n)
7099	0.030302	cell division cycle 42 (GTP binding	NM_001791	Hs.146409	NP 426359
	• ,-	protein, 25kDa) (CDC42), transcript			_
*		variant 1, mRNA /cds=(105,680)			
×7.		/gb=NM_001791 /gi=16357470	ė.		
		/ug=Hs.146409 /len=2183			
7151	0.034358		NM_001379	Hs.77462	NP_001370
,	0 0	(DNMT1), mRNA /cds=(238,5088)			
	0)	/gb=NM_001379 /gi=4503350			9 0
-	- 80	/ug=Hs.77462 /len=5434			
7165	0.043827	zinc finger protein 25 (KOX 19) (ZNF25),		Hs.5856	NP_659448
		mRNA /cds=(106,1476) /gb=NM_145011			
		/gi=24462252 /ug=Hs.5856 /len=3736			
7175	0.01911	AGENCOURT_6853421 NIH_MGC_99	BQ064669	Hs.380699	
		cDNA clone IMAGE:5926418 5', mRNA		*	
	Tr.	sequence /clone=IMAGE:5926418		•	
		/clone_end=5' /gb=BQ064669	ĺ	1	
	t	/gi=19893520 /ug=Hs.380699 /len=969			
7176	0.016648	tumor protein, translationally-controlled 1	NM_003295	Hs.401448	NP_003286
'	Sec	(TPT1), mRNA /cds=(95,613)			
		/gb=NM_003295 /gi=4507668		· ·	,
7400	0.000055	/ug=Hs.401448 /len=830			
7186	0.026653	chromosome 9 open reading frame 7	NM_017586	Hs.119285	NP_060056
		(C9orf7), mRNA /cds=(59,577)			
	*	/gb=NM_017586 /gi=8922115			
7000	0.012400	/ug=Hs.119285 /len=2695	NIM 004500	11- 400070	ND 001550
7236	0.013463	eukaryotic translation initiation factor 3,	NM_001568	Hs.106673	NP_001559
		subunit 6 48kDa (EIF3S6), mRNA			
		/cds=(23,1360) /gb=NM_001568			
7260	0.020420	/gi=4503520 /ug=Hs.106673 /len=1510	AV005557	Us 440774 "	
7268	0.020428	cDNA: FLJ21904 fis, clone HEP03585.	AK025557	Hs.110771	
	٠, ,	/gb=AK025557 /gi=10438108			* 3
	**	/ug=Hs.110771 /len=2224		L.,,	l:

Spo	t p-valu	Description	Gene	Unigene	Protein
Opo	, b		Accession No.	Accession	Accession
	`.	* *	Adocasión no:	No.	No.
7272	0.034358	hypothetical protein FLJ11021 similar to	NM_023012	Hs.81648	NP_075388
	.   0.00 1000	splicing factor, arginine/serine-rich 4	7,020012	110,01010	, <u>_</u> <u>_</u> <u>_</u> <u>_</u>
100		(FLJ11021), mRNA /cds=(767,1375)			•
		/gb=NM_023012 /gi=20127619		·	
	<b>:</b> .	/ug=Hs.81648 /len=1878		() ()	
7278	0 024972	KIAA0648 protein (KIAA0648), mRNA	NM_015200	Hs.31921	NP_056015
	0.02 10 12	/cds=(232,4125) /gb=NM_015200	10200	110.0102,1	
		/gi=22094120 /ug=Hs.31921 /len=6744	·	0.00	*
7288	3 0.028428	KIAA0800 gene product (KIAA0800),	NM_014703	Hs.118738	NP_055518
	0.020.20	mRNA /cds=(169,4692) /gb=NM_014703		110.110700	000010
		/gi=7662315 /ug=Hs.118738 /len=5984			
	*	79. 7002010749 110. 110700 7611 0007		*	
7314	0.01004	chromosome 11 open reading frame 10	NM 014206	Hs.90918	NP_055021
		(C11orf10), mRNA /cds=(56,295)		7	
0.0		/gb=NM_014206 /gi=7656933			
		/ug=Hs.90918 /len=418	*		
7320	0.00274	RNA-binding region (RNP1, RRM)	NM 018107	Hs.4997	NP_060577
1		containing 4 (RNPC4), mRNA		1.0.1001	
		/cds=(187,1461) /gb=NM_018107			
1		/gi=21361701 /ug=Hs.4997 /len=2442		* * * *	
732	1 0.021876	translocase of inner mitochondrial	NM 006335	Hs.20716	NP 006326
		membrane 17 A (yeast) (TIMM17A),			
		mRNA /cds=(8,523) /gb=NM_006335	. 60	* *	
		/gi=5454119 /ug=Hs 20716 /len=1645	* * * * * * * * * * * * * * * * * * * *		
7349	9 0.030302	dermatopontin (DPT), mRNA	NM_001937	Hs.80552	NP_001928
		/cds=(7,612) /gb=NM_001937			
0		/gi=4755134 /ug=Hs 80552 /len=717	•	<b>`</b>	
7356	0.041279		NM 001831	Hs.75106	NP_001822
		40,40, sulfated glycoprotein 2,	_		
	-	testosterone-repressed prostate	,		
		message 2, apolipoprotein J) (CLU),			
	1	mRNA /cds=(48,1397) /gb=NM_001831			g a file
1		/gi=4502904 /ug=Hs.75106 /len=1676			7
			, , , , , , , , , , , , , , , , , , ,		
7.35	7 0.041279	chromosome 6 open reading frame 33	NM_133367	Hs.239388	NP_588608
		(C6orf33), mRNA /cds=(165,1229)			*
		/gb=NM_133367 /gi=19115959	*		
	#	/ug=Hs.239388 /len=4650			
736	3 0.043827	small acidic protein (SMAP), mRNA	NM_014267	Hs.78050	NP_055082
		/cds=(137,688) /gb=NM_014267			
		/gi=20070245 /ug=Hs.78050 /len=1504	•		
736	9   0.012525	cadherin 2, type 1, N-cadherin (neuronal)	NM_001792	Hs.161	NP_001783
		(CDH2), mRNA /cds=(206,2926)			
		/gb=NM_001792 /gi=14589888	• 😁	2	
		/ug=Hs.161 /len=4122			
7378	3 0.001915	regulator of G-protein signalling 10	NM_002925	Hs.82280	NP_002916
	1	(RGS10), mRNA /cds=(44,547)	<b>\</b>	*	,
1		/gb=NM_002925 /gi=11184225			
		/ug=Hs.82280 /len=664	[		

Spot	p-valu	Description	Gen	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No
7387	0.032261	ribosomal protein L4 (RPL4), mRNA	NM_000968	Hs.286	NP_000959
		/cds=(57,1340) /gb=NM_000968			
		/gi=16579884 /ug=Hs.286 /len=1449		<u> </u>	
7405	0.028428	MAGE-E1 protein (MAGE-E1), mRNA	NM_030801	Hs.7457	NP_803881
1		/cds=(146,1390) /gb=NM_030801	٠.		
		/gi=13540587 /ug=Hs.7457 /len=2997			
7414	0.0062	tetraspanin similar to TM4SF9 (DC-	NM_030927	Hs.101395	NP_112189
	, ,	TM4F2), mRNA /cds=(79,891)	00		, ,
	7	/gb=NM_030927 /gi=13569888		. '	
		/ug=Hs.101395 /len=2556			
7418	0.026653	similar to KIAA1795 protein (H. sapiens)	XM_059632		
7400	0.000040	(LOC133247), mRNA	VII. 074400	-	
7483	0.009313	hypothetical gene supported by	XM_074428		2
7500	0.046504	XM_074428 (LOC123440), mRNA	AJ421269	11- 004446	NP_061185
7508	0.046501	mRNA for RCC1-like protein (TD-60 gene) /cds=(236,1804) /gb=AJ421269	AJ42 1269	Hs.284146	NP_001185
-00		/gi=27526612 /ug=Hs.284146 /len=4114			
* -		/gi-2/320012/ug=145.204140/left=4   14 	\$ -\$-		,
7510	0.015521	hypothetical protein MGC14327	NM_053045	Hs.231029	NP 444273
1 /010	0.010021	(MGC14327), mRNA /cds=(225,635)	11111_000040	113.201023	1111210
1		/gb=NM 053045 /gi=16596685			
		/ug=Hs.231029 /len=1576	* .	,	
7533	0.036549	pleiomorphic adenoma gene-like 1	NM_006718	Hs.75825	NP_006709
		(PLAGL1), transcript variant 2, mRNA			
, ·		/cds=(2242,3633) /gb=NM_006718			
	*	/gi=27894292 /ug=Hs.75825 /len=4816	·		*
7550	0.026653	hypothetical protein FLJ20343	NM_017775	Hs.252692	NP_060245
,		(FLJ20343), mRNA /cds=(19,1524)			
]	•	/gb=NM_017775 /gi=22547158		]	
		/ug=Hs.252692 /len=2784	*		
7564	0.026653	paired basic amino acid cleaving system	NM_002570	Hs.170414	NP_612198
		4 (PACE4), transcript variant 1, mRNA			
	•	/cds=(315,3224) /gb=NM_002570 /	-		
		/gi=20336178 /ug=Hs.170414 /len=4553		\$1.	
7578	0.004064	hypothetical protein DKFZp586G0123	NM 013386	Hs.24713	NP_037518
1210	0.004961	(DKFZp586G0123), mRNA	14111-012200	JNS.241 13	NF_03/310
	3	/cds=(25,315) /gb=NM_013386			
10		/gi=9558726 /ug=Hs.24713 /len=1294			*
7592	0.036549	KIAA1221 protein (KIAA1221), mRNA	NM 032186	Hs.173001	NP 115562
	0.000010	/cds=(129,4037) /gb=NM 032186			
		/gi=24496786 /ug=Hs.173001 /len=5531	1		
	t.				
7614	0.012525	ALS2CR3 gene for amyotrophic lateral	AB038962		
		sclerosis 2, candidate 3, exon 14			· .
7683	0.032277	zinc finger protein 302 (ZNF302), mRNA	NM_018675	Hs.125287	NP_061145
		/cds=(337,1773) /gb=NM_018675		-	}
		/gi=11034834 /ug=Hs.125287 /len=2978	İ		
<u> </u>	l	<u> </u>	L	<u> </u>	

Spot	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
7714	0.041279	hypothetical protein MGC40107	NM_152766	Hs.94316	NP_689979
-80		(MGC40107), mRNA /cds=(40,381)			
1	·	/gb=NM_152766 /gi=22749498		}	
		/ug=Hs.94316 /len=495		-	
7716	0.026653	IFNAR gene (HSIFNAR) for interferon	X60459		
		alpha/beta receptor			
7717	0.024972	similar to putative (H. sapiens)	XM_059351		
- 1		(LOC129401), mRNA	: :		
7730	1.00	MTB (MTB) mRNA, complete cds	AF348994	Hs.333727	NP_783321
1		/cds=(80,265) /gb=AF348994	0		
		/gi=28190031 /ug=Hs.333727 /len=408			·
7738	0.030302	te65d01.x1 Soares_NFL_T_GBC_S1	Al377292 .	Hs.410753	
		cDNA clone IMAGE:2091553 3', mRNA			
		sequence /clone=IMAGE:2091553	0 00	*	*
*-		/clone_end=3' /gb=Al377292			
		/gi=4187145 /ug=Hs.410753 /len=238			
7789	0.023381	EST (DKFZp564A043 clone	AL050007		
<u></u>		DKFZp564A043)			
7851	0.032277	capillary morphogenesis protein 2	NM_058172	Hs.5897	NP_477520
		(CMG2), mRNA /cds=(46,783)	:		• .
	` .	/gb=NM_058172 /gi=17158002			* .
		/ug=Hs.5897 /len=2026		· _	
7868	0.049308	EST(yx98h12.s1 Soares melanocyte	N24829		·
7000	0.040007	2NbHM cDNA clone IMAGE:269831 3')	1114 007000	10040	ND 040500
7923	0.043827	Tara-like protein (HRIHFB2122),	NM_007032	Hs.40342	NP_619538
		transcript variant 1, mRNA		'	
,		/cds=(176,1957) /gb=NM_007032	-10-		,
7925	0.046504	/gi=20336765 /ug=Hs.40342 /len=2687 EST(ng19d12.s1 NCI_CGAP_Lip2 cDNA	A A E O 1 0 2 2		
/925	0.046501	clone IMAGE:929879 similar to contains	AA301023		
		Alu repetitive element; contains element	٤	*.	
-		MSR1 repetitive element)			
}			·	-	
7928	0.049308	hypothetical protein HSPC195	NM_016463	Hs.356509	<del> </del>
, 52.0	3,04000	(HSPC195), mRNA /cds=(293,889)	1.1.10 10400	1.15.00000	
		/gb=NM_016463 /gi=20070365			*
1.0		/ug=Hs.356509 /len=1108			
7943	0.001915	EST (AV754618 TP cDNA clone	AV754618	*	
	4.5.70.0	TPGAAA04 5')	1		
7992	0.004569	brain cDNA clone:QccE-22013, full insert	AB060197	<u> </u>	· · · · · · · · · · · · · · · · · · ·
		sequence	,		
8017	0.041279	secreted frizzled-related protein 5	NM 003015	Hs.279565	NP 003006
		(SFRP5), mRNA /cds=(182,1135)			_
1		/gb=NM 003015 /gi=8400734			1
		/ug=Hs.279565 /len=1905			·
8018	9.88E-04		NM_001070	Hs.21635	NP_001061
		/cds=(25,1380) /gb=NM_001070	_	*	
		/gi=4507730 /ug=Hs.21635 /len=1568		_	
8018	9.88E-04	tubulin, gamma 1 (TUBG1), mRNA /cds=(25,1380) /gb=NM_001070	NM_001070	Hs.21635	NP_001061

Spot	p-value	Description	Gene	Unigene	Protein
	8	*	Accession No.	Accession No.	Accession No.
8030	0.041279	FLJ23497 (FLJ23497), mRNA	NM 025089	Hs.288498	NO.
		/cds=(624,1091) /gb=NM 025089	_	* *	
		/gi=13376647 /ug=Hs.288498 /len=1929	600		
<u> </u>			,	e e	
8036	0.012525	mitogen-activated protein kinase kinase	NM_003188	Hs.7510	NP_663306
	• •	kinase 7 (MAP3K7), transcript variant A,			
	,	mRNA /cds=(306,2045) /gb=NM_003188		3 (3)	* 00
•		/gi=21735560 /ug=Hs.7510 /len=2912			
		*		1	
8046	0.011644	cDNA FLJ10423 fis, clone	AK001285	Hs.106909	
, ,		NT2RP1000259 /gb=AK001285	* , .		
-		/gi=7022444 /ug=Hs 106909 /len=1837			
8080	0.024972	tumor necrosis factor receptor	NM_002546	Hs.81791	NP_002537
		superfamily, member 11b			
		(osteoprotegerin) (TNFRSF11B), mRNA			
* .		/cds=(252,1457) /gb=NM_002546		*	
0	-	/gi=22547122 /ug=Hs.81791 /len=2291	·-	i at	
8137	0.020055	cartilage acidic protein 1 (CRTAC1),	NM_018058	Hs.326444	ND 000529
0137	0.030000	mRNA /cds=(319,1575) /gb=NM_018058		ITS.320444	NP_060528
		/gi=8922351 /ug=Hs.326444 /len=2178	0		
		/gi=0922331 /dg=115.320444 /left=2176			
8163	0.041279	NADH dehydrogenase (ubiquinone) 1	NM_002491	Hs.109760	NP_002482
]."		beta subcomplex, 3, 12kDa (NDUFB3),	11111_002-101	113.100700	111 _002-102
ļ	,	mRNA /cds=(253,549) /gb=NM_002491			
٠.		/gi=4505360 /ug=Hs.109760 /len=693			* *
		, , , , , , , , , , , , , , , , , , ,	8		
8182	0.049308	general transcription factor IIH,	NM_001515	Hs.191356	NP_001506
, ,		polypeptide 2, 44kDa (GTF2H2), mRNA	_		<del>-</del>
		/cds=(1,1188) /gb=NM_001515		*	
		/gi=6681761 /ug=Hs.191356 /len=1188			
8198	0.016648	PHD zinc finger protein XAP135	NM_133325	Hs.7759	NP_579866
	-	(XAP135), transcript variant 2, mRNA	•		
'	· .	/cds=(222,1448) /gb=NM_133325	*		
	1 2 2 3 1 2 3 1 2 3 1	/gi=19747275 /ug=Hs.7759 /len=1583			
8199	0.005835	hypothetical protein MGC18216	NM_152452	Hs.104679	NP_689665
		(MGC18216), mRNA /cds=(2207,2374)			
		/gb=NM_152452 /gi=22748948			
10000	0.000465	/ug=Hs.104679 /len=3270	1114 007070	11. 000740	ND DOCCO
8223	0.028428	FK506 binding protein 9, 63 kDa	NM_007270	Hs.302749	NP_009201
•		(FKBP9), mRNA /cds=(457,885)		· .	
		/gb=NM_007270 /gi=24307926			
8227	0.004205	/ug=Hs.302749 /len=2517	NM 017040	Un 22256	ND 060390
0227	0.004205	hypothetical protein FLJ20628 (FLJ20628), mRNA /cds=(23,1456)	NM_017910	Hs.32356	NP_060380
		/gb=NM_017910 /gi=13435382		1	
		/ug=Hs.32356 /len=1846			<b>]</b> .
<u> </u>	1	1/09-1 15.52550 Nett-1040	1		

Spot	p-value	Description	Gene	Unigene	Protein
1,44			Accession No.	Accession	Accession
·		# - ip		No.	No.
8231	0.007397	peptide-histidine transporter 4 (PTR4),	NM_145648	Hs.355660	NP_663623
		mRNA /cds=(59,1792) /gb=NM_145648			ý.
1 .		/gi=21717815 /ug=Hs.355660 /len=2807			
8240		mitochondrion, complete genome	NC_001807	3 2 2 2 3	
8241	0.002161	hypothetical protein MGC3196	NM_024084	Hs.309161	
()		(MGC3196), mRNA /cds=(178,291)		=	
		/gb=NM_024084 /gi=13129079		+	
		/ug=Hs.309161 /len=603	A-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1		
8243	0.023381	T-cell lymphoma invasion and	NM_012454	Hs.12598	NP_036586
		metastasis 2 (TIAM2), mRNA			4:
		/cds=(51,3284) /gb=NM_012454			
0046	0.044070	/gi=6912703 /ug=Hs.12598 /len=4586	NINA 040007	11- 422400	ND 020400
8246	0.041279	Ras-GTPase activating protein SH3 domain-binding protein 2 (KIAA0660),	NM_012297	Hs.433496	NP_036429
	0	mRNA /cds=(121,1569) /gb=NM 012297	(1)		
		/gi=19923398 /ug=Hs.433496 /len=4210			- *
		/g = 19925596 /ug=H5.455496 /iefl=4210			
8258	0.036549	EST(zb77f03.s1 Soares senescent	N94450		NP 073600
0200	0.000040	fibroblasts NbHSF cDNA clone 309629			14070000
	1,7	3')		· .	
8262	0.043827	HSPC166 protein (HSPC166), mRNA	NM_014186	Hs.279836	NP 054905
1 "		/cds=(19,615) /gb=NM_014186			
		/gi=7661827 /ug=Hs.279836 /len=1318			*
8311	0.015521	clone IMAGE:5295441, mRNA	BC043222	Hs.405253	
	* * * * * * * * * * * * * * * * * * *	/gb=BC043222 /gi=28175025	, 1	.: * .	
		/ug=Hs.405253 /len=2712	<u> </u>		
8345	0.034358	hypothetical protein FLJ35613	NM_173653	Hs.30022	NP_775924
		(FLJ35613), mRNA /cds=(126,2063)		φ.	
		/gb=NM_173653 /gi=27734934	ان ،		
0005	0.040007	/ug=Hs.30022 /len=3568	A)A(070.457		
8395	0.043827	EST xp73h11.x1 NCI_CGAP_Ov40	AW270457		
		cDNA clone IMAGE:2746053 3' similar			
,	* 1	to contains Alu repetitive element;contains element MER32			
		repetitive element;	*		
8417	0.032277	EST QV4-FT0005-110500-203-e03	AW949100		
		FT0005			
8432	8.95E-04	EST 7f59d09.x1	BE677740		
(a) 180		Soares_NSF_F8_9W_OT_PA_P_S1		*	* *
		H.sapiens cDNA clone IMAGE:3298961	*	*	· .
	. *	3'	·	* *	o'
8435	0.00274	BX099435 NCI_CGAP_Co8 cDNA clone	BX099435	Hs.126589	
		IMAGp998M083951, mRNA sequence		*	•.
:		/clone=IMAGp998M083951_;_IMAGE:15		*	
		59599 /gb=BX099435 /gi=27829993			
	ā	/ug=Hs 126589 /len=659	; - *		
		310	·		·

Spot	p-value	Description	Gene	Unigene	Protein
				Accession	Accession
-	* * *			No.	No.
8443	0.004569	UI-H-EU1-bag-b-11-0-UI.s1	BQ448425	Hs.438826	
6		NCI_CGAP_Ct1 cDNA clone UI-H-EU1-	**		
	* • •	bag-b-11-0-UI 3', mRNA sequence			i ta i
,		/clone=UI-H-EU1-bag-b-11-0-UI		ė.	
=		/clone_end=3' /gb=BQ448425	* *0		
		/gi=21251537 /ug=Hs.438826 /len=1023			17
8457	0.030303	EST (T98494 ye60e05.s1 Soares fetal	T98494		
0437	0.030302	liver spleen 1NFLS cDNA clone	190494		
	. 8	IMAGE: 122144 3')			
8460	0.020453	AV705591 ADB cDNA clone ADBCGF11	AV705591	Hs.287350	<del> </del>
0.00		5', mRNA sequence /clone=ADBCGF11	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	113.20700	
		/clone_end=5' /gb=AV705591			
	r.	/gi=10722889 /ug=Hs.287350 /len=677			
			- · · · · · · · · · · · · · · · · · · ·		
8489	0.036549	CLK4 mRNA sequence /cds=(154,1515)	AF212224	Hs.406557	* - *
		/gb=AF212224 /gi=9437514			
	٠	/ug=Hs.406557 /len=1865			100
8499	0.026653	hypothetical protein FLJ30999	NM_152461	Hs.129166	NP_689674
0		(FLJ30999), mRNA /cds=(302,703)	*\		**
*		/gb=NM_152461 /gi=22748964			- ,
0500	0.000540	/ug=Hs.129166 /len=2067	AVA (0.00 574	115 400000	
8500	0.036549	EST375644 MAGE resequences, MAGH	AVV963571	Hs.182962	
		cDNA, mRNA sequence /gb=AW963571 /gi=8153407 /ug=Hs 182962 /len=672	÷	-	10
		/gi=013340/ /dg=115.102902/len=0/2	*	·	100
8501	0.021876	hypothetical protein FLJ40137	NM 173478	Hs.412708	NP 775749
		(FLJ40137), mRNA /cds=(149,1141)			
		/gb=NM_173478 /gi=27735056		·	
		/ug=Hs.412708 /len=2241			, i * *
8529	0.041279	EST (602645742F1 NIH_MGC_76 clone	BG618375		
		IMAGE:4767299 5')			
8547	0.011644	cDNA FLJ36837 fis, clone	AK094156	Hs.36475	• •
	4 =	ASTRO2011422. /gb=AK094156	·	8	
0550	0.046649	/gi=21753158 /ug=Hs.36475 /len=3302	VICOUSOCS	115 404600	* * * * * * * * * * * * * * * * * * * *
8550	0.0 10048	cDNA FLJ36544 fis, clone TRACH2006378. /gb=AK093863	AK093863	Hs.101689	
		/gi=21752807 /ug=Hs.101689 /len=2670		· ·	
		17 02007 7ug=113, 10 1003 /left=2070			
8553	0.032277	EST (we35d08.x1 NCI_CGAP_Lü24	AI701473	* / 4 4	
		cDNA clone IMAGE:2343087 3' similar			
	0) 0	to contains L1.t1 L1 repetitive element )			*
		· Y	.2	unia.	
8570	0.024972	EST hz28e05.x1 NCI_CGAP_GC6	BE466897	4.3	
		cDNA clone IMAGE:3209312 3'			
8577	0.049308	RC5-FT0194-271100-022-B06 FT0194	BF858635	Hś.270272	
	= ,	cDNA, mRNA sequence /gb=BF858635			
		/gi=12246379 /ug=Hs.270272 /len=590			
	<u> </u>			L	

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
		-		No.	No.
8595	0.046501	ribosomal protein L3 (RPL3), mRNA	NM_000967	Hs.119598	NP_000958
		/cds=(27,1238) /gb=NM_000967	_	·	
÷ .		/gi=16507968 /ug=Hs.119598 /len=1311	*	e	
			*		
8604	0.041279	wg14b12.x1	AI800904	Hs.132105	
		Soares_NSF_F8_9W_OT_PA_P_S1			
		cDNA clone IMAGE:2365055 3', mRNA	••		
		sequence /clone=IMAGE:2365055			. No. 1
		/clone_end=3' /gb=Al800904		. V	
		/gi=5366376 /ug=Hs.132105 /len=537		· ·	
8610	0.014461	EST, cDNA /gb=AW816379 /gi=7909373	AW816379	Hs.335018	
		/ug=Hs.335018 /len=603			
8622	0.005834	FLJ30623 fis, clone CTONG2001748	AK055185	Hs.351574	NP_079050
		/cds=UNKNOWN /gb=AK055185			1
•• ***		/gi=16549855 /ug=Hs.351574 /len=2870			
*s	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	<u></u>			
8623	0.015521	cDNA FLJ31753 fis, clone	AK056315	Hs.349283	
		NT2RI2007468. /gb=AK056315		*	
		/gi=16551681 /ug=Hs.349283 /len=2361	*		÷ .
	72				
8624	0.014461	mRNA; cDNA DKFZp313C0935 (from	AL832706	Hs.433110	
	÷	clone DKFZp313C0935) /gb=AL832706	*		
	**	/gi=21733285 /ug=Hs.433110 /len=3270	4	4	
0040	0.004045	1.00140 4.NOL OOAD LINKO DNA	D0070705	11- 440000	
8649	0.001915	nah90b12.x1 NCI_CGAP_HN19 cDNA	BG272785	Hs.440690	* *
		clone IMAGE:4257766 similar to P39194	. * •	1	
		ALU SUBFAMILY SQ SEQUENCE		*	
·. •		CONTAMINATION WARNING ENTRY			
	iRi	[1] ;contains Alu repetitive element;, mRNA sequence			* .
	1.	/clone=IMAGE:4257766 /gb=BG272785	* "		*
		/gi=12982288 /ug=Hs.440690 /len=360		Ġ.	
	*	/g -  2962266/ug-H5.440696/lell-366		_	
8653	0.000313	EST, cDNA /clone=DKFZp586F2021	AL047579	Hs.310753	* *
0000	0.009313	/gb=AL047579 /gi=4728575	1,1041313	11.13.0 107.00	
		/ug=Hs.310753 /len=431	-		:
8661	0.011644	UI-H-EI1-azf-b-12-0-UI.s1	BQ003897	Hs.446354	†
5001,	3.011044	NCI_CGAP_EI1 cDNA clone	24000001	1, 13.7-7009-7	* .
	,	IMAGE:5847851 3', mRNA sequence		Δ.	-
		/clone=IMAGE:5847851 /clone_end=3'			
	*	/gb=BQ003897 /gj=19728797		1	1
		/ug=Hs.446354 /len=1034	2 2 2		1
8662	0.007397	ts93d11.x1 NCI_CGAP_GC6 cDNA	Al631165	Hs.196952	<del> </del>
5502		clone IMAGE:2238837 3', mRNA			4.
		sequence /clone=IMAGE:2238837			
		/clone_end=3' /gb=Al631165		*2	
1.		/gi=4682495 /ug=Hs.196952 /len=537			
8669	0.012525	cDNA FLJ10190 fis, clone	AK001052	Hs.274546	
7777		HEMBA1004753. /gb=AK001052			V * Y

Spot	p-value	Description	G ne	Unigene	Protein
			Acc ssion No.	Accession No.	Accession No.
8673	0.005835	jun1.P1.D7 conorm cDNA 3', mRNA	AI535800	Hs.369112	NO.
	.0.0000	sequence /clone end=3' /gb=Al535800			
		/gi=4449935 /ug=Hs.369112 /len=480		*	
8675	0.041279	UI-H-EI0-ayo-a-20-0-UI.s1	BQ004581	Hs.412459	
		NCI_CGAP_EI0 cDNA clone			
		IMAGE:5841307 3', mRNA sequence		•	
	·	/clone=IMAGE:5841307 /clone end=3'		8 "-7"	
		/gb=BQ004581 /gi=19729481			
		/ug=Hs 412459 /len=1095			
8680	0.014457	hypothetical protein FLJ32234	NM_152551	Hs.13366	NP 689764
		(FLJ32234), mRNA /cds=(37,471)	<del>-</del>	•	
		/gb=NM_152551 /gi=22749140			
		/ug=Hs.13366 /len=3051			
8685	0.036549	Similar to ubiquitin protein ligase E3A	BC040187	Hs.25320	
		papilloma virus E6-associated protein,		*	. *
		Angelman syndrome), clone		1	
		IMAGE:4811444, mRNA /gb=BC040187		*	
		/gi=25455694 /ug=Hs.25320 /len=4823	0 2		· .
				. * .	
8686	0.005835	mRNA; cDNA DKFZp564P016 (from	AL049337	Hs.132571	
-		clone DKFZp564P016) /gb=AL049337	9	,	*
		/gi=4500118 /ug=Hs.132571 /len=1938			
8689	0.021876	ESTs, cDNA, 3' end	AL044007	Hs.95663	
		/clone=DKFZp434l2028 /clone_end=3'	• •	*	
ļ		/gb=AL044007 /gi=5432235			
	,	/ug=Hs.95663 /len=535			
8695	0.038855	HNC36-1-D2.R HNC Normal Cartilage)	BG924955	Hs.351383	
		cDNA, mRNA sequence /gb=BG924955			
		/gi=14319478 /ug=Hs.351383 /len=722			
8707	0.041279	tc93c11.x1 NCI_CGAP_CLL1 cDNA	Al475669	Hs.309348	
	*	clone IMAGE:2073716 3' similar to		*	
-		contains Alu repetitive element;, mRNA	0.	. *	
		sequence /clone=IMAGE:2073716	,		
		/clone_end=3' /gb=Al475669			
0700	0.0000==	/gi=4328714 /ug=Hs.309348 /len=487	A5004540	110 250440	
8709	0.032277	clone alpha_est218/52C1 mRNA	AF001542	Hs.356442	
		sequence /gb=AF001542 /gi=2529714	· · · _		· ·
0740	0.00445	/ug=Hs.356442 /len=2992	DUEGO767	<del>                                     </del>	NP 005339
8710		EST(cDNA clone IMAGE:6617359 5'.)	BU569767 BU617862	Hs.441168	INE_003338
8715	[ U.UZ3381	UI-H-DF0-bet-a-18-0-UI.s1	DU01/802	[[75.44   108	
	-20	NCI_CGAP_DF0 cDNA clone UI-H-DF0-			
		bet-a-18-0-UI 3', mRNA sequence /clone=UI-H-DF0-bet-a-18-0-UI	. ,	1	
		/clone_end=3' /gb=BU617862			
		/gi=23284077 /ug=Hs.441168 /len=1092	•		
	*	/gi-202040// /dg-115.44   100 /leli-1092	,		
<u> </u>	<u> </u>			I,	<u> </u>

Snot	p-value	Description	G ne	Unigene	Protein
Opor	P value	Description		Accession	Accession
	*			No.	No.
8720	0.024972	UI-H-EU0-azs-p-18-0-UI.s1	BQ183906	Hs.356538	
		NCI_CGAP_Car1 cDNA clone IMAGE:			0
-		5853185 3', mRNA sequence			
		/clone=IMAGE:_5853185 /clone_end=3'			. **
	÷	/gb=BQ183906 /gi=20359457			
		/ug=Hs.356538 /len=1068			-
8727	0.028428	Similar to L1 repeat, Tf subfamily,	BC030623	Hs.227591	
		member 14, clone IMAGE:4820809,	.*		
	,	mRNA /gb=BC030623 /gi=22539740			
		/ug=Hs.227591 /len=2185	``	*	
8754	0.028428	602072454F1 NCI_CGAP_Brn67 cDNA	BF530944	Hs.319823	· 10 8
		clone IMAGE:4215325 5', mRNA			
-		sequence /clone=IMAGE:4215325	* - 5 * *		
	- 3: -	/clone_end=5' /gb=BF530944			
	<u> </u>	/gi=11618307 /ug=Hs.319823 /len=686			
8755	0.021876	UI-H-EI1-azd-l-09-0-UI.s1	BQ003406	Hs.269493	
		NCI_CGAP_EI1 cDNA clone	9 (	·	
		IMAGE:5847320 3', mRNA sequence		*	
, , , , , , , , , , , , , , , , , , ,	•	/clone=IMAGE:5847320 /clone_end=3			*
,		/gb=BQ003406 /gi=19728306	. 1		1
		/ug=Hs.269493 /len=1055		11 70 514 505	
8757	0.00684	602319564F1 NIH_MGC_89 cDNA	BG249501	Hs.281067	
		clone IMAGE:4415078 5', mRNA	19	*	=
		sequence /clone=IMAGE:4415078	. *		
		/clone_end=5' /gb=BG249501			
0764	0.024250	/gi=12759329 /ug=Hs.281067 /len=976	AL137501	Hs.306470	
8764	0.034356	mRNA; cDNA DKFZp761G241 (from	AL 13/501	IDS.300470	
		clone DKFZp761G241) /gb=AL137501 /gi=6808146 /ug=Hs.306470 /len=3018			
8774	0.020452	EST(cDNA clone IMAGE:4257808	BG272788	1 1 1	
0//4	0.020433	similar to contains Alu repetitive element;			
				,	
8777	0.030305	U-E-EO1-ajc-l-12-0-Ul.r1 UI-E-EO1	BM718946	Hs.364651	
"'''	0.000002	cDNA clone UI-E-EO1-ajc-I-12-0-UI 5',	× 10040	1.13.304031	-
		mRNA sequence /clone=UI-E-EO1-ajc-l-		-	*
1	0	12-0-UI /clone_end=5' /gb=BM718946		•	,
		/gi=19037365 /ug=Hs.364651 /len=1031			
		1.5. 1.5551.5557.4g 1.15.554051.71611=1001	. ,		
8780	0.00299	MR2-CI0186-291100-010-a06 CI0186	BF814502	Hs.446594	-1
		cDNA, mRNA sequence /gb=BF814502		, ,	
		/gi=12147047 /ug=Hs.446594 /len=530			·
8794	0.032277	AGENCOURT_8475922	BQ721341	Hs.128076	
		Lupski_sympathetic_trunk cDNA clone	*		* **
		IMAGE:6195208 5', mRNA sequence			
		/clone=IMAGE:6195208 /clone_end=5'			
		/gb=BQ721341 /gi=21860238	*		
		/ug=Hs.128076 /len=1186	· 0 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	<u></u>	

Spot	p-valu	D scription	G ne	Unig ne	Protein
Opot	p iaia			Acc ssion	Accession
			Accession No.	No.	No.
8800	3 53F-04	UI-H-FH1-bfi-o-08-0-UI.s1	CA427422	Hs.182545	NO.
0,000	0,002 0 1	NCI_CGAP_FH1 cDNA clone UI-H-FH1-		110.102010	
		bfi-o-08-0-UI 3', mRNA sequence			
		/clone=UI-H-FH1-bfi-o-08-0-UI			9 7
		/clone_end=3' /gb=CA427422			
		/gi=24790148 /ug=Hs.182545 /len=1150		. *	
•		791 247 00 140 70g 110. 1020 10 71cm 1100			*
8826	0.043827	cDNA FLJ25058 fis, clone CBL04608.	AK057787	Hs.350624	
0020	0.010021	/cds=(139,639) /gb=AK057787	,	1.0.00002	
	1	/gi=16553726 /ug=Hs.350624 /len=1808			
		, g, , , , , , , , , , , , , , , , , ,			
8827	0.020453	ob11d04.s1 NCI_CGAP_Kid3 cDNA	AA872730	Hs.125229	7 ·
00=:		clone IMAGE:1323367 3' similar to	7 3 3 4 1 4 1 5 4		
		contains Alu repetitive element contains			
, ,		element LTR5 repetitive element;			
-		mRNA sequence			*
100		/clone=IMAGE:1323367 /clone end=3'			
		/gb=AA872730 /gi=2968852	*		
×		/ug=Hs.125229 /len=586			
8836	0.026653	No significant match	SEQ.ID.No.33		
8863	0.036549	EST(cDNA clone IMAGE:290115 3'	N63269	10 W AL. 2	1-14 + 11 H H
		similar to contains Alu repetitive			
		element;contains element MSR1	*	·	
/0		repetitive element;)	7		
8865	0.01004	cDNA FLJ12091 fis, clone	AK022153		* -
-		HEMBB1002582			
8909	0.036549	WW domain-containing adapter with a	NM_100264	Hs.70333	NP_567823
		coiled-coil region (WAC), transcript			
		variant 2, mRNA /cds=(332,2140)	·		
		/gb=NM_100264 /gi=18379329			*
		/ug=Hs.70333 /len=3088		•	*
8913	0.002294	EST xc94a04.x1 NCI_CGAP_Brn35	AW090604		
	*	cDNA clone IMAGE:2591886 3' similar		*	
. (		to contains element MSR1 repetitive			
		element;			*
8914	0.020596	EST (PM1-CT0247-101199-003-h12	AW852630		7 7 7
		CT0247		Ī.	
8946	0.014461	hypothetical protein FLJ33282	NM_152388	Hs.346509	
		(FLJ33282), mRNA /cds=(225,1523)		. *	
1	* *	/gb=NM_152388 /gi=22748830			
	<u> </u>	/ug=Hs.346509 /len=2078			
8963	0.032277	EST(IL2-HT0433-020200-041-F07_1	BE161204		
L		HT0433)			
8974	0.046501	BX094154 Soares fetal liver spleen	BX094154	Hs.12962	
		1NFLS cDNA clone IMAGp998P17654,			
		mRNA sequence	X *		
		/clone=IMAGp998P17654_;_IMAGE:293	* * *		. "
t .	•	632 /gb=BX094154 /gi=27826950			a .
	1	/ug=Hs.12962 /len=758	<u>ļ </u>	<u> </u>	

S	pot	p-value	Description	Gene	Unig ne	Protein
		<i>a</i> .		Accession No.	Accession	Accession
_						No.
89	975	0.011644	7e58g12.x1	BE644873	Hs.417404	
			Soares_NSF_F8_9W_OT_PA_P_S1		*	; *
			cDNA clone IMAGE:3286726 3', mRNA			*
			sequence /clone=IMAGE:3286726		-	
, .	•		/clone_end=3' /gb=BE644873			
L			/gi=9969184 /ug=Hs.417404 /len=494			
89	976	0.036549	wg12a04.x1	AI800735	Hs.115122	Υ.
			Soares_NSF_F8_9W_OT_PA_P_S1			
ŀ			cDNA clone IMAGE:2364846 3', mRNA			
			sequence /clone=IMAGE:2364846			• 00
Ē			/clone_end=3' /gb=AI800735			
L			/gi=5366129 /ug=Hs.115122 /len=555			*
90	027	0.023381	UI-H-EU0-azt-n-21-0-UI.s1	BQ183977	Hs.421341	
			NCI_CGAP_Car1 cDNA clone IMAGE:	2	.9. 0	-
,	*	5 +4	5853524 3', mRNA sequence			. *
			/clone=IMAGE:_5853524 /clone_end=3'			
*			/gb=BQ183977 /gi=20359528			
		i 1	/ug=Hs.421341 /len=1142	18		
	. `		*			£.* ×
90	029	0.020453	ol54a01.s1 Soares_NFL_T_GBC_S1	AA917705	Hs.190264	
			cDNA clone IMAGE:1527240 3' similar			HC
		\.	to contains Alu repetitive element;,		a design	•
1		,	mRNA sequence	•	0	
	2 .		/clone=IMAGE:1527240 /clone_end=3'		8	
	( ×		/gb=AA917705 /gi=3057595		():	,
ľ			/ug=Hs.190264 /len=515			*
9	030	0.046501	EST(cDNA RC0-NT0113-300500-011-	BF366806	4	
		.,	g05 NT0113)			*
9	062	0.043827	gh54d02.x1	AI240813	Hs.368570	7.4
		,	Soares_fetal_liver_spleen_1NFLS_S1	·		
	. (		cDNA clone IMAGE:1848483 3' similar		+	1 1
			to contains MER30 b3 MER30 repetitive	,		
			element ;, mRNA sequence			
			/clone=IMAGE:1848483 /clone_end=3'			
			/gb=Al240813 /gi=3836210		*	
	•	L.	/ug=Hs.368570 /len=459	•		· :
9	080	0.032277	EST(cDNA clone IMAGE:4999711 5')	BI092644		NP_004883
-	101		clone IMAGE:5261213, mRNA	BC036485	Hs.26418	
			/gb=BC036485 /gi=22209057			- B
		. *	/ug=Hs.26418 /len=2880			
9	106	0.046501	yz39f06.s1 Morton Fetal Cochlea cDNA	N66393	Hs.102754	
			clone IMAGE:285443 3', mRNA	,		
1 .			sequence /clone=IMAGE:285443	•		
-		1		i	1	1 .
			/clone_end=3' /gb=N66393 /gi=1218518			-

Spot	p-value	Description	Gene	Unigene	Protein
· ) '			Accession No.	Accession	Accession
9108	0.001747	UI-H-EI0-aye-c-17-0-UI.s1	CA447385	<b>No.</b> Hs.420740	No.
3100	0.001747	NCI_CGAP_EI0 cDNA clone UI-H-EI0-	CA447303	105.4 <u>2</u> 0740	X .
				(	
1	1.00	aye-c-17-0-UI 3', mRNA sequence		* •	\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*
		/clone=UI-H-EI0-aye-c-17-0-UI			9.0 (1.0)
		/clone_end=3' /gb=CA447385	,		
0400	0.004070	/gi=24811805 /ug=Hs.420740 /len=812	1111000077		
9129		EST(cDNA.	AW896077		
9131	0.01004	ESTs, cDNA, 5' end	BF342391	Hs.30469	NP_055313
		/clone=IMAGE:4148900 /clone_end=5'			
		/gb=BF342391 /gi=11289392	41 00		· .
		/ug=Hs.30469 /len=803			
9137	0.034358	cDNA FLJ31919 fis, clone	AK056481	Hs.400872	
		NT2RP7004964. /gb=AK056481			
		/gi=16551895 /ug=Hs.400872 /len=4013			
					9
9147	0.046501	602507046F1 NIH_MGC_79 cDNA	BG435458	Hs.191168	
	-	clone IMAGE:4604315 5', mRNA			. *
		sequence /clone=IMAGE:4604315		·	
		/clone_end=5' /gb=BG435458	*	÷	
	4	/gi=13341964 /ug=Hs.191168 /len=672	Feb. 1980	* :	
9148	0.00684	DKFZp434M2216 (from clone	AL137295	Hs.199429	NP_004632
,		DKFZp434M2216) /cds=UNKNOWN			
		/gb=AL137295 /gi=6807756		;	
		/ug=Hs.199429 /len=1035	1	v ***	* .
9153	0.015521	AGENCOURT_8584280	BQ876563	Hs.346743	
7,777	+	Lupski sympathetic trunk cDNA clone			· .
		IMAGE:6192820 5', mRNA sequence		*	
		/clone=IMAGE:6192820 /clone_end=5'			
		/gb=BQ876563 /gi=22268571	· .		107
. '		/ug=Hs.346743 /len=925			
9154	0.004205	mRNA; cDNA DKFZp564B213 (from	AL049240	Hs.380268	1 10 00 1
ÿ 104	0.004209	clone DKFZp564B213) /gb=AL049240	17,049240	119.300200	
		/gi=4499973 /ug=Hs.380268 /len=767			
9155	0.034350	cDNA FLJ36544 fis, clone	AK093863	Hs.101689	19 a 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
9155	0.034336		Wiringgoog	IU 1009	,
		TRACH2006378. /gb=AK093863	•		
		/gi=21752807 /ug=Hs.101689 /len=2670		1	
0400	0.00000	CCT/alasanta NILOLID -DNA -lasa	Docozo		
9169	0.00326	EST(placenta Nb2HP cDNA clone	R25670		
		IMAGE:132920 3' similar to contains Alu			<i>-</i>
		repetitive element; contains L1 repetitive			.*
X 1==	0.00==	element ;)	D. 474 2 2 2 2		ļ
9179	0.00632	UI-E-EJ1-ajf-o-07-0-UI.r1 UI-E-EJ1	BM718282	Hs.439477	1
		cDNA clone UI-E-EJ1-ajf-o-07-0-UI 5',			
		mRNA sequence /clone=UI-E-EJ1-ajf-o-			· ·
		07-0-UI /clone_end=5' /gb=BM718282		_	
	*	/gi=19036470 /ug=Hs.439477 /len=1095	. :		
	<u> </u>		.0 * *		

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
* ·				No.	No.
9182	0.041279	os71f06.x1 NCI_CGAP_GC2 cDNA	AI082470	Hs.135463	
		clone IMAGE:1610819 3', mRNA			
1.		sequence /clone=IMAGE:1610819	*		0.
	+,	/clone_end=3' /gb=Al082470			
		/gi=3419262 /ug=Hs.135463 /len=521		- *	
9189	0.00632	clone IMAGE:5265581, mRNA	BC035165	Hs.400548	
		/gb=BC035165 /gi=23272508	•		+
1 .		/ug=Hs.400548 /len=2237	* *		-
9190	0.017843	DKFZP564D116 protein	NM_015631	Hs.181185	NP_056446
		(DKFZP564D116), mRNA			
	. '	/cds=(676,1965) /gb=NM_015631		•	
		/gi=24308108 /ug=Hs.181185 /len=2637			•
1	*				
9230	0.01911	hn49c02.x1 NCI_CGAP_Co17 cDNA	AW770800	Hs.371969	
		clone IMAGE:3026978 3' similar to			
		contains MER5.b1 MER5 repetitive			
		element ;, mRNA sequence		-X-	
		/clone=IMAGE:3026978 /clone end=3'	l *. *:	1.5	
		/gb=AW770800 /gi=7702847		- 1	
*		/ug=Hs.371969 /len=463			
9232	0.011644	clone IMAGE:5265853, mRNA	BC037736	Hs.397840	
	*	/gb=BC037736 /gi=23337068		7	
		/ug=Hs.397840 /len=3811		9.7	
9235	3.53E-04	cDNA FLJ13558 fis, clone	AK023620	Hs.86043	
		PLACE1007743. /gb=AK023620			
,		/gi=10435601 /ug=Hs.86043 /len=2271		=	***
9243	0.043827	AV700621 GKC cDNA clone GKCDKF09	AV700621	Hs.191445	
		3', mRNA sequence /clone=GKCDKF09	7	3.1	·
100		/clone_end=3' /gb=AV700621			
i.		/gi=10302592 /ug=Hs.191445 /len=809		. * Y	
	7	* * * * * * * * * * * * * * * * * * * *			·
9259	0.016648	th92f12.x1	AI435504	Hs.443955	
		Soares_NSF_F8_9W_OT_PA_P_S1	*		
. ,	=	cDNA clone IMAGE:2126159 3' similar			
. '		to SW:DOC2_MOUSE P98078	-		
	7 ×	MITOGEN-RESPONSIVE	i -		
		PHOSPHOPROTEIN ISOFORMS P96,	. "		
		P93 AND P67. ;, mRNA sequence			
		/clone=IMAGE:2126159 /clone_end=3'			
1 .	:	/gb=Al435504 /gi=4303646			
J	•	/ug=Hs.443955 /len=545			
9266	0.005382	clone FLB2932 mRNA sequence	AF138859	Hs.274405	4 T. T.
		/gb=AF138859 /gi=7340965			
		/ug=Hs.274405 /len=2990			
9270	0.028428	602122561F1 NIH_MGC_56 cDNA	BF668349	Hs.44731	
,	ile.	clone IMAGE:4279766 5', mRNA			. " . "
] .		sequence /clone=IMAGE:4279766			
} '		/clone_end=5' /gb=BF668349	·		·
	84	/gi=11942244 /ug=Hs.44731 /len=906			·
9281	0.015521	EST(cDNA clone MDSDHE04 5')	AV759672	W. S	

Spot	p-value	Description	Gene	Unigene	Protein
		*	Accession No.	Accession	Accession
			•	No.	No.
9298	0.021876	ad47h05.s1 Stratagene lung carcinoma	AA669458	Hs.445542	
		937218 cDNA clone IMAGE:884889 3'		1	
		similar to gb:X51956_rna1 GAMMA			
Ī		ENOLASE Alu repetitive		,	
- \$-		element;contains element TAR1	:		
		repetitive element ;, mRNA sequence	:		
	, *	/clone=IMAGE:884889 /clone_end=3'		-	
		/gb=AA669458 /gi=2630957	•		
		/ug=Hs.445542 /len=926			
9318		No significant match	SEQ.ID.No.102		
9327	0.009313	EST, mRNA; cDNA DKFZp566M063	AL110194	·	NP_002119
,	0	(from clone DKFZp566M063)			
9350	0.028428	No significant match, ORF+2(389~530)	SEQ.ID.No.87	•	
9351		No significant match, ORF+3(126~266)	SEQ.ID.No.91		
9354	0.017843	No significant match (ORF:-		7	
·		3:151~300[150])	SEQ.ID.No.60		*
9369	0.049308	UI-E-EJ0-ahj-l-23-0-UI.r1 UI-E-EJ0	BM701102	Hs.63236	
		cDNA clone UI-E-EJ0-ahj-I-23-0-UI 5',			·
		mRNA sequence /clone=UI-E-EJ0-ahj-l-		*	
ĺ	*	23-0-UI /clone_end=5' /gb=BM701102			
		/gi=19014360 /ug=Hs.63236 /len=1511			
9390	0.021876	ribosomal protein L13a (RPL13A),	NM_012423	Hs.389335	NP_036555
	*	mRNA /cds=(23,634) /gb=NM_012423	*	-	
ĺ	,	/gi=14591905 /ug=Hs.389335 /len=1142			1
9392	0.00274	AGENCOURT_6400386 NIH_MGC_67	BM799714	Hs.356635	
		cDNA clone IMAGE:5495662 5', mRNA			
ĺ		sequence /clone=IMAGE:5495662			e .
ĺ		/clone_end=5' /gb=BM799714			
i		/gi=19116537 /ug=Hs.356635 /len=1153			
9427	0.023381	Enah/Vasp-like (EVL), mRNA	NM 016337	Hs.241471	NP_057421
. • :=:		/cds=(62,1318) /gb=NM_016337			
		/gi=7706686 /ug=Hs.241471 /len=1833	*	,	` `
9459	0.041279	ubiquinol-cytochrome c reductase	NM 006294	Hs.131255	NP_006285
		binding protein (UQCRB), mRNA	-		
		/cds=(54,389) /gb=NM 006294			
		/gi=20070231 /ug=Hs.131255 /len=965	*		· X-
9466	0.030302	hypothetical protein FLJ10891	NM_018260	Hs.274169	NP 060730
		(FLJ10891), mRNA /cds=(128,1525)			
		/gb=NM 018260 /gi=8922743			
		/ug=Hs.274169 /len=2864		-	
9475	0.001915	hypothetical protein FLJ20624	NM_017906	Hs.52256	NP_060376
		(FLJ20624), mRNA /cds=(80,1255)			
		/gb=NM_017906 /gi=8923576			
		/ug=Hs.52256 /len=1554	/		
9497	0.028428	myotubularin related protein 9 (MTMR9),	NM_015458	Hs.48802	NP_056273
10731		1 •	I =		
5731		mRNA /cds=(83,1732) /gb=NM_015458			1
J-431		/gi=19923423 /ug=Hs.48802 /len=7081			

Spot	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession	Accession
			,	No.	No.
9508	0.023381	similar to RIKEN cDNA 1810055D05	NM_145261	Hs.349177	NP_660304
		(LOC131118), mRNA /cds=(125,475)			· -
	*	/gb=NM_145261 /gi=21687101			
		/ug=Hs.349177 /len=580			
9526	0.020453	C6orf37 mRNA, complete cds	AF350451	Hs.10784	NP 060103
		/cds=(294,1607) /gb=AF350451			
		/gi=21427109 /ug=Hs.10784 /len=5571			
9589	0.021876	abhydrolase domain containing 3	NM_138340	Hs.13377	NP_612213
j.	,	(ABHD3), mRNA /cds=(110,1339)	1 - 5 - 1 - 5		
	:	/gb=NM_138340 /gi=23397662	,		
		/ug=Hs.13377 /len=2049	· ·		
9590	0.024972	cDNA FLJ30977 fis, clone	AK055539	Hs.133015	NP 849156
	0.02 1072	HHDPC2000095, highly similar to	/11000000	113.100010	_043130
		Cricetulus griseus layilin mRNA.	1		=:
		/cds=(338,1462) /gb=AK055539			
		/gi=16550287 /ug=Hs.133015 /len=2067			
		/gi=10000207 /ug=Hs.100010 /left=2007		:	
9596	0.040308	vimentin (VIM), mRNA /cds=(123,1523)	NM 003380	Hs.297753	ND 000005
9590	0.049306		NIVI_003380	HS.297753	NP_000995
	1	/gb=NM_003380 /gi=4507894			
9617	0.020202	/ug=Hs.297753 /len=1851	A1 4 5 7 4 C O	11- 000404	
9017	0.030302	mRNA; cDNA DKFZp761B0823 (from	AL157462	Hs.306484	
	*	clone DKFZp761B0823) /gb=AL157462			ŀ
0000	0.005005	/gi=7018477 /ug=Hs.306484 /len=5085	D0040500	11.0407	
9632	0.005835	clone MGC:9947 IMAGE:3876105,	BC013590	Hs.2437	*
	, '	mRNA, complete cds /cds=(51,2216)	<b>l</b>		
	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	/gb=BC013590 /gi=15488925	' '	8 .	*
0005	0.044070	/ug=Hs.2437 /len=2651			
9665	0:041279	EST(df64h05.y1 Morton Fetal Cochlea	AW024055	,	
		clone IMAGE:2488569 5') (5e-06 match)			
2004	0.04000=	DVA EL LIBORA C			-
9684	0.043827	cDNA FLJ40989 fis, clone	AK098308	Hs.325568	
		UTERU2015108. /gb=AK098308	,		
		/gi=21758297 /ug=Hs.325568 /len=2316	. *		
12402	1 21 22 2				
9712	0.008631	wl54c05.x1 NCI_CGAP_Brn25 cDNA	AI864553	Hs.371597	
		clone IMAGE:2428712 3', mRNA			
		sequence /clone=IMAGE:2428712			
		/clone_end=3' /gb=AI864553			
		/gi=5528660 /ug=Hs.371597 /len=474	;		
9728	0.030302	EST(ow54e12.s1	AI022887		1
		Soares_parathyroid_tumor_NbHPA			1
		clone IMAGE:1650670 3')	- •		
9730	0.014461	601862578F1 NIH_MGC_53 cDNA	BF207870	Hs.396179	
		clone IMAGE:4082082 5', mRNA	,		
		sequence /clone=IMAGE:4082082	·		-
· .		/clone_end=5' /gb=BF207870			*
		/gi=11101456 /ug=Hs.396179 /len=756		14.	_ a as-us
9736	0.00684	EST(wl38a07.x1 NCI_CGAP_Ut1 clone IMAGE:2427156 3')	AI858415		NP_079457

Spot	p-value	D scription	G ne	Unigene	Protein
- CPC	p raids	5 001.pag.		Accession	Accession
	,		Acc 33ion No.	No.	No.
9758	0.004205	UI-E-DX0-agr-j-18-0-UI.s1 UI-E-DX0	BM667357	Hs.436172	NO.
1. 5, 55	0.004200	cDNA clone UI-E-DX0-agr-j-18-0-UI 3',	DIVIDO7 007	113.400172	
	9.1	mRNA sequence /clone=UI-E-DX0-agr-j-			•
		18-0-UI /clone_end=3' /gb=BM667357			
00	*	/gi=18975188 /ug=Hs.436172 /len=983	-		
9774	0.021876	cDNA FLJ36605 fis, clone	AK093924	Hs.379100	
3114	0.02 1070	TRACH2015316, highly similar to	AR093924	115.579100	
		VIMENTIN. /cds=(631,1317)	-8.		
	a ,	/gb=AK093924 /gi=21752883 /		1.0	
		/ug=Hs.379100 /len=2665			
9784	0.043827		NM 031461	Uo 192264	ND 412640
9/04	0.043027		NIVI_03 146 1	Hs.182364	NP_113649
÷-		/cds=(376,1878) /gb=NM_031461			8
	,	/gi=21314740 /ug=Hs.182364 /len=2962		00	*
0706	0.020055		A1 447505	11- 4055	10000
9796	บ.บอุชุชออ	mRNA; cDNA DKFZp564C2063 (from	AL117595	Hs.4055	
	9	clone DKFZp564C2063) /gb=AL117595		· · · · · · · · ·	1 m
0044	0.040040	/gi=5912159 /ug=Hs.4055 /len=1444	D0044000	11. 50404	
9814	0.010816	clone MGC:20208 IMAGE:3936339,	BC014000	Hs.58461	
1	·) ·	mRNA, complete cds /cds=(330,1832)			* *
. *	100	/gb=BC014000 /gi=15559281			
0000	0.004500	/ug=Hs.58461 /len=2733	D00070		- 12 12 12 12 1
9830	0.001592	mRNA for KIAA0219 gene, partial cds.	D86973	Hs.75354	
_		/cds=(1,8029) /gb=D86973 /gi=20521847			
0000	0.04044	/ug=Hs.75354 /len=8608			1
9833	0.01911	AGENCOURT_6861057 NIH_MGC_99	BQ066467	Hs.446485	*
*		cDNA clone IMAGE:5931113 5', mRNA			
100		sequence /clone=IMAGE:5931113	pe:		
		/clone_end=5' /gb=BQ066467			0
		/gi=19895513 /ug=Hs 446485 /len=1029		a a	
0055	0.010.100		1111 0000-0		
9855	0.013463	potent brain type organic ion transporter	NM_020372	Hs 373498	NP_065105
	,	(BOCT), transcript variant 1, mRNA	±		-8.7
		/cds=(57,1673) /gb=NM_020372	,	, '	
		/gi=21361833 /ug=Hs.373498 /len=2090		,	
0000			N. 4 000554		ND: 005040
9869	0.00145	Nedd4 family interacting protein 1	NM_030571	Hs.9788	NP_085048
		(NDFIP1), mRNA /cds=(105,770)			
		/gb=NM_030571 /gi=13386479	·	40° 0	
0004	0.034070	/ug=Hs.9788 /len=1837	NIM COOACO	U- 5007	ND 000450
9891	J.U.UZ [8/6]	isocitrate dehydrogenase 2 (NADP ),	NM_002168	Hs.5337	NP_002159
	,	mitochondrial (IDH2), nuclear gene			
		encoding mitochondrial protein, mRNA	· · ·		9
		/cds=(87,1445) /gb=NM_002168	e¥e	1	
0007	0.000453	/gi=28178831 /ug=Hs.5337 /len=1740	NIM COCACA	LID 402000 1	ND 000470
9907	0.020453	glucuronidase, beta (GUSB), mRNA	NM_000181	Hs.183868	NP_000172
	4	/cds=(27,1982) /gb=NM_000181			
0000	0.024070	/gi=4504222 /ug=Hs.183868 /len=2191	DC027740	Un 40040	- x
9909	0.027876	clone IMAGE:5263531, mRNA	BC037740	Hs.18016	
		/gb=BC037740 /gi=22902216		• •	
<u></u>	L	/ug=Hs.18016 /len=5036	<u> </u>	<u> </u>	

Spot	p-value	Description	Gen	Unigene	Protein
2.5			Accession No.	Accession	Accession
-1			1111	No.	No.
9911	0.007397	DKFZP586A0522 protein	NM_014033	Hs.288771	NP_054752
		(DKFZP586A0522), mRNA			
		/cds=(21,755) /gb=NM_014033			
		/gi=13378140 /ug=Hs.288771 /len=1705			
9918	0.022381	chromosome 20 open reading frame 108	NM 080821	Hs.352413	NP_543011
3310	0.023301	(C20orf108), mRNA /cds=(41,619)	14141_000021	1115.552415	141 _040011
		/gb=NM_080821 /gi=18201877			
		/ug=Hs.352413 /len=3026			
9934	0.020453	aconitase 2, mitochondrial (ACO2),	NM_001098	Hs.300463	NP 001089
	0.020 100	nuclear gene encoding mitochondrial		1.0.000	
		protein, mRNA /cds=(21,2363)			e
1.		/gb=NM_001098 /gi=4501866	e <sub>2</sub>		
		/ug=Hs.300463 /len=2467	.*		· _ ·
9953	0.026653	Fatty acid binding protein 1, liver	NM_012556		
		(Fabp1), mRNA			
9960	0.005835	similar to weakly similar to glutathione	BC029424	Hs.283072	
		peroxidase 2, clone MGC:32677		* * * * * * * * * * * * * * * * * * * *	
		IMAGE:4285958, mRNA, complete cds			*
		/cds=(35,664) /gb=BC029424	e		
1.		/gi=20810222 /ug=Hs.283072 /len=1398	+		
9972	0.032277	caldesmon 1 (CALD1), transcript variant	NM_033138	Hs.325474	NP_149347
	* .	1, mRNA /cds=(230,2611)	,		
		/gb=NM_033138 /gi=15149460			* *
9982	0.047042	/ug=Hs.325474 /len=3610	NM_020038	Hs.90786	NP_064422
9902	0.01/643	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3),	NIVI_U2UU36	IUS 901.00	INP_004422
	7	transcript variant MRP3B, mRNA		٠.	-81
		/cds=(71,1603) /gb=NM_020038		*	10
		/gi=9955973 /ug=Hs.90786 /len=5380			*
10026	0.01004	dishevelled associated activator of	NM 014992	Hs.197751	NP_055807
	3.3.337	morphogenesis 1 (DAAM1), mRNA			
	- X-	/cds=(126,3362) /gb=NM 014992	5 **		
İ	1	/gi=21071076 /ug=Hs.197751 /len=4256			
				-	
10039	0.038855	keratinocytes associated protein 2	NM_173852	Hs.374854	NP_776251
1		(KCP2), mRNA /cds=(1,489)			
		/gb=NM_173852 /gi=27777660			*
		/ug=Hs.374854 /len=489		. Tales service	3
10064	0.041279	KIAA0570 gene product (KIAA0570),	XM_002692		
12.2		mRNA		10.555	115 00 5 5 5 5
10095	0.026653	O-sialoglycoprotein endopeptidase	NM_017807	Hs.108894	NP_060277
	0.00	(OSGEP), mRNA /cds=(130,1137)			
		/gb=NM_017807 /gi=8923379			
10404	0.000077	/ug=Hs.108894 /len=1394	VIA 1040500		<del> </del>
10101	0.032277		XM_040593		
	<u> </u>	(LOC94680), mRNA	L	1	

Spot	p-value	Description	Gen	Unig ne	Protein
			Accession No.	Accession	Accession
10102	0.023381	hypothetical protein FLJ23445	NM 025075	No. Hs.288151	No. NP_079351
.0.0.	0.020001	(FLJ23445), mRNA /cds=(44,658)	11111_020070	113.200101	_0,000
		/gb=NM 025075 /gi=13376622			
		/ug=Hs.288151 /len=963	٠.	*	
10116	0.024972	splicing factor 1 (SF1), mRNA	NM_004630	Hs.180677	NP_004621
		/cds=(383,2254) /gb=NM 004630		, , , , , , , , , , , , , , , , , , , ,	
-		/gi=4759339 /ug=Hs.180677 /len=3131	*	• .	-
10134	0.01911	xl59d02.x1 NCI_CGAP_Pan1 cDNA	AW190111	Hs.377837	
		clone IMAGE:2678979 3', mRNA			*
. *		sequence /clone=IMAGE:2678979			
	1	/clone_end=3' /gb=AW190111			· ·
		/gi=6464591 /ug=Hs.377837 /len=248			
10148	0.043827	EST(qo26g10.x1 NCI_CGAP_Lu5 clone	AI342863		
		IMAGE:1909698 3' contains Alu repeat)			
10170	0.043827	EST (ts95a10.x1 NCI_CGAP_GC6	Al635513		***
10170		cDNA clone IMAGE:2239002 3')			
10179	0.00684	EST (wq27e08.x1 NCI_CGAP_Kid11	AI953360		NP_620149
40400		IMAGE:2472518 3')	D14000000		n ·
10196	0.038855	UI-CF-DU1-aav-k-08-0-UI.s1 UI-CF-DU1	BM983293	Hs.424609	:
		cDNA clone UI-CF-DU1-aav-k-08-0-UI			**
		3', mRNA sequence /clone=UI-CF-DU1- aav-k-08-0-UI /clone_end=3'			
		/gb=BM983293 /gi=19607660			
100	1	/ug=Hs.424609 /len=684			
10217	0.028428	EST (wi53c12.x1 NCI_CGAP_Co16	Al762075		NP_002884
10211	0.020420	cDNA clone IMAGE:2393974 3')	/ 11 02070	X-	141 _002004
10226	0.043827	wm98f08.x1 NCI_CGAP_Ut2 cDNA	Al889396	Hs.212245	
		clone IMAGE:2444007 3' similar to	u		
		contains Alu repetitive element; contains			
3. 4	1-1	element MIR repetitive element ;, mRNA	*	4	
• .		sequence /clone=IMAGE:2444007			
		/clone_end=3' /gb=AI889396		·	
		/gi=5594560 /ug=Hs.212245 /len=434			
·			*		
10236	0.043827	hypothetical protein MGC4701	NM_024511	Hs.421054	NP_078787
		(MGC4701), mRNA /cds=(149,1585)			·
		/gb=NM_024511 /gi=24308290			
10047	0.040400	/ug=Hs 421054 /len=1686	M40005		-
10247		vimentin (VIM) gene	M18895		ND 690074
10276	0.043027	Hypothetical protein(cDNA sequence FLJ11311 fis, clone PLACE1010102)	AK002173		NP_689971
		(=cDNA sequence DKFZp566J2146)		1.	
10277	0.00274	likely ortholog of mouse embryonic	NM_017611	Hs.274453	NP_060081
.0217	0.00274	epithelial gene 1 (EEG1), mRNA	1.3.1.2.1.01.1	1, 10.2, 14400	1.11 _00000
		/cds=(319,1794) /gb=NM_017611	* .		
	<u> </u>	/gi=18252046 /ug=Hs.274453 /len=2630			
	aya.	1	200		
10282	0.041279	EST (7o83a06.x1 NCI_CGAP_Kid11	BF197462		V ===

Spot	p-value	Description	Gen	Unigene	Protein
	*		Accession No.	Accession	Accession
				No.	No
10283	0.041279	EST xs47d05.x1 NCI_CGAP_Kid11	AW269335		NP_476500
	1000000	cDNA clone IMAGE:2772777 3'			
10286	0.007397	Similar to cell death activator CIDE-3,	BC043599	Hs.432698	
		clone MGC:50748 IMAGE:5204770,			9.
		mRNA, complete cds /cds=(432,617)			
<b>)</b>		/gb=BC043599 /gi=27694390	*	,	
40000	â aa ia=a	/ug=Hs.432698 /len=1832			
10289	0.024972	EST RC3-HT0593-170300-011-c10	BE177303		
40004	0.000400	HT0593	41/00/007		<del> </del>
10304	0.028428	cDNA FLJ14175 fis, clone	AK024237	Hs.288613	."
		NT2RP2002979. /gb=AK024237			
		/gi=10436564 /ug=Hs.288613 /len=3493			
40007	0.004050	FOTOGOLO A NOTICO A DI CALCADA	A1445000		
10307	0.034358	EST(ti95f04.x1 NCI_CGAP_Gas4 cDNA	AI445690		
40045	0.00000	clone IMAGE:2139775 3')	DE450004		
10315	0.030302	EST ( MR0-HT0407-010200-008-g12	BE159321		
100.40	0.004070	HT0407	DUZ 40004	050740	ļ
10346	0.021876	UI-E-EO1-aiv-e-19-0-UI.s1 UI-E-EO1	BU742864	Hs.356716	
, *	8	cDNA clone UI-E-EO1-aiv-e-19-0-UI 3',		100	,
*		mRNA sequence /clone=UI-E-EO1-aiv-e-	•	+ 0 10	÷
1		19-0-UI /clone_end=3' /gb=BU742864	-		
	· · ·	/gi=23689787 /ug=Hs.356716 /len=1044		·**	2
10347	0.038855	hypothetical protein dJ122O8.2	NM 020466	Hs.268115	NP 065199
10347	0.030033	(DJ122O8.2), mRNA /cds=(34,300)	NIVI_020400	IU8.500112	INE_000199
[		/gb=NM_020466 /gi=20070310	·		
	• • • • •	/ug=Hs.268115 /len=902			
10364	0.005382	EST (QV3-NN1023-130500-178-g10	AW902437	***************************************	<u> </u>
10004	0.000002	INN1023)	7.002457		
10379	0 041279	EST (tc71e05.x1 Soares_NhHMPu_S1	AI804457		NP_002067
10075	0.041270	cDNA clone IMAGE:2070080 3')	711004437		_002007
10386	0.00274	UI-H-BW0-ajj-h-09-0-UI.s1	AW298400	Hs.438172	
10000	0.00214	NCI_CGAP_Sub6 cDNA clone		113.450172	
3	7	IMAGE:2732033 3', mRNA sequence			7.
		/clone=IMAGE:2732033 /clone_end=3'	1		
ė	] .	/gb=AW298400 /gi=6704960	·		
		/ug=Hs.438172 /len=635	*		
10408	0.044761	yr31a03.r1 Soares fetal liver spleen	R98895	Hs.125823	<del>                                     </del>
		1NFLS cDNA clone IMAGE:206860 5'	*		`
}		similar to contains MER19 repetitive		**	- 7-
		element ;, mRNA sequence			. ,
: 0.		/clone=IMAGE:206860 /clone_end=5'			
l · .		/gb=R98895 /gi=985496 /ug=Hs.125823	4		
	1	/len=377		1	-
10418	0.049308	602152595F1 NIH_MGC_81 cDNA	BF672139	Hs.19479	<u> </u>
		clone IMAGE:4293719 5', mRNA	,	···	
]		sequence /clone=IMAGE:4293719	1		ļ
	1 3	_ · · · · · · · · · · · · · · · · · · ·	-		1
		/clone_end=5' /gb=BF672139	_		

Spot	p-valu	D scription	Gene	Unigene	Protein
				Accession	Accession
· · ·				No.	No.
10471	0.012525	hypothetical protein FLJ14596	NM_032809	Hs.325309	NP_116198
	•	(FLJ14596), mRNA /cds=(1324,1968)	<del></del>		
	1.5	/gb=NM_032809 /gi=19923651	9		. 8
		/ug=Hs.325309 /len=3597			
10482	0.046501	EST(cDNA clone IMAGE:4588661 5')	BG422853		
10498	0.044761	wo45d05.x1 NCI_CGAP_Gas4 cDNA	Al926493	Hs.213840	
		clone IMAGE:2458281 3' similar to		3 1	
	•	contains element XTR repetitive element	,	-1	
		,, mRNA sequence	• •		
		/clone=IMAGE:2458281 /clone_end=3'	,		
		/gb=Al926493 /gi=5662457			.
		/ug=Hs.213840 /len=509			
10504	0.003866	AGENCOURT_8152128	BU145410	Hs.304440	
		Lupski_dorsal_root_ganglion cDNA			
		clone IMAGE:6184005 5', mRNA	***		. •
		sequence /clone=IMAGE:6184005			* -
		/clone_end=5' /gb=BU145410			
		/gi=22658942 /ug=Hs.304440 /len=889			
10529	0.026653	df27e02.w1 Morton Fetal Cochlea cDNA	BI492664	Hs.345490	
	•	clone IMAGE:2484578 3', mRNA	,		· .
		sequence /clone=IMAGE:2484578			
		/clone_end=3' /gb=Bl492664	• .		
	. •	/gi=15332008 /ug=Hs.345490 /len=657			
10531	0.020453	mRNA; cDNA DKFZp686J172 (from	AL832206	Hs.56896	
		clone DKFZp686J172) /gb=AL832206			· · · · · · · · · · · · · · · · · · ·
·		/gi=21732751 /ug=Hs.56896 /len=6055	:		
10536	0.037211	nascent-polypeptide-associated complex	NM_005594	Hs.32916	NP_005585
	. *	alpha polypeptide (NACA), mRNA			
	1.	/cds=(26,673) /gb=NM_005594			
		/gi=5031930 /ug=Hs.32916 /len=797			
10539	0.024972	ribosomal protein, large, P1 (RPLP1),	NM_001003	Hs.424299	NP_000994
	*	mRNA /cds=(130,474) /gb=NM_001003		·	
-8		/gi=16905511 /ug=Hs.424299 /len=512	•		
10553	0.000550	FOT/-DNA -i issa Of-04/4070 OF	Α Δ 4 6 5 7 0 0		
10551	0.003552	EST(cDNA clone IMAGE:814978 3'	AA465709		
	,	similar to TR:E91737 E91737 REVERSE	1		* *
	. ,	TRANSCRIPTASE HOMOLOG (L1			
		REPETITIVE ELEMENT; contains L1.t1			
-	:	L1 repetitive element;)			, ,
10558	0.017042	ESTs, cDNA /clone=IMAGE:1372579	AA833868	Hs.156300	
10008	0.017843		~~033000	175.130300	
	-	/gb=AA833868 /gi=2908636		. 00	
10550	0.04044	/ug=Hs.156300 /len=495	BM691757	Uo 11255	
10559		UI-E-CL1-afg-c-18-0-UI.r1 UI-E-CL1	DINIOS LÁSA	Hs.11355	
	```	cDNA clone UI-E-CL1-afg-c-18-0-UI 5',	<b>.</b> .		
		mRNA sequence /clone=UI-E-CL1-afg-c-	1 .		
	,	18-0-UI /clone_end=5' /gb=BM691757	·		
		/gi=19005015 /ug=Hs.11355 /len=1234			
Ļ	<u> </u>	L	1	L,	<u>L.</u>

Spot	p-valu	Description	G n	Unigene	Protein
. "			Accession No.	Accession	Accession
40504	0.047040	200148 4 1101 0 0 4 5 1110 5 114		No.	No.
10561	0.017843	wn03h10.x1 NCI_CGAP_Ut2 cDNA	AI924266	Hs.370113	
		clone IMAGE:2444419 3', mRNA			
	N	sequence /clone=IMAGE:2444419			
		/clone_end=3' /gb=Al924266			9
140-00	0.000710	/gi=5660230 /ug=Hs.370113 /len=514			
10583	0.030746	AV700930 GKC cDNA clone	AV700930	Hs.285894	
l l		GKCBRB12 3', mRNA sequence			8
*	•	/clone=GKCBRB12 /clone_end=3'	•		
		/gb=AV700930 /gi=10302901		-	
40500	0.047040	/ug=Hs.285894 /len=746	NIA 000040	11 6 000	1
10593	0.017843	twisted gastrulation 1 (Drosophila)	NM_020648	Hs.247302	NP_065699
4.6		(TWSG1), mRNA /cds=(106,777)		<b>1</b> -	.00
		/gb=NM_020648 /gi=21314788	4 5 4	•	•
10622	0.000242	/ug=Hs.247302 /len=3693	DC024244	11- 20700	
10623	0.009313	clone IMAGE:5276765, mRNA	BC031314	Hs.26766	
	1)1	/cds=UNKNOWN /gb=BC031314	*		
10624	0.021076	/gi=21410747 /ug=Hs.26766 /len=1000 AGENCOURT_6417307 NIH_MGC_67	BM799896	Ula 204020	
10024	0.021070	cDNA clone IMAGE:5492062 5', mRNA	DIVI 7 99896	Hs.304926	"
		sequence /clone=IMAGE:5492062		•	
		/clone_end=5' /gb=BM799896	* *		
		/gi=19116719 /ug=Hs.304926 /len=913			
10629	<u> </u>	ac74b05.x5 Stratagene lung (#937210)	AI791153	Hs.444952	A X
10029	0.043500	cDNA clone IMAGE:868305 3' similar to	A1791133	ITIS.444952	
		contains Alu repetitive element;, mRNA			
		sequence /clone=IMAGE:868305		i .	[
		/clone_end=3' /gb=AI791153		14	
		/gi=5338869 /ug=Hs.444952 /len=498	*		-
-		7gi 000000 7ug 110. 144002 7içil 400	,		
10636	0.007397	cDNA FLJ13571 fis, clone	AK023633	Hs.116278	
		PLACE1008405. /gb=AK023633	, 11.02000	110.110270	*
	* '	/gi=10435617 /ug=Hs.116278 /len=2484			,
		Section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the sect			
10644	0.021876	EST(cDNA clone GKCEND03 5')	AV683165		
10657		cDNA FLJ34771 fis, clone	AK092090	Hs.433010	
,		NT2NE2003150. /gb=AK092090			
. ,	*:	/gi=21750599 /ug=Hs.433010 /len=2424	- 1		i i
		3		*	
10658	0.012525	hypothetical protein MGC10233	NM_152715	Hs.29041	NP 689928
		(MGC10233), mRNA /cds=(547,1389)	_		_
		/gb=NM_152715 /gi=22749416	* .	W.	
·		/ug=Hs.29041 /len=3915			
10661	0.013463	ip18c02.y1 HR85 islet cDNA clone	CA777576	Hs.115779	
	,	IMAGE:6217706 5', mRNA sequence			[
,		/clone=IMAGE:6217706 /clone_end=5'	İ	'	
·		/gb=CA777576 /gi=26015451	(1)		
		/ug=Hs.115779 /len=700	*	]	

Spot	p-value	D scription	Gene	Unigene	Protein
			Accession No.		Accession
	1 2 2 1 2 2 1 2			No.	No.
10666	0.017843	EST384170 MAGE resequences, MAGL	AW971961	Hs.136340	
		cDNA, mRNA sequence /gb=AW971961			
	0	/gi=8161927 /ug=Hs.136340 /len=642		-	
The section is not	*.			× •	<u> </u>
10705	0.015521	No significant match,		* * *	
		ORF+2(386~529),+3(3~107)	SEQ.ID.No.2		
10729	0.01911	myc-induced nuclear antigen, 53 kDa	NM_032778	Hs.23294	NP_116167
		(MINA53), transcript variant 2, mRNA		] * •	100
		/cds=(214,1608) /gb=NM_032778		0.2	
		/gi=23346417 /ug=Hs.23294 /len=2221			
10732	0.046501	EST(Kawakami zebrafish DRA Danio	AW343514		
1	· · · · · · · · · · · · · · · · · · ·	rerio cDNA clone 2640570 3')			
10746	0.017843	No significant match			
		(ORF:+3:69~302[234])	SEQ:ID.No.27		
10765	0.024972	EST oy92c03.x1	Al076100		
		Soares_fetal_liver_spleen_1NFLS_S1			
		H.sapiens cDNA clone IMAGE:1673284			
		3'			
10773	0.026653	EST (RC3-CT0254-300800-022-g07	BE927223		
		CT0254)			1
10777	0.01911	EST (wm51f05.x1 NCI_CGAP_Ut2	AI871724		
	1 - 1 - 2 - 2	IMAGE:2439489 3')			
		EST (ADB cDNA clone ADBAKA02 5')	AV704531		
10782	0.023381	EST (cDNA clone IMAGE:120476 3'	T95469		
40700	0.004070	similar to			
10786	0.021876	EST (MR0-SN0040-060400-001-h09	AW867719		. * .
40700	å aggeta	SN0040)	1		
10798	0.026653	EST (ta16g05.x1 NCI_CGAP_Lym5	AI471814		
40700	0.000050	IMAGE:2044280 3')	1111001000		1 102
10799	0.026653	cDNA FLJ11934 fis, clone	AK021996	Hs.261699	•
	•	HEMBB1000510. /gb=AK021996			
	1	/gi=10433305 /ug=Hs.261699 /len=2599	Ţ.,		
10005	0.000077	FOT ( 104 144 4 5 4 5 4 1	1.045000		•
10805	0.032277	EST(ak84d11.s1 Barstead spleen	AA845289	-00	
		HPLRB2 cDNA clone IMAGE:1414581 3'	,		
	*	similar to contains MER10.t3 MER10			13
40047	0.040040	repetitive element)	DE504000		
10817	0.016648	EST(hz33h07.x1 NCI_CGAP_GC6	BE504880		
40040	0.000450	cDNA clone IMAGE:3209821 3')			
10842	0.020453	EST (nc45b12.s1 NCI_CGAP_Pr3 cDNA	AA229160		
		clone IMAGE:1011071 similar to	4.		
10047	0.005005	contains Alu repetitive element)	NINA 000005	11. 0000	ND 445004
10847	0.005835	hypothetical protein MGC3200	NM_032305	Hs.9088	NP_115681
	0	(MGC3200), mRNA /cds=(108,764)	•		
.		/gb=NM_032305 /gi=14150063	· ·		*
10000	0.000040	/ug=Hs.9088 /len=1191	NO 004007	* -	
10860	0.009313	mitochondrion, complete genome	NC_001807		10. 3

Spot	p-value	Description	Gene	Unigene	Protein
				Accession	Accession
			<u> </u>	No.	No.
10861	0.032277	UI-CF-EC1-aea-g-11-0-UI.s1 UI-CF-EC1	BU688263	Hs.336400	
		cDNA clone UI-CF-EC1-aea-g-11-0-UI	* * *		
		3', mRNA sequence /clone=UI-CF-EC1-		٠.	
-2		aea-g-11-0-UI /clone_end=3'			·
		/gb=BU688263 /gi=23544886			*
1		/ug=Hs.336400 /len=528		×	
10863	0.002294	EST(TCBAP1E0695 Pediatric pre-B cell	BE243837		NP_006241
		acute lymphoblastic leukemia Baylor-			
		HGSC project=TCBA clone			*
		TCBAP0695)			
10888	0.034358	UI-H-DH0-aul-j-10-0-UI.s1	BM994461	Hs.434057	
		NCI_CGAP_DH0 cDNA clone			
	0	IMAGE:5871081 3', mRNA sequence			
		/clone=IMAGE:5871081 /clone_end=3'		8 33	
ľ .		/gb=BM994461 /gi=19719362			e i
		/ug=Hs.434057 /len=2059			
10899	0.007397	ad44d12.x5 Stratagene lung carcinoma	AI732123	Hs.446065	
1		937218 cDNA clone IMAGE:884567 3'	•		
1		similar to contains Alu repetitive			
		element;contains L1.t1 L1 repetitive			
)		element ;, mRNA sequence			-
1		/clone=IMAGE:884567 /clone_end=3'			
1		/gb=Al732123 /gi=5053258			
		/ug=Hs.446065 /len=484			
10909	0.017843	EST (MR1-SN0062-100500-002-g03	AW868480		
		SN0062 cDNA)			
10926	0.015521	EST(yp57a07.s1 Soares fetal liver	H37798		
		spleen 1NFLS cDNA clone	. 0	*	
		IMAGE:191508 3' similar to			
		gb:X56411_rna1 ALCOHOL			
1 7		DEHYDROGENASE CLASS II PI			
		CHAIN)			·
10937	0.024972	hypothetical protein MGC16384	NM_053048	Hs.274268	NP_444276
1		(MGC16384), mRNA /cds=(450,602)		8	1 4
		/gb=NM_053048 /gi=16596689			*
10010	0.004050	/ug=Hs.274268 /len=1599	41.000000	11- 050047	
10940	0.034358	mRNA; cDNA DKFZp686K192 (from	AL832209	Hs.259347	
Ì		clone DKFZp686K192) /gb=AL832209		*	
	3	/gi=21732754 /ug=Hs.259347 /len=6707			
10040	0.017042	mDNA, aDNA DVEZ-547K0040*/f	AL 920500	Uo 274224	
10943	0.017843	mRNA; cDNA DKFZp547K0918 (from	AL832566	Hs.271324	
		clone DKFZp547K0918) /gb=AL832566		· ·	
	Į	/gi=21733141 /ug=Hs.271324 /len=1883	*	1	
10947	0.041270	ESTs, cDNA /gb=AW959468	AW959468	Hs.188738	<del>                                     </del>
10947	0.041279		VAA99400	1715. 100/30	1
10950	0.03304	/gi=8149152 /ug=Hs.188738 /len=767 cDNA FLJ38913 fis, clone	AK096232	Hs.50094	NP_835224
10950	0.023301	NT2NE2008017. /gb=AK096232	1/1/090232	113.50034	147_050224
		/gi=21755673 /ug=Hs.50094 /len=2555	, ,	*	
<u> </u>	L	1/91-2 17 3307 3 749-118,30034 /1611-2333	1		<del></del>

Snot	p-value	Description	Gene	Unigene	Prot in
Opol	P value	Description		Accession	Accession
			7,000331011 140	No.	No.
10958	0.028428	FLJ30424 fis, clone BRACE2008881,	AK054986	Hs.21423	
		weakly similar to ZINC FINGER	-		) T
		PROTEIN 195 /cds=UNKNOWN			
	•	/gb=AK054986 /gi=16549625			
		/ug=Hs.21423 /len=2144		. "	4-0
10969	0.01911	cDNA FLJ37747 fis, clone	AK095066	Hs.289068	
		BRHIP2022986. /gb=AK095066			,
		/gi=21754256 /ug=Hs.289068 /len=3097			
*					
10979	0.00145	mRNA full length insert cDNA clone	AL359062	Hş.41271	
\$	٠.	EUROIMAGE 1913076. /gb=AL359062			
		/gi=8518189 /ug=Hs.41271 /len=1779	_* 1	· · · · · · · · ·	*
10989	0.011644	BX102645 NCI_CGAP_Brn23 cDNA	BX102645	Hs.146883	
15		clone IMAGp998L144327, mRNA			
, ,	,	sequence		1 2	
		/clone=IMAGp998L144327_;_IMAGE:17			
		03965 /gb=BX102645 /gi=27831887	8 2 2		
		/ug=Hs.146883 /len=786	- (C - v		*
11002	0.024972	AU119153 HEMBA1 cDNA clone	AU119153	Hs.288615	
7	, v.	HEMBA1005152 5', mRNA sequence			80
		/clone=HEMBA1005152 /clone_end=5'			7 0
	*	/gb=AU119153 /gi=10934388			
		/ug=Hs.288615 /len=820			
11004	0.00684	Similar to UDP-N-acetyl-alpha-D-	BC037341	Hs.351204	*
		galactosamine:polypeptide N-			• . •
		acetylgalactosaminyltransferase 9			
	i .	(GalNAc-T9), clone MGC:43305			( )
1 .		IMAGE:5265475, mRNA, complete cds	-		*
. *		/cds=(416,2239) /gb=BC037341		.*	
		/gi=22713621 /ug=Hs.351204 /len=2525		*	
		EST(cDNA 3'.	BM264491		
11046	0.009313	wc25f11.x1 NCI_CGAP_Kid11 cDNA	Al678258	Hs.174257	
	.8.	clone IMAGE:2316237 3', mRNA		,	
		sequence /clone=IMAGE:2316237		-)(-	
* **		/clone_end=3' /gb=Al678258			
11055	0.005000	/gi=4888440 /ug=Hs.174257 /len=585	11/000101	11 100000	
11052	0.005382	cDNA FLJ40815 fis, clone	AK098134	Hs.432620	
	*	TRACH2010600. /gb=AK098134	·		
		/gi=21758081 /ug=Hs.432620 /len=2814	a		: *
44055	0.044044	7100-024	DE400000	11- 440007	<del>                                     </del>
11057	0.011644	7/80c03.x1	BF196920	Hs.419997	
		Soares_NSF_F8_9W_OT_PA_P_S1			+
		cDNA clone IMAGE:3527788 3' similar		3	
		to TR:O88246 O88246 MSZF14 ;,	ψ.		
		mRNA sequence		4.	
		/clone=IMAGE:3527788 /clone_end=3'			
		/gb=BF196920 /gi=11085469		*	
<u> </u>	<u> </u>	/ug=Hs.419997 /len=511	<u> </u>	l	L.,

Spot	p-value	D scription	Gene	Unigene	Protein
	y . •		Accession No.	Accession	Accession
	<u> </u>		<u>.</u>	No.	No.
11061	0.015521	clone IMAGE:3887266, mRNA	BC015512	Hs.88013	
		/gb=BC015512 /gi=15930151	÷ "		
		/ug=Hs.88013 /len=1505			
11063	0.017843	clone alpha_est218/52C1 mRNA	AF001542	Hs.356442	
		sequence /gb=AF001542 /gi=2529714			
51		/ug=Hs.356442 /len=2992			
11081		cDNA /clone=IMAGE:997623	AA533447	Hs.312989	NP_000601
		/gb=AA533447 /gi=2277543	*		
,		/ug=Hs.312989 /len=474			
11082	0.014461	UI-1-BB1p-avc-e-03-0-UI.s1	BU754312	Hs.355575	
		NCI_CGAP_PI6 cDNA clone UI-1-BB1p-		. 0	
		avc-e-03-0-UI 3', mRNA sequence		0	
	=	/clone=UI-1-BB1p-avc-e-03-0-UI			
* *		/clone_end=3' /gb=BU754312			7.
-	- 1	/gi=23713100 /ug=Hs.355575 /len=1086			
				• .	
11083	0.032277	EST(cDNA clone IMAGE:2675214 3')	AW189289		NP_001116
11090	0.007994	UI-H-FT1-bhv-c-13-0-UI.s1	CA748480	Hs.22883	
.,		NCI_CGAP_FT1 cDNA clone UI-H-FT1-	V)(0		
		bhv-c-13-0-UI 3', mRNA sequence			
		/clone=UI-H-FT1-bhv-c-13-0-UI			
		/clone_end=3' /gb=CA748480			40.
		/gi=25568160 /ug=Hs.22883 /len=1102			
11116	0.016648	cDNA FLJ33668 fis, clone	AK090987	Hs.346796	
		BRAMY2028565. /gb=AK090987			· · · ·
	1	/gi=21749256 /ug=Hs.346796 /len=2294			
11125	0.049308	EST(cDNA clone IMAGE:2815110 3')	AW268719		
11126	0.012525	full length insert cDNA clone ZD64C04	AF088052	Hs.384557	
		/gb=AF088052 /gi=3523258			
		/ug=Hs.384557 /len=831			
11192	0.01911	RC4-HT0277-160200-013-d07 HT0277	BE151126	Hs.158600	
		cDNA, mRNA sequence /gb=BE151126			
		/gi=8613847 /ug=Hs.158600 /len=571	×		-
11202	0.01911	AV699513 GKC cDNA clone GKCDLA08	AV699513	Hs.131366	
0		3', mRNA sequence /clone=GKCDLA08			
		/clone_end=3' /gb=AV699513	=		
	ļ.,	/gi=10301484 /ug=Hs.131366 /len=793	*	. *	
11215	0.003866	Novel, ORF+3(39~203)	SEQ.ID.No.53		
11253		hypothetical protein similar to beta-	NM_018096	Hs.85570	NP_060566
		transducin family (FLJ10458), mRNA	_		*
].		/cds=(14,1471) /gb=NM_018096		9	
		/gi=20070287 /ug=Hs.85570 /len=2593			
11295	0:013463	collagen, type V, alpha 1 (COL5A1),	NM_000093	Hs.146428	NP_000084
		mRNA /cds=(383,5899) /gb=NM_000093	_		_
			1	1	1
	9	/gi=16554578 /ug=Hs.146428 /len=6496	00		1 '

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11303	0.00632	S100 calcium binding protein A1 (S100A1), mRNA /cds=(114,398) /gb=NM_006271 /gi=5454031 /ug=Hs.433503 /len=607	NM_006271	Hs.433503	NP_006262
11316	0.026979	KIAA1721 protein, partial cds /cds=UNKNOWN /gb=AB051508 /gi=12697986 /ug=Hs.117102 /len=8047	AB051508	Hs.117102	NP_071904
11318	0.016693	SAR1 protein (SAR1), mRNA /cds=(125,721) /gb=NM_020150 /gi=21361614 /ug=Hs.110796 /len=3003	NM_020150	Hs.110796	
11335	0.012525	COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717	NM_004375	Hs.241515	NP_004366
11339	0.026653	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(1758,3863) /gb=NM_024524 /gi=21362055 /ug=Hs.324507 /len=5226	NM_024524	Hs.324507	NP_078800
11379	0.007994	hypothetical protein FLJ20038 (FLJ20038), mRNA /cds=(274,720) /gb=NM_017634 /gi=8923043 /ug=Hs.72071 /len=2571	NM_017634	Hs.72071	NP_060104
11383	0.023381	DKFZP586G011 protein (LAP1B), mRNA /cds=(56,1444) /gb=NM_015602 /gi=24308098 /ug=Hs.234265 /len=3275	NM_015602	Hs.234265	NP_056417
11387	0.049308	df22c07.w1 Morton Fetal Cochlea cDNA clone IMAGE:2484085 3', mRNA sequence /clone=IMAGE:2484085 /clone_end=3' /gb=BI492292 /gi=15331636 /ug=Hs.379172 /len=359	BI492292	Hs.379172	
11397	0.038855	Niemann-Pick disease, type C2 (NPC2), mRNA /cds=(116,571) /gb=NM_006432 /gi=20149580 /ug=Hs.433222 /len=929	NM_006432	Hs.433222	NP_006423
11399	0.016648	density-regulated protein (DENR), 7 mRNA /cds=(111,707) /gb=NM_003677 /gi=27501445 /ug=Hs.22393 /len=2766	NM_003677	Hs.22393	NP_003668
11401	0.01911	hypothetical protein PRO1843 (PRO1843), mRNA /cds=(965,1255) /gb=NM_018507 /gi=8924082 /ug=Hs.2833330 /len=1268	NM_018507	Hs.283330	NP_060977

Spot	p-value	Description	Gene	Unigene	Protein
		Q	Accession No.	Accession	Accession
	**	- Carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carlo de la carl	B-22-12-1	No.	No.
11407	0.023381	Similar to proline synthetase co-	BC012334	Hs.301959	NP_009129
, i		transcribed (bacterial homolog), clone			
1	·	MGC:2667 IMAGE:3546307, mRNA,			
		complete cds /cds=(67,894)			
	3	/gb=BC012334 /gi=15147390			
14505	0.405.04	/ug=Hs.301959 /len=2580	D. 1000000	050005	
11537	8.10E-04	UI-H-DF1-auf-c-04-0-UI.s1	BM992029	Hs.358825	-
		NCI_CGAP_DF1 cDNA clone			
,	1 .	IMAGE:5868603 3', mRNA sequence	9	,	+
.'	,	/clone=IMAGE:5868603 /clone_end=3'		·	
*	,	/gb=BM992029 /gi=19711418			
11500	0.047040	/ug=Hs.358825 /len=1052			
11539	0.017843	mRNA for KIAA1327 protein, partial cds.	AB037748	Hs.106204	
		/cds=(1,5417) /gb=AB037748			
	. "	/gi=20521883 /ug=Hs.106204 /len=6687	,	·	
44551	0.000055	EOT (16784)	A)A(004744		ND 057405
11554	0.038855	EST(df27f12.y1 Morton Fetal Cochlea	AW021741		NP_057485
44570	0.044070	clone IMAGE:2484646 5')	A14/200074		
11576	0.041279	EST(CM4-ST0276-101299-059-d05	AW392874	,	
44500	7.005.04	ST0276)	A)A(000045	11- 420700	
11582	7.33E-04	RC1-NN0073-090500-012-f02 NN0073	AW898615	Hs.130729	,
		cDNA, mRNA sequence /gb=AW898615	· .	* .	
		/gi=8062820 /ug=Hs 130729 /len=660			· .
11585	0.041279	EST (yd08e03.r1 clone 24895 5')	T80443	<u> </u>	
11596		hypothetical protein cDNA	AL162046		NP_060717
' '		DKFZp761K1115 (from clone			
		DKFZp761K1115); partial cds		, ,	
11598	0.036549		NM_016282	Hs.43436	NP_057366
		mRNA /cds=(141,824) /gb=NM_016282			
-00		/gi=19923436 /ug=Hs.43436 /len=2642		l .	
					÷
11600	0.00274	similar to spermatid WD-repeat protein	NM_145241	Hs.133331	NP_660284
		(LOC114987), mRNA /cds=(238,1338)			
		/gb=NM_145241 /gi=21687047			
		/ug=Hs.133331 /len=3121			<u> </u>
11604	0.038855	EST(ae50c06.s1 Stratagene lung	AA600135		
- 0		carcinoma 937218 clone IMAGE:950314			
	*	3' contains Alu repeat)			
11606	0.006723	UI-H-DT1-avz-k-14-0-UI.s1	BQ015886	Hs 22607	
/		NCI_CGAP_DT1 cDNA clone			
/ /		IMAGE:5886469 3', mRNA sequence	1	1	1
		/clone=IMAGE:5886469 /clone_end=3'			*
		/gb=BQ015886 /gi=19751163			
		/ug=Hs.22607 /len=1207			
11621	0.032277		NM_005177	Hs.267871	NP_005168
1		subunit a isoform 1 (ATP6V0A1), mRNA		,	
		/cds=(168,2663) /gb=NM_005177			
-	,,	/gi=19913417 /ug=Hs.267871 /len=4139			
L	<u>L</u>		<u> </u>	<u> </u>	1

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11629		EST(qd99f10.x1 Soares_testis_NHT clone IMAGE:1737643 3')	AI143918		NP_005714
11671	0.004205	UI-H-DP0-avb-p-04-0-UI.s1 NCI_CGAP_Fs1 cDNA clone IMAGE:5877363 3', mRNA sequence /clone=IMAGE:5877363 /clone end=3'	BQ020727	Hs.446656	
*	*	/gb=BQ020727 /gi=19756005 /ug=Hs.446656 /len=1208	*		*
11674	•	EST (qa48c04.x1 Soares_NhHMPu_S1 IMAGE:1689990 3')	AI123338		
11678 11680		EST (RC3-CT0369-261299-011-h06 CT0369) EST ys96h09.r1 Soares retina N2b5HR	AW860070 H84275		,
11684	*	cDNA clone IMAGE:222689 5' cDNA: FLJ21311 fis, clone COL02167.	AK024964	Hs.173933	NP_005586
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	/gb=AK024964 /gi=10437390 /ug=Hs.173933 /len=3216			
11699	0.036549	hypothetical protein MGC5306 (MGC5306); mRNA /cds=(207,1043) /gb=NM_024116 /gi=13129135 /ug=Hs.301732 /len=2336	NM_024116	Hs.301732	NP_077021
11746	0.034358	ribosomal protein L26-like 1 (RPL26L1), mRNA /cds=(43,480) /gb=NM_016093 /gi=17017971 /ug=Hs.110165 /len=723	NM_016093	Hs.110165	NP_057177
11783	0.034358	cDNA FLJ20709 fis, clone KAIA1124, highly similar to D86324 mRNA for CMP- N-acetylneuraminic acid. /gb=AK000716 /gi=7020978 /ug=Hs.24697 /len=3488	AK000716	Hs.24697	
11789	0.012525	high mobility group nucleosomal binding domain 4 (HMGN4), mRNA /cds=(239,511) /gb=NM_006353 /gi=23238232 /ug=Hs.236774 /len=1980	NM_006353	Hs.236774	NP_006344
11800	0.024972	RAN binding protein 2-like 1 (RANBP2L1), transcript variant 1, mRNA /cds=(78,5375) /gb=NM_005054 /gi=19718754 /ug=Hs.179825 /len=7164	NM_005054	Hs.179825	NP_115636
11806	0.028428	DKFZp434K0172 (from clone DKFZp434K0172) /cds=UNKNOWN /gb=AL122084 /gi=6102892 /ug=Hs 121073 /len=3447	AL122084	Hs.121073	NP_060570
11860	0.017843	FOXJ2 forkhead factor (FHX), mRNA /cds=(490,2214) /gb=NM_018416 /gi=8923841 /ug=Hs.120844 /len=4873	NM_018416	Hs.120844	NP_060886

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
11879	0.049308	interleukin-1 receptor-associated kinase	NM_016123	Hs.142295	NP 057207
		4 (IRAK4), mRNA /cds=(50,1432)			4
-		/gb=NM_016123 /gi=7705840	*	<b>}</b> •	
	•	/ug=Hs.142295 /len=2817	• 0		** *
11898	0.002877	intersectin 2 (ITSN2), transcript variant 1,	NM 006277	Hs. 166184	NP 671494
		mRNA /cds=(242,5332) /gb=NM_006277			_
		/gi=22325384 /ug=Hs.166184 /len=6092		. '	
	•				a a
11923	0.002508	unidentified mRNA, partial sequence.	U43604	Hs.159901	*
] .		/gb=U43604 /gi=1171236			
	* '	/ug=Hs.159901 /len=1677			
11926	0.043827	hypothetical protein FLJ13611	NM_024941	Hs.282958	NP 079217
-		(FLJ13611), mRNA /cds=(207,1271)	7		<b>-</b>
		/gb=NM_024941 /gi=13376418			
		/ug=Hs.282958 /len=2726			
11927	0.026653	CCR4-NOT transcription complex,	NM 004779	Hs.26703	NP 004770
-		subunit 8 (CNOT8), mRNA	· - T		√ <u> </u>
		/cds=(245,1123) /gb=NM 004779	- 3		
		/gi=24496777 /ug=Hs.26703 /len=2489			
11949	0.038855	spermine synthase (SMS), mRNA	NM 004595	Hs.89718	NP_004586
		/cds=(102,1202) /gb=NM 004595			
		/gi=21264340 /ug=Hs.89718 /len=1717		-1 -1	
11955	0.041279	mRNA for KIAA0935 protein, partial cds.	AB023152	Hs.12183	
,		/cds=(1,2472) /gb=AB023152	-		
		/gi=4589513 /ug=Hs.12183 /len=6189	€'		
11957	0.044761	DKFZp564I112 (from clone	AL110136	Hs.47679	
		DKFZp564I112) mRNA; cDNA		* .	4
	1 1	/cds=UNKNOWN /gb=AL110136	*		
		/gi=5817031 /ug=Hs.47679 /len=1885			
11973	0.015521	mitochondrion, complete genome	NC_001807		
11985	0.046501	protocadherin beta 16 (PCDHB16),	NM_020957	Hs.147674	NP_066008
		mRNA /cds=(1156,3486)			
		/gb=NM_020957 /gi=14195604	*-		
		/ug=Hs.147674 /len=4827			
11987	0.030746	hypothetical protein BC008647	NM_138376	Hs.102480	NP_612385
		(LOC91875), mRNA /cds=(41,1363)	= ,		. – ,
_		/gb=NM_138376 /gi=24308431		*	
•		/ug=Hs.102480 /len=1845			
12003	0.026653	EST(zi39c11.s1 Soares fetal liver spleen	AA680133		NP_660208
	.*	1NFLS S1 cDNA clone 433172 3')	*	[ •	
12004	0.004569	hypothetical L1 protein (third intron of	JU0033		JU0033
<u> </u>		gene TS)			
12021	0.020453	chromosome 18 open reading frame 1	NM_004338	Hs.153498	NP_004329
	k.	(C18orf1), mRNA /cds=(243,989)	/-		
	'	/gb=NM_004338 /gi=4757883	: 1		
		/ug=Hs.153498 /len=8093		*	
12022	0.047541	kinesin family protein 3B (KIF3B)	NM_004798		NP_004789

Spot	p-value	Description	Gene	Unigene	Protein
Opoc	p value			Acc ssion	Accession
			Accession No.	No.	No.
12059	0.038855	K-EST0221887 L17N670205n1 cDNA	CB161859	Hs.436333	140.
		clone L17N670205n1-41-A03 5', mRNA			
0.7		sequence /clone=L17N670205n1-41-A03	·		
	-(-	/clone_end=5' /gb=CB161859	Υ		
	*	/gi=28147985 /ug=Hs.436333 /len=481		·	
12074	0.019217	EST(as88c04.x1 Barstead colon	Al735066	.04	- 100
		HPLRB7 clone IMAGE:2335782 3'		-	
* .		TR:Q13538 Q13538 ORF2: FUNCTION			·
		UNKNOWN; contains Alu repeat)			* _
12120	0.017843	mRNA; cDNA DKFZp761O0611 (from	AL834155	Hs.22969	
		clone DKFZp761O0611) /gb=AL834155	· ·		
		/gi=21739631 /ug=Hs.22969 /len=4502			
12141	0.044761	EST (zc24f10.s1	W43004		
	,	Soares_senescent_fibroblasts_NbHSF	,		
	- :	IMAGE:323275 3')(contains Alu			
	-	repetitive element)			*
12155	0.011644	EST AV734861 cdA H.sapiens cDNA	AV734861		
. * .		clone cdAAPC07 5'			
12158	0.030134	PTK2 protein tyrosine kinase 2 (PTK2),	NM_153831	Hs.740	NP_722560
	* 17	transcript variant 1, mRNA			
٠.		/cds=(231,3389) /gb=NM_153831			*
	•	/gi=27886591 /ug=Hs.740 /len=4453			•
12160	0.011586	DKFZp564P1871_s1 564 (synonym:	AL037446	Hs.208747	
		hfbr2) cDNA clone DKFZp564P1871 3',			·
	*	mRNA sequence	44.4		
		/clone=DKFZp564P1871 /clone_end=3'			
		/gb=AL037446 /gi=5406837			
		/ug=Hs.208747 /len=556			
12163	0.016648	mRNA, cDNA DKFZp434l2129 (from	AL832450	Hs.376999	
		clone DKFZp434l2129) /cds=(1,655)	. ()	(	•
*		/gb=AL832450 /gi=21733015	,	8	
		/ug=Hs.376999 /len=2100			
12165	8.10E-04	EST CM3-HT0185-061099-021-c03	BE144941	1	
		HT0185 cDNA	-		
12178	0.034358	EST (of53c02.s1 NCI_CGAP_CNS1	AA836671		
		IMAGE:1427906)			1
12183	0.004961	cDNA sequence (cDNA FLJ14256 fis,	AK024318		NP_073743
	*	clone PLACE1000007, weakly similar to	. ,		
5.		PROBABLE UBIQUITIN CARBOXYL-	100		
'		TERMINAL HYDROLASE R10E11.3)		0	
		Length = 3176			,
12184	0.030302	cDNA FLJ11086 fis, clone	AK001948	Hs.272240	*
	0	PLACE1005266. /gb=AK001948			
<u> </u>	<u> </u>	/gi=7023529 /ug=Hs.272240 /len=1899			, ,
12189	0.038855	EST AV750486 NPC H.sapiens cDNA	AV750486		
<u></u>		clone NPCDCF06 5'		<del> </del>	
12207	0.004205	phytoceramidase, alkaline (PHCA),	NM_018367	Hs.23862	NP_060837
		mRNA /cds=(59,862) /gb=NM_018367			
L		/gi=19923526 /ug=Hs.23862 /len=3404			

Spot	p-value	D scription	Gene	Unig ne	Protein
		* 1	Accession No.	Accession	Accession
12213	0.036549	repetitive sequence (ALU SUBFAMILY	P39188	No.	No.
12210	0.000040	J)	1 00 100		*
12229	0.013463	clone IMAGE:3924941, mRNA	BC029341	Hs.391380	
		/gb=BC029341 /gi=20379505	*	, , , , , , , , , , , , , , , , , , , ,	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
		/ug=Hs.391380 /len=1657			
12243		mRNA; cDNA DKFZp313P0434 (from	AL832702	Hs.125019	
		clone DKFZp313P0434) /gb=AL832702		*	
		/gi=21733281 /ug=Hs.125019 /len=2995			).
12244	0.00299	EST(601812732F1 NIH_MGC_54 cDNA	BF211120	a-	NP_071942
		clone IMAGE:4047222 5')		-	
12251	0.021876	AGENCOURT_10616002	BU963194	Hs.422374	
1		NIH_MGC_141 cDNA clone			
		IMAGE:6744199 5', mRNA sequence	·	*	
0		/clone=IMAGE:6744199 /clone_end=5'	j.		
		/gb=BU963194 /gi=24192766			
		/ug=Hs.422374 /len=939			:
12252	0.015521	UI-E-CL1-afb-k-21-0-UI.s1 UI-E-CL1	BM665519	Hs.159501	
		cDNA clone UI-E-CL1-afb-k-21-0-UI 3',			
		mRNA sequence /clone=UI-E-CL1-afb-k-			<u>.</u>
		21-0-UI /clone_end=3' /gb=BM665519			
		/gi=18972482 /ug=Hs.159501 /len=1100			
10050	0.000050	Ection 1	D0000404	11-7004	ND 004040
12259	0.026653	EST (Similar to pleckstrin homology,	BC008191	Hs.7984	NP_004218
ĺ		Sec7 and coiled/coil domains 3, clone			
		MGC:5340 IMAGE:2984886, complete	ů.	· ·	
		cds /cds=(3,542) /gb=BC008191		'	
12261	0.023381	/gi=14198262/ug=Hs.7984 /len=3720) UI-E-EO1-aid-o-06-0-UI.s1 UI-E-EO1	BM677516	Hs.443680	
12201	0.023361	cDNA clone UI-E-EO1-aid-o-06-0-UI 3',	DIVIO77510	HS.443000	
} .	, -	mRNA sequence /clone=UI-E-EO1-aid-o-	}		100
	3	06-0-UI /clone end=3' /gb=BM677516		•	
		/gi=18987412 /ug=Hs.443680 /len=1044		~	
		10307 + 12 / ug = 113.4+00000 / icit = 1044		-	
12284	0.00326	EST384170 MAGE resequences, MAGL	AW971961	Hs.136340	
	, , , , , , , , , , , , , , , , , , ,	cDNA, mRNA sequence /gb=AW971961		0	
	1.	/gi=8161927 /ug=Hs.136340 /len=642	*		
	~ . ·				
12290	0.021876	EST(yd74f02.s1 Soares fetal liver spleen	T79796		
		1NFLS cDNA clone IMAGE:113979 3'			
	l.	similar to contains Alu repetitive element)		100%	
			;		
12296	0.00299	EST(yy85f03.r1	N50310	,	
		Soares_multiple_sclerosis_2NbHMSP		]	
		clone IMAGE:280349 5' similar to		,	2
		contains Alu repetitive element)			
12322	0.030302	EST(DKFZp547L234_r1 547 (synonym:	AL134310		
		hfbr1) cDNA clone DKFZp547L234 5')	I		<u> </u>

Spot	p-value	Description	Gene	Unigene	Protein
* .			Accession No.	Accession	Accession No.
12323	0.011644	hypothetical protein DKFZp564D1378	NM_032124	<b>No.</b> Hs.318401	NP 115500
		(DKFZP564D1378), mRNA			
		/cds=(125,904) /gb=NM_032124			
		/gi=14149776 /ug=Hs.318401 /len=2195			
12326	0.036549	EST(UI-H-BI3-akh-f-06-0-UI.s1	AW449287		
12029		NCI_CGAP_Sub5 cDNA clone			-
		IMAGE:2734235 3')			,
12329	0.007397	EST(RC2-CT0298-300100-014-d01	AW604547	-}	NP_000981
		СТ0298)			
12335	0.010816	EST (603205161F1 NIH_MGC_97 cDNA	BI462159		NP_006234
10050	0.000540	clone IMAGE:5270895 5')	414/000450	1 4000	
12352	0.036549	UI-H-BI2-ahm-d-05-0-UI.s1	AW293452	Hs.16228	
*	٠	NCI_CGAP_Sub4 cDNA clone IMAGE:2727224 3', mRNA sequence			
,		/clone=IMAGE:2727224 /clone_end=3'	-		
		/gb=AW293452 /gi=6700088	:		0
		/ug=Hs.16228 /len=634		*	
12371	0.005259	ESTs, cDNA, 5' end /clone=BMFBFE06	AV756341	Hs.244273	
		/clone_end=5' /gb=AV756341			
		/gi=10914189 /ug=Hs.244273 /len=766		30	
12374	0.039601	ESTs, cDNA	BG194574	Hs.221776	,
		/gb=BG194574/gi=13716261			
12388	0.036540	/ug=Hs.221776 /len=853 EST(cDNA clone IMAGE:4398135 5')	BF984363	-	
12412		cDNA / IL3-NT0294-060401-533-D04	BI041924		
1,5-1,5	0.010010	NT0294	51041024	,	
12424	0.004569	mRNA; cDNA DKFZp564B076 (from	AL049313	Hs.21103	·
		clone DKFZp564B076) /gb=AL049313			
		/gi=4500086 /ug=Hs.21103 /len=2208			
12426	0.036549	602590145F1 NIH_MGC_76 cDNA	BG564169	Hs.444093	
		clone IMAGE:4724074 5', mRNA			4
		sequence /clone=IMAGE:4724074			
		/clone_end=5' /gb=BG564169			
12430	0.013463	/gi=13571821 /ug=Hs.444093 /len=792 mRNA, cDNA DKFZp686J19116 (from	AL833458	Hs.428760	
12450	0,010403	clone DKFZp686J19116) /gb=AL833458	AL000400	113.420700	
		/gi=21734100 /ug=Hs.428760 /len=3297		·	÷
				. 3 4	
12431	0.004961	ESTs, cDNA /gb=AW993259	AW993259	Hs.113105	
, .·		/gi=8253410 /ug=Hs.113105 /len=678			
12433	0.041279	cDNA FLJ14388 fis, clone	AK027294	Hs.9812	ŀ
		HEMBA1002716. /gb=AK027294			
12425	0.029400	/gi=14041878 /ug=Hs.9812 /len=1673	DC027740	Up:19046	
12435	J U.UZ8428	clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216	BC037740	Hs.18016	
		/ug=Hs.18016 /len=5036		÷	[
<u> </u>	l ,,	pag 110.100 to holl 0000	L	<del></del>	<del>ل ا</del>

Spot	p-value	Description	Gene Accession No.	Unigen Accession	Prot in Acc ssion
12436	0.026652	UI-H-BW0-ajn-d-08-0-UI.s1	AW297946	<b>No.</b> Hs.444392	No.
12430	0.020003	NCI CGAP Sub6 cDNA clone	AVV23/340	115.444592	97
		IMAGE:2732223 3', mRNA sequence		]	
•	*,			· ·	
		/clone=IMAGE:2732223 /clone_end=3'		8	
		/gb=AW297946 /gi=6704582		-	
10.150	0.044404	/ug=Hs.444392 /len=807	4 4 9 9 9 4 9 9	11 07044	
12453	0.014461	EST, cDNA, 3' end	AA398482	Hs.97641	
9	·	/clone=IMAGE:726989 /clone_end=3'			· ·
	. *	/gb=AA398482 /gi=2051592		Ì	00.
		/ug=Hs.97641 /len=397			
12489	0.00684	MR2-Cl0186-291100-010-a06 Cl0186	BF814502	Hs.446594	
		cDNA, mRNA sequence /gb=BF814502			
	.00	/gi=12147047 /ug=Hs.446594 /len=530			
12494	0.024972	cDNA FLJ39046 fis, clone	AK096365	Hs.9856	
		NT2RP7010612. /gb=AK096365			
,		/gi=21755841 /ug=Hs.9856 /len=2161	X		
12499	0.004205	EST(cDNA clone IMAGE:4823837 5')	BG720040		NP 079229
12520		EST(Embryonic Heart cDNA Library	AI617050	. 03	
•=====		Danio rerio cDNA 5' )			- ()
12529	0.014461	cDNA FLJ36544 fis, clone	AK093863	Hs.101689	
12020	0.077107	TRACH2006378. /gb=AK093863			0.
	-	/gi=21752807 /ug=Hs.101689 /len=2670			
12530	0.024972	AGENCOURT_7566238 NIH_MGC_92	BQ226831	Hs.21887	
12000	0.02-072	cDNA clone IMAGE:6043519 5', mRNA	D G Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z	11.0.2 100.	
		sequence /clone=IMAGE:6043519			٠.
		/clone_end=5' /gb=BQ226831			
	1	/gi=20408231 /ug=Hs.21887 /len=1223	}		, ,
12531	0.023381	wt59c09.x1 NCI_CGAP_Pan1 cDNA	Al955766	Hs.329191	<del> </del>
12331	0.023301	clone IMAGE:2511760 3', mRNA	A1300700	113.323131	
. 1.	* * *	seguence /clone=IMAGE:2511760			
	•	1 .	*	**	
-		/clone_end=3' /gb=Al955766	-	·	
40504	0.000055	/gi=5748076 /ug=Hs:329191 /len=496	A A 740440		ND 060910
		EST(cDNA clone IMAGE:1270440 3')	AA748418	11. 40070	NP_060819
12555	0.0,16648	ESTs, cDNA, 5' end	BG698090	Hs.12876	
		/clone=IMAGE:4802969 /clone_end=5'			
	1	/gb=BG698090 /gi=13965026			
		/ug=Hs.12876 /len=985			*
12568	0.009313	EST, cDNA, 3' end	AA927945	Hs.292141	
	Ì	/clone=IMAGE:1541875 /clone_end=3'			
		/gb=AA927945 /gi=3076689			
		/ug=Hs.292141 /len=354			
12572	0.002508	EST, clone IMAGE:4151959, mRNA	BC011194	Hs.367863	
	-	/cds=UNKNOWN /gb=BC011194			
		/gi=15277441 /ug=Hs.367863 /len=1842			·
	1			J	}

Spot	p-value	Description	Gene	Unigene Accession	Protein Accession
			Accession No.		
10574	0.000400	ULU EDO pues 5 45 O UL 04	DO00000	No.	No.
12574	0.028428	UI-H-ED0-awx-b-15-0-UI.s1	BQ020068	Hs.396278	,
		NCI_CGAP_ED0 cDNA clone			
		IMAGE:5824814 3', mRNA sequence	• •		
		/clone=IMAGE:5824814 /clone_end=3'	1 2		
.· "	*	/gb=BQ020068 /gi=19755345	* *		
		/ug=Hs.396278 /len=1351			
12593	0.047541	No significant match,			
		ORF+2(71~409),+1(121~384)	SEQ.ID.No.94		
12618	0.030302	No significant match			•
		(ORF:+1:52~230[180])	SEQ.ID.No;28	. :	
		No significant match, ORF+3(156~314)	SEQ.ID.No.77		
12655	0.005835	zt59c06.s1 Soares_testis_NHT cDNA	AA398215	Hs.290951	3,11
7		clone IMAGE:726634:3', mRNA		`	
	9	sequence /clone=IMAGE:726634	÷		
- 1	*	/clone_end=3' /gb=AA398215			
		/gi=2051324 /ug=Hs.290951 /len=427			
12669	0.00632	hypothetical protein FLJ31438	NM_152385	Hs.24423	NP 689598
		(FLJ31438), mRNA /cds=(347,2107)	T		_
		/gb=NM_152385 /gi=22748824			
		/ug=Hs.24423 /len=2266			49
12680	0.030302	EST (CM3-HT0528-010200-086-f04	BE169870		
		HT0528)			
12695	0.004961	mitochondrion, complete genome	NC 001807		· · · · · · · · · · · · · · · · · · ·
12697		mitochondrion, complete genome	NC 001807		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
12703		EST(CM2-BT0366-271299-061-e10	BE068039	,	
12700	0.000010	BT0366)	D200000		*
12729	0.005835	xg60a08.x1 NCI_CGAP_Ut4 cDNA clone	AW168110	Hs.277648	
12720	0.000000	IMAGE:2632694 3', mRNA sequence	/ ( ) ( )	110.2170-0	1
		/clone=IMAGE:2632694 /clone end=3'		0	
	ľ	/gb=AW168110 /gi=6399635			
		/ug=Hs.277648 /len=475			
12731	0.024072	BX099644 NCI_CGAP_Kid3 cDNA clone	DV000644	Hs.125353	100 00 00
12/31	0.024972	IMAGp998A103336, mRNA sequence	DA099044	1118.125555	, ,
				8	
	. (	/clone=IMAGp998A103336_;_IMAGE:13		•	
0.		23153 /gb=BX099644 /gi=27830124			
	1 .	/ug=Hs.125353 /len=472			Ĭ
10700	0.004070		110 004007	,	We will be a second
		mitochondrion, complete genome	NC_001807		
12733	0.0249/2	cDNA, 3' end /clone=IMAGE:2726753	AW293323	Hs.255182	
*		/clone_end=3' /gb=AW293323			* *
7 5 20 -		/gi=6699885 /ug=Hs.255182 /len=354		1 . 20 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	* .
12734	0:021876	mRNA for FLJ00201 protein.	AK074129	Hs.353001	
	-	/cds=(1,2119) /gb=AK074129	,		
.*=		/gi=18676605 /ug=Hs.353001 /len=4443			
		3			<u></u>
12755	0.034358	EST(yf27d03.s1 Soares fetal liver spleen	R09539		
	}	1NFLS cDNA clone IMAGE:128069 3')	,	<i>p</i> •	
<u> </u>				· · ·	

Spot	p-value	Description	Gen	Unigene	Protein
			Acc ssion No.	Accession	Accession
				No.	No.
12763	0.030302	UI-H-FG0-bct-g-21-0-UI.s1	BU627064	Hs.85999	
		NCI_CGAP_EN1_2 cDNA clone UI-H-			,
		FG0-bct-g-21-0-UI 3', mRNA sequence		-8-	
- ·		/clone=UI-H-FG0-bct-g-21-0-UI	11. 9		())
		/clone_end=3' /gb=BU627064	. *		
		/gi=23293278 /ug=Hs.85999 /len=1075			
12765	0.021876	EST (RC5-BT0663-050400-012-H04	BE085097		
		BT0663 cDNA)			
12779	0.032277	UI-H-DF1-auk-m-15-0-UI.s1	BM991622	Hs:24252	
		NCI_CGAP_DF1 cDNA clone		-50	
	.0	IMAGE:5870774 3', mRNA sequence	*		
	1	/clone=IMAGE:5870774 /clone_end=3'	. *		
		/gb=BM991622 /gi=19711011		:	
	111	/ug=Hs.24252 /len=1094			
12805	0.044761	clone IMAGE:3633225, mRNA	BC012758	Hs.356377	
		/gb=BC012758 /gi=15706478			
		/ug=Hs.356377 /len=1914		. "	
12807	0.030302	hypothetical protein BC014320	NM_138785	Hs.240767	NP_620140
		(LOC116254), mRNA /cds=(28,1020)		*	·
	a	/gb=NM_138785 /gi=20302037			
		/ug=Hs.240767 /len=1143			
12818	0.041279	7a42b09.x1 NCI_CGAP_GC6 cDNA	BE551502	Hs.445382	
		clone IMAGE:3221369 3', mRNA			
		sequence /clone=IMAGE:3221369	1 1		
}		/clone_end=3' /gb=BE551502			
		/gi=9793194 /ug=Hs.445382 /len=553			
12837	0.024972	cDNA, 5' end /clone=IMAGE:5214599	BI911779	Hs.13370	NP_054763
. *		/clone_end=5' /gb=Bl911779			
		/gi=16175651 /ug=Hs.121740 /len=818		1.	
12838	0.032277	EST(mRNA from cd34 stem cells Homo	AF150252		
	-	sapiens cDNA clone CBFBDE10)	1		
					*
12839	0.020453	EST383336 MAGE resequences, MAGL	AW971247	Hs.348501	
		cDNA, mRNA sequence /gb=AW971247			0.0
		/gi=8161092 /ug=Hs.348501 /len=578			
<u> </u>	2 2 2 3				
12843	0.001199	cDNA clone IMAGE:123789 3' similar to	R01434		
00		contains Alu repetitive element;contains		i	
	,	THR repetitive element ; Soares fetal			
	. * (	liver spleen 1NFLS		. 4	
	. 2022		0.12		
12846	0.00684	EST, cDNA, 5' end	AL137968	Hs.256115	
		/clone=DKFZp761D0315 /clone_end=5'			1
		/gb=AL137968 /gi=6854648			
		/ug=Hs.256115 /len=523		.:	
12876	0.034358	cDNA FLJ36999 fis, clone	AK094318	Hs.343588	
	}	BRACE2007518. /gb=AK094318	1 .		1
		/gi=21753354 /ug=Hs.343588 /len=2283			*
-					

Spot	p-valu	Description	Gene Accession No.	Unigene Acc ssion No.	Protein Accession No.
12879	0.041279	hypothetical protein FLJ22415	NM_024769	Hs.135121	NP_079045
1.20.0	0.011210	(FLJ22415), mRNA /cds=(342,1463)	0200	110.100 121	0.00.0
		/gb=NM_024769 /gi=13376114			-
		/ug=Hs.135121 /len=2627	÷		
12888	0.003552	yp57c03.s1 Soares fetal liver spleen	H37807	Hs.418023	<u> </u>
12000	0.000002	1NFLS cDNA clone IMAGE:191524 3'	1.0.00.	110.110020	<u>,</u>
•		similar to contains L1 repetitive element			}
		;, mRNA sequence			• 40 •
1		/clone=IMAGE:191524 /clone end=3'		*	] •
		/gb=H37807 /gi=907306 /ug=Hs.418023			
		/len=461			
12891	0.002294	cDNA FLJ38472 fis, clone	AK095791	Hs.50150	
12001	0.002204	FEBRA2022148. /gb=AK095791	7 (1000751	113.00100	
		/gi=21755125 /ug=Hs.50150 /len=2454	Y . Y		8 1
12896	0.005382	cDNA FLJ30298 fis, clone	AK054860	Hs.351546	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
12030	0.000002	BRACE2003172. /gb=AK054860	711004000	113.5515.55	
	-	/gi=16549479 /ug=Hs.351546 /len=2659			
		10049479 /ug=118.55 1546 /iei1=2059			
12897	0.010816	EST(cDNA clone IMAGE:6106210 5'.)	BQ438562		NP 005339
12898		603395193F1 NIH_MGC 90 cDNA	BI871283	Hs.443147	141_000009
12030	0.032211	clone IMAGE:5405278 5', mRNA	DIO7 1203	118.445147	•
		sequence /clone=IMAGE:5405278			
] a ·		/clone_end=5' /gb=BI871283			
1		/gi=16044958 /ug=Hs.443147 /len=845		n. j.	. 1
12903	0.00684	cDNA FLJ33097 fis, clone	AK057659	Hs 415317	
12303	0.00004	TRACH2000775. /gb=AK057659	AK037039 1.	113.410017	
		/gi=16553423 /ug=Hs.415317 /len=2977			
7	*	/g = 1033342374g=113.41337771en=2977  -			. 0
12921	0.021876	BX106452 NCI_CGAP_Gas4 cDNA	BX106452	Hs.200841	
12321	0.02 1070	clone IMAGp998N095583, mRNA	DX 100432	113.200041	
,		sequence			*
		/clone=IMAGp998N095583_;_IMAGE:22	· .		
		55816 /gb=BX106452 /gi=27834105	-X-		
		/ug=Hs.200841 /len=458	3.7		
12924	0.046501	UI-H-BI3-alm-f-10-0-UI.s1	AW452027	Hs.440660	1 10
12024	0.040001	NCI_CGAP_Sub5 cDNA clone	7.44-102027	113.110000	
		IMAGE:2737314 3', mRNA sequence			٠.
		/clone=IMAGE:2737314 /clone end=3'	a :	*.	-
		/gb=AW452027 /gi=6992803			
	: .	/ug=Hs.440660 /len=755		1	
12933	0.01004	cDNA FLJ34764 fis, clone	AK092083	Hs.111583	-
1,2000	0.01004	NT2NE2002311. /gb=AK092083		1.16. 1.1666	
1		/gi=21750590 /ug=Hs.111583 /len=2552	ν,		<u> </u>
		2 17 00000 rug=113. 1 1 1000 /ieii=2002.	4	:	
12941	0.00853	MR2-CI0186-291100-010-a06 CI0186	BF814502	Hs.446594	A 7 0 1
1,5371	. 0.00000	cDNA, mRNA sequence /gb=BF814502	014002	1110.770007	
		/gi=12147047 /ug=Hs.446594 /len=530	*		· ·
] .					] .
<u> </u>		<u> </u>	<u> </u>	<u> </u>	L

12947					
12947			Accession No.	Accession	Accession
12947				No.	No.
		UI-H-BI1-acd-d-04-0-UI.s1	AW135924	Hs.224883	
		NCI_CGAP_Sub3 cDNA clone	. ,		
. 1		IMAGE:2713783 3', mRNA sequence			: :
[		/clone=IMAGE:2713783 /clone_end=3'		. *	
1		/gb=AW135924 /gi=6140057			
		/ug=Hs.224883 /len=834			
12953		cDNA, 3' end /clone=IMAGE:436024	AA699991	Hs.348162	,
		/clone_end=3' /gb=AA699991			
		/gi=2702954 /ug=Hs.348162 /len=614	ļ		
12958		ov45a11.x1 Soares_testis_NHT cDNA	AI073470	Hs.233388	
		clone IMAGE:1640252 3', mRNA		,	. *
		sequence /clone=IMAGE:1640252	*	l · .	
,		/clone_end=3' /gb=AI073470	* 0		ì
		/gi=3400114 /ug=Hs.233388 /len=565			
12986	0.038855	mRNA; cDNA DKFZp564B222 (from	AL049974	Hs.100261	
		clone DKFZp564B222) /gb=AL049974		-8-	-
10000		/gi=4884224 /ug=Hs.100261 /len=2315			
12989		clone IMAGE:5268470, mRNA	BC040580	Hs.426563	, 1
**		/gb=BC040580 /gi=26251834			. ,
10000		/ug=Hs.426563 /len=3344	1114 470005		115-5-5-5
12999	0.020596	hypothetical protein FLJ32440	NM_173685	Hs.344478	NP_775956
		(FLJ32440), mRNA /cds=(228,971)	*		
		/gb=NM_173685 /gi=27734760			\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
40005		/ug=Hs.344478 /len=1258	4.4000500	11 100001	
13005	0.008631	zx55g04.r1	AA203502	Hs.192991	
·		Soares_fetal_liver_spleen_1NFLS_S1		l <sub>a.</sub>	
		cDNA clone IMAGE:446454 5', mRNA		*	
	, *-	sequence /clone=IMAGE:446454	18		i i
		/clone_end=5' /gb=AA203502			
13014		/gi=1799213 /ug=Hs.192991 /len=952 cDNA FLJ13334 fis, clone	AK023396	Hs.269091	
13014	0.041279	OVARC1001846. /gb=AK023396	MN023390	IU2769091	
		/gi=10435315 /ug=Hs.269091 /len=2361			9
	*	7gi=10+333137dg=118.2090917len=2301			
13021	0.012483	EST(cDNA clone GLCAOE01 3')	AV646538		
		UI-H-CO0-atn-a-07-0-UI.s1	BM988193	Hs.28107	
	0.010021	NCI CGAP Sub9 cDNA clone		113.20107	
		IMAGE:5861653 3', mRNA sequence			, a
	•	/clone=IMAGE:5861653 /clone_end=3'	. *		
	* .	/gb=BM988193 /gi=19707582			
	- ×	/ug=Hs.28107 /len=1022	*		
13032	0.004569	EST(cDNA clone UI-R-CA0-axe-a-12-0-	BE113844	7	
	.,	UI 3' )		-2	٥
13033	0.011644	EST(cDNA clone IMAGE:4455676 5')	BG166249	<del></del>	712
		chromosome 3 clone RP11-627J17,	AC112211		
]		WORKING DRAFT SEQUENCE, 4			[.
		unordered pieces	**		
13064	0.026653	No significant match (ORF:-		-	
	Ì	1:37~186[150])	SEQ.ID.No.63		

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession No.	Accession
13076	0.041279	UI-H-BI1-abw-h-07-0-UI.s1	AW138111	Hs.436560	No.
		NCI_CGAP_Sub3 cDNA clone IMAGE:2713572 3', mRNA sequence /clone=IMAGE:2713572 /clone_end=3'	) 	. )	-
		/gb=AW138111 /gi=6142429 /ug=Hs.436560 /len=800			
13100	-	No significant match (ORF:+3.6~221[216])	SEQ.ID.No.64		
13112	0.00684		NM_000850	Hs.348387	NP_671490
		transcript variant 1, mRNA /cds=(310,966) /gb=NM_000850 /gi=23065554 /ug=Hs.348387 /len=1436			
13128	0.038855	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA /cds=(81,362) /gb=NM_000609	NM_000609	Hs.237356	NP_000600
		/gi=10834987 /ug=Hs.237356 /len=3541			
13132	0.019217	endosome-associated FYVE-domain protein (ENDOFIN), mRNA /cds=(249,4868) /gb=NM_014733	NM_014733	Hs.83790	NP_055548
13183	0.012525	/gi=7662047 /ug=Hs.83790 /len=6632 translocation related non-coding gene	AF044579	Hs.375632	<del> </del>
	1	(TNRG10) mRNA, complete sequence /gb=AF044579 /gi=3095103		110.07002	
		/ug=Hs.375632 /len=2726		,	:.
13187	0.049308	smooth muscle cell-expressed and macrophage conditioned medium-	NM_020351	Hs.283100	NP_065084
	*	induced protein smag-64 (LOC57086), mRNA /cds=(360,560) /gb=NM_020351 /gi=9966814 /ug=Hs.283100 /len=2828			*
13194	0.015521	putative serine-rich protein mRNA, partial cds (AF246705.1)	AF246705	Hs.32922	NP_060102
13213	0.049308	DNA sequence from clone RP4-550H1 on chromosome 20q11.1-11.22 Contains a high mobility group protein pseudogene, a novel gene, the 5' end of	AL035420	*	
i i		the EPB41L1 gene encoding Erythrocyte membrane protein band 4.1-like 1 protein (KIAA0338), ESTs, STSs, GS>		*	
13260	0.043827	UBX domain containing 2 (UBXD2), mRNA /cds=(156,1682) /gb=NM_014607 /gi=24307964 /ug=Hs.77495 /len=3867	NM_014607	Hs.77495	NP_055422
13302	6.62E-04	nuclear pore complex protein (NUP107), mRNA /cds=(116,2893) /gb=NM_020401 /gi=9966880 /ug=Hs.236204 /len=3131	NM_020401	Hs.236204	NP_065134

Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
	* '		Accession ino.		
13339	0.026653	mRNA for KIAA1133 protein, partial cds.	AB051436	<b>No.</b> Hs.318584	No.
10000	0.020000	/cds=(1,2676) /gb=AB051436	7000 1400	115.510504	
		/gi=13195720 /ug=Hs.318584 /len=6542			
,		/gi=13193/20/dg=119.310304 /ieii=0342			
13342	0.00632	RNA guanylyltransferase and 5'-	NM_003800	Hs.27345	NP_003791
		phosphatase (RNGTT), mRNA	- 00	8	
		/cds=(289,2082) /gb=NM_003800		·	
		/gi=4506562 /ug=Hs.27345 /len=4546			
13366	0.038855	hypothetical protein DKFZp434I1916	NM_032245	Hs.334641	NP_115621
1.		(DKFZp434l1916), mRNA	**		
		/cds=(144,563) /gb=NM_032245	,		• .
	·	/gi=14149959 /ug=Hs.334641 /len=800			
13376	0.023381	hypothetical protein FLJ20276	NM_017738	Hs.270502	NP_060208
		(FLJ20276), mRNA /cds=(134,3388)		0.00	
	20 .	/gb≍NM_017738 /gi=8923250	*		*
		/ug=Hs.270502 /len=4790			
13380	0.026653	similar to HYPOTHETICAL 34.0 KDA	NM_033416	Hs.91579	NP_219484
		PROTEIN ZK795.3 IN CHROMOSOME			
		IV (MGC19606), mRNA /cds=(18,893)	*		
		/gb=NM_033416 /gi=15529981		. 0	*
	**	/ug=Hs.91579 /len=1074			
13406	0.00684	yh68a05.s1 Soares placenta Nb2HP	R32301	Hs.386871	
	,	cDNA clone IMAGE:134864 3', mRNA			
10		sequence /clone=IMAGE:134864			
	107	/clone_end=3' /gb=R32301 /gi=788144			Î
		/ug=Hs.386871 /len=246			
13490	0.003866	mRNA; cDNA DKFZp586G1917 (from	AL117453	Hs.306343	:
		clone DKFZp586G1917) /gb=AL117453		- 44	
		/gi=5911904 /ug=Hs.306343 /len=3532			
13513	0.004961	EST(PM3-SN0020-270300-001-h08	AW865025		NP_115668
Ĺ <u>.</u>		SN0020)	*	,	
13515	0.030302	EST(hh87d03.x1 NCI_CGAP_GU1 clone	AW627545		
		IMAGE:2969765 3' contains Alu repeat)			
13524	0.012525	hypothetical protein DKFZp586C1924	NM_032273	Hs.108338	NP_115649
-		(DKFZp586C1924), mRNA		1	1.
,		/cds=(106,693) /gb=NM_032273	9		
		/gi=14150016 /ug=Hs 108338 /len=782			
13545	0.045752	yg03b02.s1 Soares infant brain 1NIB	R42618	Hs.12700	* ***
,		cDNA clone IMAGE:30959 3', mRNA			
*	<b>'</b> .	sequence /clone=IMAGE:30959		*	
	1	/clone_end=3' /gb=R42618 /gi=817379			
	<u> </u>	/ug=Hs.12700 /len=441			
13553	0.011586	EST(zw71a05.r1 Soares_testis_NHT	AA432328		
		cDNA clone IMAGE:781616 5' similar to		1	
		contains Alu repetitive element)			
13571	0.049815	EST (7d70f02.x1 NCI_CGAP_Lu24	BE673855 <sup>₹</sup>		1
		IMAGE:3278331 3')		<u> </u>	
13596	0.046501	insulin-like growth factor II receptor	AF069333		
l	I	(IGF2R) gene, partial cds			*

Spot	p-value	D scription	G ne	Unigene	Protein
		9	Accession No.	Accession	Accession
				No.	No.
13615	0.010816	mRNA full length insert cDNA clone	AJ420560	Hs.93231	
į		EUROIMAGE 1476475 /gb=AJ420560	4	ž.	*
		/gi=17066424 /ug=Hs.93231 /len=1346			
13619	0.024441	FLJ30633 fis, clone CTONG2002418,	AK055195	Hs.331328	NP_079031
	• •	weakly similar to Homo sapiens scaffold		* *	
		attachment factor B (SAF-B) mRNA			
		(AK055195.1)			·
13634	0.023381	non-SMC (structural maintenance of	NM_145080	Hs.284295	NP_659547
		chromosomes) element 1 protein			
\	· '	(NSE1), mRNA /cds=(24,794)		\ ·	
		/gb=NM_145080 /gi=21489972		}	,
		/ug=Hs.284295 /len=992			
13649	0.036549	Similar to heparan sulfate 6-O-	BC001196	Hs.6363	NP_004798
[		sulfotransferase, clone IMAGE:3355592,			
*		mRNA, partial cds /cds=(0,518)			
	•	/gb=BC001196 /gi=12654712 ,	50		
		/ug=Hs.6363 /len=3220			·
13665	0.038855		NM_003350	Hs.79300	NP_003341
		2 (UBE2V2), mRNA /cds=(22,459)			
	00.	/gb=NM_003350 /gi=12025664			
	- 77	/ug=Hs.79300 /len=1535		<u> </u>	
13674	0.028428	mRNA for KIAA1826 protein, partial cds.	AB058729	Hs.266782	
1		/cds=(1312,2454)/gb=AB058729		1	
1.	1)	/gi=14017868 /ug=Hs.266782 /len=4066		_	
-					
13677	0.005835	KIAA1377 protein, partial cds	AB037798	Hs.188790	
]	0	/cds=UNKNOWN /gb=AB037798			
		/gi=7243134 /ug=Hs.188790 /len=3916			
13700	0.032277	DJ467N11.1 protein, FLJ13127 fis, clone	AK023189	Hs.143917	NP_071374
		NT2RP3002911 /cds=UNKNOWN			
) -		/gb=AK023189 /gi=10435003			
		/ug=Hs 143917 /len=3073			
1000					<u></u>
13731	0.00274	diacylglycerol O-acyltransferase homolog	NM_032564	Hs.334305	NP_115953
* '		2 (mouse) (DGAT2), mRNA			
)		/cds=(777,1670) /gb=NM_032564	*		ì
] . ]		/gi=14211870 /ug=Hs.334305 /len=2713		***	*
140740	0.055.04	DNA DVEZ - 454N0047 (f	AL 020040	11- 205040	
13746	8.95E-04	mRNA; cDNA DKFZp451N2217 (from	AL832616	Hs.335812	
		clone DKFZp451N2217) /gb=AL832616		<b>,</b>	
}		/gi=21733191 /ug=Hs.335812 /len=4940		}	-
12700	0.022700	likok ortholog of marios hamaria is disast	NIM 0440EC	Ho 7017	ND 054375
13768	0.032788	likely ortholog of mouse hypoxia induced	NM_014056	Hs.7917	NP_054775
		gene 1 (HIG1), mRNA /cds=(93,374)			
,		/gb=NM_014056 /gi=7661619			
12704	0.040504	/ug=Hs.7917 /len=1362	DN740044	115 124252	
13784	0.040501	cDNA, 5' end /clone=UI-E-EJ0-ahh-n-05-	DIVI / 1694 1	Hs.134353	1
1		0-UI /clone_end=5' /gb=BM716941			-
L	إحصيجا	/gi=19030199 /ug=Hs.134353 /len=640	ــــــــــــــــــــــــــــــــــــــ	L	ــــــــــــــــــــــــــــــــــــــ

Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession No.
13791	0.028425	hypothetical protein FLJ12787	NM_032175	No. Hs.100134	NP 115551
10751	0.020425	(FLJ12787), mRNA /cds=(19,876)	14141_002770	1115.100154	141 -119001
v.		/gb=NM_032175 /gi=14149856	. , . ×	1	
		/ug=Hs.100134 /len=2751		)	
13795	0.017843	hypothetical protein FLJ21302	NM_022901	Hs.128071	NP_075052
, 0, 00	0.017040	(FLJ21302), mRNA /cds=(91,1203)	11111_022001	113.120011	_0,0002
		/gb=NM_022901 /gi=12597640		1	
- 1		/ug=Hs.128071 /len=3160	y -	<b>l</b> .	
13814	0.036549	mRNA for KIAA0292 gene, partial cds.	AB006630	Hs.201668	
1001,	0.000010	/cds=(1,5152) /gb=AB006630	7.1200000	1.10.20.000	
	٠,	/gi=2564331 /ug=Hs.201668 /len=6542		,	
13834	0.036549	hypothetical protein FLJ20186	NM 017702	Hs.62771	NP 060172
,1000-1	0.000010	(FLJ20186), mRNA /cds=(128,721)	11111_011102	113.02111	111 _000112
		/gb=NM 017702 /gi=8923176		1	
o.		/ug=Hs.62771 /len=869			
13857	0.001747	mRNA full length insert cDNA clone	AL109709	Hs.167456	<del> </del>
.000		EUROIMAGE 43432. /gb=AL109709	,	1.10.197.190	
		/gi=9187596 /ug=Hs.167456 /len=2091			
13885	0.032277	EST DKFZp434H1418_r1 434	AL048856	11111	NP 006531
,,,,,,,		(synonym:htes3) cDNA clone	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		50055.
		DKFZp434H1418		3	
13922	0.028428	cDNA FLJ36579 fis, clone	AK093898	Hs.48653	<del> </del>
		TRACH2012647. /gb=AK093898.			
		/gi=21752852 /ug=Hs.48653 /len=2318			*
13923	0.01911	mRNA for KIAA1754 protein, partial cds.	AB051541	Hs.28501	NP 203755
		/cds=(32,1816) /gb=AB051541		Х,	
		/gi=12698052 /ug=Hs.28501 /len=4088		2	
13945	0.007397	EST(tx88e11.x1 NCI_CGAP_Ut4 clone	Al690725		
		IMAGE:2276684 3' contains Alu repeat)			
			*	.*	1
13952	0.046501	cDNA FLJ13342 fis, clone	AK023404	Hs.255890	
		OVARC1001950. /gb=AK023404	*		
		/gi=10435328 /ug=Hs.255890 /len=2490			0.0
				*	x
13956	0.021876	zh79h09.s1	W92715	Hs.59358	7
		Soares_fetal_liver_spleen_1NFLS_S1			•
		cDNA clone IMAGE:418337 3', mRNA			1
		sequence /clone=IMAGE:418337	8	<b>1</b>	
		/clone_end=3' /gb=W92715 /gi=1421867	1 1		1
	-	/ug=Hs.59358 /len=397		0.7	
13959	0.030302	wi63d02.x1 NCI_CGAP_Kid12 cDNA	AI762877	Hs.369625	1
		clone IMAGE:2397987 3', mRNA	1		ľ
		sequence /clone=IMAGE:2397987			
		/clone_end=3' /gb=Al762877	1		1
	}	/gi=5178544 /ug=Hs.369625 /len=467			*
13982	0.007284	EST(nv54h12.r1 NCI_CGAP_Ew1 cDNA	AA721522		
	1	clone IMAGE:1233671)		1	I

Spot	p-value	Description	Gene	Unig n	Protein
			Accession No.	Accession No.	Accession No.
13991	0.032277	cDNA FLJ35303 fis, clone	AK092622	Hs.131689	NO.
		PROST2009571. /gb=AK092622			
		/gi=21751255 /ug=Hs.131689 /len=2442	* *	e .	
13992		EST oi10c01.s1 NCI_CGAP_GC4	AA872487		NP_055862
		IMAGE:1476096 3'		*	
14014	0.011644	transmembrane, prostate androgen	NM_020182	Hs.83883	NP_064567
	,	induced RNA (TMEPAI), mRNA	*		
		/cds=(321,1184) /gb=NM_020182	*	**	*
		/gi=21361840 /ug=Hs.83883 /len=4839			
14033	0.026653	EST yt98a02.r1	H96454		
		Soares_pineal_gland_N3HPG cDNA			
	1001 2 10 2 2 7 7	clone IMAGE:232298 5	7 2 2 2 2 2 2 2 3 4 4		777
14052	0.01004	EST(tc73e11.x1 Soares_NhHMPu_S1	Al379321	0.	
4.400.1	0.00000.1	clone IMAGE:2070284 3')	NINA 450407	11- 47404	ND cocco
14064	0.002294	hypothetical protein FLJ33918	NM_152407	Hs.17121	NP_689620
-		(FLJ33918), mRNA /cds=(491,856)			* * *
* .		/gb=NM_152407 /gi=22748862			
14000	0.000055	/ug=Hs.17121 /len=2811	A A C 4 O O O A		
14080	0.038855	EST(af08g07.s1 Soares_testis_NHT	AA610081		90
14093	0.024250	cDNA clone IMAGE:1031100 3') v-myc myelocytomatosis viral oncogene	NM 002467	Hs.79070	NP 002458
14093	0.034336	(avian) (MYC), mRNA /cds=(559,1878)	NIVI_002407	ns./90/0	INP_002456
	Ÿ	/gb=NM_002467 /gi=12962934			
		/ug=Hs.79070 /len=2121			75.0
14111	0.00632	hypothetical protein MGC3121	NM 024031	Hs.293629	NP 076936
17111	0.00002	(MGC3121), mRNA /cds=(179,1936)	14141_024001	119.20020	141 _070000
l .		/gb=NM_024031 /gi=13128979			
		/ug=Hs.293629 /len=2063		• 0	
14130	0.012525	EST (yx14d09.r1 Soares melanocyte	N23550		
		2NbHM IMAGE:261713 5')			4.5
14156	0.023381	EST(nw90a09.s1 NCI_CGAP_Pr12	AA937853	7	
		cDNA clone IMAGE:1253848)			*
14177	0.025245	hypothetical protein BC008207	NM_138386	Hs.267130	NP_612395
ĺ		(LOC92345), mRNA /cds=(195,1679)	<del>,</del>	, ,	
. 4.		/gb=NM_138386 /gi=19923910		- 3	
,		/ug=Hs.267130 /len=1919		-	i. '
14184		EST(clone IMAGE:2509657 3')	AI955713	3	
14187	0.034358	EST(RC5-HT0581-210300-021-B05	BE175638		
·		HT0581)			
14225	0.00684	clone 23933 mRNA sequence	U79273	Hs.239483	
	1	/gb=U79273 /gi=1710239			· ·
4 .555		/ug=Hs.239483 /len=1440	D14475045	11. 445.55	
14226	0.014461	AGENCOURT_6480263 NIH_MGC_92	BM475617	Hs.445483	
		cDNA clone IMAGE:5575699 5', mRNA		* * .	
		sequence /clone=IMAGE:5575699	,		
		/clone_end=5' /gb=BM475617	*		
		/gi=18524659 /ug=Hs.445483 /len=1135	*, *, &		i) i
,	<u> </u>		<u> </u>	<u> </u>	I

Snot	p-valu	Description	Gene	Unigene	Protein
Shor	p-valu	Description		Accession	Accession
		*	Accession No.	No.	No.
14235	0.041279	hypothetical protein MGC45400	NM_153333	Hs.389734	NP_699164
14200	0.04/12/3	(MGC45400), mRNA /cds=(245,598)	14W_10000	M3.009/104	141-099104
1.6		/gb=NM 153333 /gi=23503246			
		/ug=Hs.389734 /len=1290		9 *	
14238	0.007004	UI-H-BI3-akh-b-10-0-UI.s1	AW449245	Hs.438347	<del> </del>
14230	0.007994	NCI CGAP Sub5 cDNA clone	AVV449245	FIS.430347 	
		IMAGE:2734051 3'; mRNA sequence			
-		/clone=IMAGE:2734051 /clone end=3'	* · · · · ·		
		/gb=AW449245 /gi=6990021		-	
		/ug=Hs.438347 /len=707	• (	(i)	
14244	0.021976	cDNA FLJ11946 fis, clone	AK022008	Hs.323231	
14244	0.021070	HEMBB1000709. /gb=AK022008	AN022000 .	1 15.32323 1	
	-	/gi=10433321 /ug=Hs.323231 /len=3241	,	•,	
		/gi=10455521 /ug=ns.525251 /leii=5241			7.3
1/2/0	0.036540	mitochondrion, complete genome	NC 001807		* * * * * * * * * * * * * * * * * * * *
14249		BX109840	BX109840	Hs.269512	
14209	0.010521	Soares_fetal_heart_NbHH19W cDNA	DV 109040	1 13.2093 12	
,		clone IMAGp998M11793, mRNA			*
	3	sequence			
		/clone=IMAGp998M11793_;_IMAGE:346	**		
			. * :		
		930 /gb=BX109840 /gi=27877881	* *	=	
14266	0.00000	/ug=Hs.269512 /len=749	A A 700000	11- 225555	
14200	0.030302	EST, cDNA /clone=IMAGE:1266535	AA729300	Hs.325555	
		/gb=AA729300 /gi=2750659	A see		
14268	0.036549	/ug=Hs.325555 /len=173 calcium/calmodulin-dependent protein	NM_172127	Hs.111460	NP 742126
14200	0.030349	kinase (CaM kinase) II delta (CAMK2D),	1/2/2/	I 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NF_/42120
		transcript variant 1, mRNA	· ·		2 1
	* :	/cds=(505,1941) /gb=NM_172127			·
:	* .	/gi=26667185 /ug=Hs.111460 /len=4098			
		19 -20001			0
14276	0.034358	FLJ11984 fis, clone HEMBB1001348	AK022046	Hs.293922	
1	0.00,1000	/cds=UNKNOWN /gb=AK022046	7 11 (0220-10	119.200022	-
		/gi=10433365 /ug=Hs.293922 /len=3161			
- *		10 10 10 10 10 10 10 10 10 10 10 10 10	* *		
14283	0.020453	ESTs, cDNA, 5' end /clone=GLCCSC04	AV720392	Hs.293568	
230	] 5.920,00	/clone_end=5' /gb=AV720392			*
- *		/gi=10817544 /ug=Hs.293568 (=ESTs,	·	,	
		Weakly similar to AF116721 112		,	
		PRO2738)	_		
14295	0.012525	cDNA: FLJ22765 fis, clone KAIA1180.	AK026418	Hs.163986	1
1 .		/gb=AK026418 /gi=10439279			× ×
	0	/ug=Hs.163986 /len=1994			73
14302	0.032277	wo01c07.x1 NCI_CGAP_Pan1 cDNA	AI934308	Hs.216635	
		clone IMAGE:2454060 3' similar to			* "
ļ ·		gb:M15353 EUKARYOTIC INITIATION		, N	
		FACTOR 4E mRNA sequence	' '		[ [
		/clone=IMAGE:2454060 /clone_end=3'			
		/gb=Al934308 /gi=5673178			
	,	/ug=Hs.216635 /len=558			
<u> </u>		J 3 J	L	L	<u> </u>

Spot	p-valu	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14307	0.01004	EST(cDNA clone IMAGE:6104513 5'.)	BQ429184		
14322	0.015521	clone IMAGE:4297077, mRNA /gb=BC017920 /gi=17389820 /ug=Hs.375771 /len=1247	BC017920	Hs.375771	*
14337	0.024972	mRNA; cDNA DKFZp686M023 (from clone DKFZp686M023) /gb=AL833547 /gi=21734192 /ug=Hs.31412 /len=7318	AL833547	Hs.31412	
14345		mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624) /gb=AL110152 /gi=5817054 /ug=Hs.94030 /len=1341	AL110152	Hs.94030	
14346	0.012525	cDNA clone CBLAPH08 5'	AV739829		
14358	0.020453	nab71h02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:3273435 3' similar to contains Alu repetitive element;	BF439932	Hs.331476	
•	* •	mRNA sequence /clone=IMAGE:3273435 /clone_end=3' /gb=BF439932 /gi=11452449 /ug=Hs.331476 /len=347			
14368	0.032277	tu62h09.x1 NCI_CGAP_Gas4 cDNA	Al679301	Hs.372588	
9		clone IMAGE:2255681 3' similar to contains Alu repetitive element, mRNA sequence /clone=IMAGE:2255681 /clone_end=3' /gb=Al679301			
,		/gi=4889483 /ug=Hs.372588 /len=497	<u> </u>	·	<b>-</b> :
14369	0.01911	ESTs, cDNA, 3' end /clone=IMAGE:2012069 /clone_end=3' /gb=Al357655 /gi=4109276 /ug=Hs.292931 /len=595	Al357655	Hs.292931	×
14373	0.005835	UI-H-EU0-azo-e-16-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:5851383 3', mRNA sequence /clone=IMAGE:5851383 /clone_end=3' /gb=BQ045026 /gi=19796008 /ug=Hs.446007 /len=1073	BQ045026	Hs.446007	
14374	0.001915	RC4-HT0277-160200-013-d07 HT0277 cDNA, mRNA sequence /gb=BE151126 /gi=8613847 /ug=Hs.158600 /len=571	BE151126	Hs.158600	
14379	0.043827	Similar to hypothetical protein FLJ20489, clone MGC:50559 IMAGE:5744381, mRNA, complete cds /cds=(290,1078) /gb=BC039535 /gi=24659157 /ug=Hs.440840 /len=2078	BC039535	Hs.440840	NP_776163
14384	0.015521	cDNA FLJ14041 fis, clone HEMBA1005780. /gb=AK024103 /gi=10436401 /ug=Hs.214783 /len=3488	AK024103	Hs.214783	

Spot	p-value	Description	Gene	Unigene	Protein
•			Accession No.	Accession	Accession
		* "		No.	No.
14386		UI-E-EJ0-aik-i-20-0-UI.r1 UI-E-EJ0	BM727413	Hs.112619	
	Transfer in	cDNA clone UI-E-EJ0-aik-i-20-0-UI 5',			
		mRNA sequence /clone=UI-E-EJ0-aik-i-		*	
. 101	·	20-0-UI /clone_end=5' /gb=BM727413		·	
		/gi=19048746 /ug=Hs.112619 /len=1667	:		
					,
14390	0:01004	BX097880 NCI_CGAP_Thy1 cDNA	BX097880	Hs.208961	7
	•	clone IMAGp998F242841, mRNA			*
		sequence	:	* .	
•		/clone=IMAGp998F242841_;_IMAGE:11		*	
		33207 /gb=BX097880 /gi=27829041			1
14393	0.000343	/ug=Hs.208961 /len=354 UI-CF-EN1-add-I-13-0-UI.s1 UI-CF-EN1	BM980639	LI- 202420	
14393	0.009313	cDNA clone UI-CF-EN1-add-I-13-0-UI 3',	PINIAOOOSA	Hs.363126	
1		mRNA sequence /clone=UI-CF-EN1-add-	= (		
		I-13-0-UI /clone_end=3' /gb=BM980639			
		/gi=19602306 /ug=Hs.363126 /len=691			
	~	/gi= 19002500 /dg=115.000120 /icii=001		•	
14394	0.028428	ESTs, cDNA, 3' end	AA719837	Hs.292589	
		/clone=IMAGE:397194 /clone end=3'			1
		/gb=AA719837 /gi=2732936			, ,
		/ug=Hs.292589 /len=480			
14403	0.009313	UI-1-BB1p-avf-c-10-0-UI.s1	BQ023219	Hs.365670	
		NCI_CGAP_PI6 cDNA clone UI-1-BB1p-	9		
4	4,	avf-c-10-0-UI 3', mRNA sequence			
		/clone=UI-1-BB1p-avf-c-10-0-UI			., .
		/clone_end=3' /gb=BQ023219		•	• -50,
		/gi=19758498 /ug=Hs.365670 /len=1038			- "
4 4 4 4 4	0,000,400	AV70.400.4.14D.G. DNIA.1	A) (70 400 4		
14414	0.028428	AV764634 MDS cDNA clone	AV764634	Hs.270532	
		MDSBZE01 5', mRNA sequence /clone=MDSBZE01 /clone end=5'	'		<i>x</i>
		/gb=AV764634 /gi=10922482			
		/gb=Av704034 /gi=10922402 /ug=Hs.270532 /len=1289			3.
14417		proteasome (prosome, macropain)	NM 002789	Hs.251531	NP 002780
' ' ' '	0.01=701	subunit, alpha type, 4 (PSMA4), mRNA	502,55	1.10.20 1001	_502760
	160	/cds=(137,922) /gb=NM_002789			
		/gi=23110940 /ug=Hs.251531 /len=1189			,
,			· ·		
14431	0.003145	cDNA clone e443-f /He443-f Adult heart,	T82627		- E
		Clontech	*		
14444		mitochondrion, complete genome	NC_001807		
14448	0.016648	cDNA FLJ30332 fis, clone	AK054894	Hs.351572	
		BRACE2007254. /gb=AK054894		-00	
		/gi=16549521 /ug=Hs.351572 /len=1800		·	
	- 1				
14449	0.001199	clone 25023 mRNA sequence	AF131817	Hs.90858	*
	Y	/gb=AF131817 /gi=4406652			
14474	0.000404	/ug=Hs.90858 /len=1466	DO745070	ļ	
14474	0.002161	EST(cDNA clone IMAGE:4850459 3')	BG745876	<u> </u>	L

Spot	p-value	Description	Gene	Unigene	Protein
	-		Accession No.	Accession	Accession
				No.	No.
14483	0.020453	cDNA FLJ34248 fis, clone	AK091567	Hs.112461	
		FCBBF4000446. /gb=AK091567			
	•	/gi=21749972 /ug=Hs.112461 /len=1623	- 1. The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of	, <i>.</i>	*
14505		No significant match (ORF:none)	SEQ.ID.No.66		
14521	0.00182	HSC15D092 normalized infant brain	Z39248	Hs.27328	
		cDNA cDNA clone c-15d09 3', mRNA			ŧ
		sequence /clone=c-15d09 /clone_end=3'			1 .
		/gb=Z39248 /gi=562440 /ug=Hs.27328			-
		/len=352	1.5		
14524	0.004569	EST (wa75f06.x1	Al685268	- 00	
××		Soares_NFL_T_GBC_S1			*
14541	0.026229	EST tz43f04.x1 NCI_CGAP_Brn52	AI863121		
		cDNA clone IMAGE:2291359 3' similar			3
		to contains Alu repetitive			
		element;contains L1.b1 L1 repetitive			*
14542	0.028428	EST xn66e12.x1 NCI_CGAP_CML1	AW195150	100000	11
	• ,	IMAGE:2699470 3' similar to contains	**		
		Alu repetitive element;	y0		
14551	0.003434	EST (ng23f02.s1 NCI_CGAP_Ov2 cDNA	AA502813		
		clone IMAGE:930267 similar to contains			
		Alu repetitive element)			_ *
14560	0.049308	TRAM-like protein (KIAA0057), mRNA	NM_012288	Hs.153954	NP_036420
		/cds=(76,1188) /gb=NM_012288	. *		*
		/gi=6912449 /ug=Hs.153954 /len=6974			
14598	0.017843	cDNA FLJ32068 fis, clone	AK056630	Hs.24758	
••		OCBBF1000114. /gb=AK056630			٠.
· _		/gi=16552085 /ug=Hs.24758 /len=2139	<u> </u>	ā.	
14612	0.041279	EST (AL536815 LTI_FL013_FBrn1 clone	AL536815	•	
	1.55	CS0DF020YK05 5')			
14613	0.047541	neuroepithelial cell transforming gene 1	NM_005863	Hs.25155	NP_005854
		(NET1), mRNA /cds=(147,1775)		1	
	•	/gb=NM_005863 /gi=19923326		,	*
		/ug=Hs.25155 /len=3236			
14614	0.020596	EST(yq95a02.r1 Soares fetal liver spleen	H56096		
		1NFLS cDNA clone IMAGE:203498.5'			
		similar to contains Alu repetitive element)		ļ. ·	·
14615	0.005259	EST zb60f02.y5	AI734267		NP_079335
٠, ٠		Soares_fetal_lung_NbHL19W cDNA			,
,		clone IMAGE:307995 5' similar to	· ·		
•		contains Alu repetitive element; contains	*	٠.	*
1 -		element LTR9 repetitive element ;		}	
14633	0.034358	EST(no86d01.s1 NCI_CGAP_AA1 cDNA	AA614000		
		clone IMAGE:1113697 3')			·
14639	0.038855	EST (no81g07.s1 NCI_CGAP_AA1	AA613881		
1		IMAGE:1113276 3')		I	·

Spot	p-value	Description	Gene	Unigen	Protein
				Accession	Accession
4 - 10 - 10 - 10 - 10 - 10 - 10 - 10 - 1		ed let		No.	No.
14643	0.028428	UI-H-FG1-bgh-l-12-0-UI:s1	BU624037	Hs.416904	7-
	,	NCI_CGAP_FG1 cDNA clone UI-H-FG1-			* ,
		bgh-l-12-0-UI 3', mRNA sequence			
	_	/clone=UI-H-FG1-bgh-I-12-0-UI	, · · · · · ·		
		/clone_end=3' /gb=BU624037	*		
	-	/gi=23290252 /ug=Hs.416904 /len=1160			
		*			
14648	0.005713	mRNA; cDNA DKFZp667J1615 (from	AL713792	Hs.120388	,
	. *	clone DKFZp667J1615) /gb=AL713792		Y .	- 12
~ 1		/gi=19584550 /ug=Hs.120388 /len=4127	4		
			4 27	1.4-4	
14663	0.001747	EST(zs14a10.r1 NCI_CGAP_GCB1	AA243380	*	NP_057315
		cDNA clone IMAGE:685146 5')	0		
14671	0.00274	UI-H-EI0-aye-c-17-0-UI.s1	CA447385	Hs.420740	
	· · · · · · · · · · · · · · · · · · ·	NCI_CGAP_EI0 cDNA clone UI-H-EI0-			
	4	aye-c-17-0-UI 3', mRNA sequence			
	8	/clone=UI-H-EI0-aye-c-17-0-UI	, Y		4 Y
	9	/clone_end=3' /gb=CA447385	===		
	*	/gi=24811805 /ug=Hs.420740 /len=812			
14694	0.022058	cDNA FLJ35910 fis, clone	AK093229	Hs.348902	
		TESTI2009987. /gb=AK093229			
•	(	/gi=21752038 /ug=Hs.348902 /len=2035		,	
			` <u> </u>		00 .
14695	0.008631	EST(cDNA clone IMAGE:1240639 3'	AA808945		i C
		similar to contains Alu repetitive element)		,	
				. ,	9
14697	0.020453	EST00015 NCI_CGAP_Lu5 cDNA clone	BF707422	Hs.298289	
	* * *	IMAGE:1568018 3', mRNA sequence			
*	1-1-	/clone=IMAGE:1568018 /clone_end=3'	*		
		/gb=BF707422 /gi=11999083	0.0		<u>,                                      </u>
		/ug=Hs.298289 /len=858	*		
14698	0.011586	EST(MR1-MT0282-191200-005-b11	BF904004		
		MT0282 cDNA )		7.	"
14700	0.020453	EST(cDNA clone IMAGE:4761963 5')	BG682907	0.00	NP_065750
14712	0.002621	mRNA; cDNA DKFZp564D193 (from	AL049252	Hs.406752	
		clone DKFZp564D193) /gb=AL049252	*		
		/gi=4499993 /ug=Hs.406752 /len=3343	1		
14714	0.016648	UI-E-CL1-afe-n-12-0-UI.s1 UI-E-CL1	BU729525	Hs.233617	* * * * * * * * * * * * * * * * * * * *
		cDNA clone UI-E-CL1-afe-n-12-0-UI 3',			
		mRNA sequence /clone=UI-E-CL1-afe-n-			
		12-0-UI /clone_end=3' /gb=BU729525		_	
<u> </u>		/gi=23652495 /ug=Hs.233617 /len=1402			
				6	
14717	0.026229	cDNA FLJ32589 fis, clone	AK057151	Hs.21342	
		SPLEN2000443. /gb=AK057151			<u></u>
<u>.</u>		/gi=16552741 /ug=Hs.21342 /len=2178		-*-	
14719	3.93E-04	EST(cDNA clone IMAGE:2387836 3'	AI760555		NP_658913
		similar to contains Alu repetitive		. ,	
		element,contains element MER22	,		1
	1	repetitive element;)	I	1	1

Spot	p-value	Description	Gene	Unigene	Protein
	* 1		Accession No.	Accession	Accession
14720	0.00684	cDNA FLJ32224 fis, clone	AK056786	No. Hs.406907	No.
		PLACE6004336. /gb=AK056786			
. 6	2	/gi=16552290 /ug=Hs.406907 /len=3076	-00		
		3			
14722	0.002877	cDNA FLJ11439 fis, clone	AK021501	Hs.287416	
		HEMBA1001299. /gb=AK021501			
•		/gi=10432697 /ug=Hs.287416 /len=1500			
*		,			
14736	0.012525	FLJ33160 fis, clone UTERU2000485	AK057722	Hs.124733	
	.,	/cds=UNKNOWN /gb=AK057722	**.		
		/gi=16553641 /ug=Hs.124733 /len=2328			
					·
14737	0.034358	clone IMAGE:5298326, mRNA	BC036198	Hs.369297	
	*.	/gb=BC036198 /gi=23271941			, 0
4.4700	. ,	/ug=Hs.369297 /len=3475	DE445000		NID 000504
14/38	0.007397	EST(cDNA clone IMAGE:3570461 3'	BF115962		NP_620584
	r	similar to contains element MER7	* *	·	
14762	0.04004	repetitive element;)	AI589443		
14763 14769		EST(cDNA clone IMAGE:2224205 3'.)	BM678100	Hs.156646	
14709	0.007994	UI-E-EJ0-aig-I-23-0-UI s1 UI-E-EJ0 cDNA clone UI-E-EJ0-aig-I-23-0-UI 3',	DIVIO76100	IDS. 100040	0
		mRNA sequence /clone=UI-E-EJ0-aig-I-			
		23-0-UI /clone_end=3' /gb=BM678100		**	
		/gi=18987996 /ug=Hs.156646 /len=1091			7
-	. 1	1000700074g 113.10004071cm 1001			
14773	0.002294	602635144F1 NCI CGAP Skn3 cDNA	BG741535	Hs.445822	·
		clone IMAGE:4780090 5', mRNA			* "
	•	sequence /clone=IMAGE:4780090			
1	.^	/clone_end=5' /gb=BG741535	· · · · ·		
		/gi=14052188 /ug=Hs.445822 /len=693		;	
14806	0.024972	cDNA FLJ14279 fis, clone	AK024341	Hs.250383	
, I ===		PLACE1005574. /gb=AK024341			
		/gi=10436703 /ug=Hs.250383 /len=2005			
	4.4				
14819	0.030134	FLJ14036 fis, clone	AK024098	Hs.306663	
		HEMBA1004709/cds=UNKNOWN			
	:	/gb=AK024098 /gi=10436394	· · ·		*
14005	0.040404	/ug=Hs.306663/len=2067	DO000E00	115 050045	
14825	0.013494	clone IMAGE:3847423, mRNA	BC020562	Hs.352245	
*	.,	/gb=BC020562 /gi=18088249			= 0
14831	0.023391	/ug=Hs.352245 /len=2742 clone IMAGE:4183899, mRNA	BC008625	Hs.55336	1
14031	0.023301	/cds=UNKNOWN /gb=BC008625	DC000020	115.00000	
		/gi=14250384 /ug=Hs.55336 /len=1413	• () *	*	
14833	0.004205	EST380251 MAGE resequences, MAGJ	AW968281	Hs.319460	
17033	0,004200	cDNA, mRNA sequence /gb=AW968281	A44900201	113.313400	
		/gi=8158016 /ug=Hs.319460 /len=689			
	·	- 3. 3.656.6748 116.616400 /ICH-003		·	
<u> </u>	1	<del></del>	<del> </del>	<del></del>	

Spot	p-value	Description	Gene Accession No.	Unigene Acc ssion No.	Protein Accession No.
14837	0.009313	EST(RC4-CT0322-261299-011-h03 CT0322 Homo sapiens cDNA, mRNA sequence)	AW857814		
14842	0.049308	mitochondrion, complete genome	NC 001807		- 1
14845		EST, cDNA /clone=IMAGE:1252723 /gb=AA888306 /gi=3003981	AA888306	Hs.327126	
14851	0.021076	/ug=Hs.327126 /len=291 UI-H-BW1-amm-h-09-0-UI.s1	BF512783	Hs.443691	
14001	0.021070	NCI_CGAP_Sub7 cDNA clone	DF312763	H5.443091	£18=.
	*	IMAGE:3070696 3', mRNA sequence /clone=IMAGE:3070696 /clone_end=3' /gb=BF512783 /gi=11597962 /ug=Hs.443691 /len=568			
14877	0.028811	EST, cDNA, 3' end	N58488	Hs.94100	NP_002086
		/clone=IMAGE:248258 /clone_end=3' /gb=N58488 /gi=1202378 /ug=Hs.94100 /len=520		*	, may 50
14879	0.011644	UI-H-FH1-bfm-c-24-0-UI.s1	CA429379	Hs.436064	
*		NCI_CGAP_FH1 cDNA clone UI-H-FH1- bfm-c-24-0-UI 3', mRNA sequence /clone=UI-H-FH1-bfm-c-24-0-UI			10 - 30 10 - 30
00 A		/clone_end=3' /gb=CA429379 /gi=24792105 /ug=Hs.436064 /len=1037			*.
14884	0.024972	602043661F1 NCI_CGAP_Brn67 cDNA clone IMAGE:4181462 5', mRNA	BF528488	Hs.433462	
	4	sequence /clone=IMAGE:4181462 /clone_end=5' /gb=BF528488 /gi=11615851 /ug=Hs.433462 /len=885			
14893	0.01004	EST375707 MAGE resequences, MAGH cDNA, mRNA sequence /gb=AW963634	AW963634	Hs 429581	
		/gi=8153470 /ug=Hs.429581 /len=750			
14906	0.007994	EST, cDNA: FLJ21479 fis, clone COL05032 /cds=UNKNOWN	AK025132	Hs.397727	NP_004710
		/gb=AK025132 /gi=10437589 /ug=Hs.139315 /len=1920	. ()	**	
14911	0.043827	UI-1-BB1p-akk-b-05-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-	BU753775	Hs 279870	
		akk-b-05-0-UI 3', mRNA sequence /clone=UI-1-BB1p-akk-b-05-0-UI		**	
-	. (	/clone_end=3' /gb=BU753775 /gi=23712051 /ug=Hs.279870 /len=1533			*
		cDNA FLJ25001 fis, clone CBL00443	AK057730		NP_203524
		No significant match, ORF-3(1~195)	SEQ.ID.No.57	<u> </u>	
14928		No significant match, ORF+1(1~249),+2(11~253)	SEQ.ID.No.79	*	
14935	0.041279	No significant match (ORF:+1:346~452[108])	SEQ.ID.No.18	*	**

Spot	p-value	D scription	G ne Accession No.	Unigene Accession No.	Protein Accession No.
14942	0.007397	EST, cDNA /gb=AW360966 /gi=6865616 /ug=Hs.6653 /len=661	AW360966	Hs.6653	NP_055942
14943	0.020596	EST, mRNA; cDNA DKFZp434P0235 (from clone DKFZp434P0235) /cds=UNKNOWN /gb=AL117519 /gi=5912035 /ug=Hs.34348 /len=1124	AL117519	Hs.396951	NP_849157
14947	0.016693	EST(cDNA clone IMAGE:3267894 3")	BF435209		-1.20
14952	0.043823	RC1-DT0029-120100-011-h01 DT0029 cDNA, mRNA sequence /gb=AW579207 /gi=7254256 /ug=Hs 414692 /len=697	AW579207	Hs.414692	
14971	0.008631	No significant match (ORF:+3: 3~180[179])	SEQ.ID.No.20		·

		TABLE 3G		* .	
Genes	Correspo	nding To Differentially Expressed Genes i	n Figure 14 - D	iabetes	- 7
	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
	Y		No	No.	No.
98	0.031226	mitochondrion, complete genome	NC 001807		
169		nuclear protein double minute 1 (MDM1),	NM_017440	Hs.12871	NP_064513
-		mRNA /cds=(93,2237) /gb=NM_017440			_
		/gi=24586654 /ug=Hs.12871 /len=2942	".		
170	0.045433	Duffy blood group (FY), mRNA	NM_002036	Hs.183	NP 00202
		/cds=(495,1511) /gb=NM_002036	-		
		/gi=4503818 /ug=Hs.183 /len=1559	,		**
183	0.022722	cDNA FLJ13209 fis, clone NT2RP4000424.	AK023271	Hs.416949	
. • •	0.022,22	/gb=AK023271 /gi=10435130		1.10, 1,00,10	
	-	/ug=Hs.416949 /len=2026			
342	0.039219		NM 004374	Hs.351875	NP 00436
072	0.000210	(COX6C), nuclear gene encoding	11111_004074	113.901070	141 _00400
		mitochondrial protein, mRNA /cds=(61,288)			ļ. :
	1	/gb=NM_004374 /gi=17999531			•
		/ug=Hs.351875 /len=444			
354	0.030210	stromal cell-derived factor 2 (SDF2), mRNA	NM 006023	Hs.118684	NP_00885
JJ4	0.039219	/cds=(40,675) /gb=NM_006923	14141_000923	1115, 110004	
		/gi=14141194 /ug=Hs.118684 /len=1075		8.8	
371	0.026691	ecotropic viral integration site 2A (EVI2A),	NM_014210	Hs.70499	NP_05502
3/1	0.020091		1410 014210	Ins./0499	MP_02202
		mRNA /cds=(220,918) /gb=NM_014210			* .
200	0.000040	/gi=7657074 /ug=Hs.70499 /len=1563	AIM 0400EE	U- 000555	ND 02020
380	0.039219	5'-3' exoribonuclease 2 (XRN2), mRNA	NM_012255	Hs.268555	NP_03638
		/cds=(86,2938) /gb=NM_012255	74.2		- "
107	0.00050	/gi=18860915 /ug=Hs.268555 /len=3445	Dist. 4.500	11. 105500	
437	0.00953	TCAAP1D11790 Pediatric acute	BM144590	Hs.425539	
		myelogenous leukemia cell (FAB M1)	. *	*	
	`.	Baylor-HGSC project=TCAA cDNA clone			
	-	TCAAP1179, mRNA sequence			`
		/clone=TCAAP1179 /gb=BM144590	*	·	*
1 2 2 2		/gi=17161827 /ug=Hs.425539 /len=178		=::::::::::::::::::::::::::::::::::::::	2 (2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
.447		acid ceramidase	U70063		NP_80859
454	0.028884	BCL2/adenovirus E1B 19kDa interacting	NM_004331	Hs.132955	NP_00432
. * *		protein 3-like (BNIP3L), mRNA			/
		/cds=(83,742) /gb=NM_004331			
• •	- 2	/gi=4757859 /ug=Hs.132955 /len=1337			
607	0.039719	ribosomal protein S27a (RPS27A), mRNA	NM_002954	Hs.311640	NP_00294
		/cds=(39,509) /gb=NM_002954	-		-
		/gi=27436941 /ug=Hs.311640 /len=541			<u> </u>
629	0.049642	nuclear cap binding protein subunit 1,	NM_002486	Hs.89563	NP_00247
		80kDa (NCBP1), mRNA /cds=(31,2403)	,	* .	
	8 .	/gb=NM_002486 /gi=4505342		*	
		/ug=Hs.89563 /len=2828			
679	0.019262	hypothetical protein LOC51255	NM_016494	Hs.11156	NP_05757
,		(LOC51255), mRNA /cds=(31,492)		***	· ·
	-	/gb=NM_016494 /gi=24475978			
		/ug=Hs.11156 /len=601			0

	p-value	nding To Diff rentially Expressed Gen s  D scription	Gene	Unigene	Protein
Shor	h-value	D SCHPHOH		_	
			Accession	Accession	Accession
703	0.020210	cytochrome b-245, beta polypeptide	No. NM 000397	<b>No.</b> Hs.88974	<b>No.</b> NP 000388
103	0.058218	(chronic granulomatous disease) (CYBB),	MM_000397	IDS.00974	INP_000360
	-	mRNA /cds=(15,1727) /gb=NM_000397		,	
		/gi=6996020 /ug=Hs.88974 /len=4266		1	
708	0.024630	cyclin L ania-6a (LOC57018), mRNA	NM_020307	Hs.4859	NP_064703
700	0.024039	/cds=(55,1635) /gb=NM_020307	NW_020307	115.4059	INF_004703
	*	/gi=9945319 /ug=Hs.4859 /len=2076	*		
766	0.033724	tissue inhibitor of metalloproteinase 3	NM 000362	Hs.245188	NP 000353
700	0.000724	(Sorsby fundus dystrophy,	14141_000502	113.243100	_000000
		pseudoinflammatory) (TIMP3), mRNA	12		
		/cds=(1189,1824) /gb=NM_000362		1	
		/gi=21536431 /ug=Hs.245188 /len=5487		j.	1
769	0.00186	platelet/endothelial cell adhesion molecule	NM 000442	Hs.78146	NP 000433
700	9.00,100	(CD31 antigen) (PECAM1), mRNA	14141_000442	113.70140	_000435
		/cds=(194,2410) /gb=NM_000442			
		/gi=21314616 /ug=Hs.78146 /len=3189			
770	0.031226	of Tom7 (S. cerevisiae) (TOM7), mRNA	NM 019059	Hs.112318	NP_061932
,,,	0.001,220	/cds=(94,261) /gb=NM 019059	11111_01000		_001302
		/gi=9506858 /ug=Hs.112318 /len=487	1.		
778	0.047644	ubiquitin-like 1 (sentrin) (UBL1), mRNA	NM_003352	Hs.81424	NP_003343
, . <u>.</u>	0.511	/cds=(132,437) /gb=NM_003352	555552	710.01121	
		/gi=20127433 /ug=Hs.81424 /len=1227			
798	0.016261	cytochrome c oxidase subunit VIIa	NM_001864	Hs.421621	NP 001855
		polypeptide 1 (muscle) (COX7A1), nuclear	, <del>-</del>		
,	. '.	gene encoding mitochondrial protein,	*		1
		mRNA /cds=(463,702) /gb=NM 001864		*	
		/gi=18105034 /ug=Hs.421621 /len=783		-	
	0.0				*
800	0.039219	protein S (alpha) (PROS1), mRNA	NM_000313	Hs.64016	NP_000304
		/cds=(147,2177) /gb=NM_000313		1	-
		/gi=4506116 /ug=Hs.64016 /len=3309			
805	0.028884	ribosomal protein S17 (RPS17), mRNA	NM_001021	Hs.5174	NP_001012
	' '	/cds=(26,433) /gb=NM_001021			
	] ''	/gi=14591913 /ug=Hs.5174 /len=515			
814	0.034411	CGI-148 protein (CGI-148), mRNA	NM_016078	Hs.87295	NP_057162
•		/cds=(300,845) /gb=NM_016078	- ,		1
		/gi=7705643 /ug=Hs.87295 /len=2070			
847	0.020932	peroxisomal biogenesis factor 3 (PEX3),	NM_003630	Hs.7277	NP_003621
	-	mRNA /cds=(64,1185) /gb=NM_003630		,	
· ·		/gi=4505726 /ug=Hs.7277 /len=1979			<u> </u>
866	0.04883	polycystic kidney disease 2 (autosomal	NM_000297	Hs.82001	NP_000288
		dominant) (PKD2), mRNA /cds=(67,2973)		1	1
	. "	/gb=NM_000297 /gi=4505834		1	1
	Ľ	/ug=Hs.82001 /len=5057			<u> </u>
908	0.005359	phosphoinositide-3-kinase, regulatory	NM_014602	Hs.83050	NP_055417
		subunit 4, p150 (PIK3R4), mRNA			1
	*	/cds=(543,4619) /gb=NM_014602	1	1	
		/gi=23943911 /ug=Hs.83050 /len=5060		I	

		nding To Differentially Expressed Genes i			
Spot	p-value	Description	Gene	Unigene	Protein
	1		Accession	Accession	Accession
			No.	No.	No.
910	0.033724	CD9 antigen (p24) (CD9), mRNA	NM_001769	Hs.1244	NP_001760
		/cds=(112,798) /gb=NM_001769			
		/gi=21237762 /ug=Hs.1244 /len=1246			
923	0.014917	eukaryotic translation initiation factor 3,	NM_003756	Hs.58189	NP 003747
		subunit 3 gamma, 40kDa (EIF3S3), mRNA	7		
	<b>,</b>	/cds=(6,1064) /gb=NM_003756		}	
		/gi=4503514 /ug=Hs.58189 /len=1280			
943	0.004381	XIST, coding sequence "a" mRNA (locus	X56199	Hs.352403	
		DXS399E). /gb=X56199 /gi=37987			
		/ug=Hs.352403 /len=1614			
953	0.031226	mRNA for KIAA0592 protein, partial cds.	AB011164	Hs.439367	
		/cds=(1,4062) /gb=AB011164 /gi=3043707			<u>.</u>
	1.00	/ug=Hs.439367 /len=4623			· '
963	0.026691	nucleoporin 153kDa (NUP153), mRNA	NM 005124	Hs.211608	NP_005115
		/cds=(201,4628) /gb=NM_005124			_555,10
		/gi=24430145 /ug=Hs.211608 /len=5687			
1006	0.014917	tissue inhibitor of metalloproteinase 4	NM 003256	Hs.190787	NP_003247
.000		(TIMP4), mRNA /cds=(60,734)	ooop.oo	1.10.100101	141 _000241
		/gb=NM_003256 /gi=4507514			
		/ug=Hs.190787 /len=1189			
1026	0.028884	methionine adenosyltransferase II, beta	NM 013283	Hs.54642	NP_037415
1020	0.020004	(MAT2B), mRNA /cds=(73,1077)	111111_013203	113.04042	141 _057415
		/gb=NM_013283 /gi=20127525			
,		/ug=Hs.54642 /len=2054		*	
1036	0.04883	mRNA for KIAA1518 protein, partial cds.	AB040951	Hs.284208	NP 056308
1000	0.04003	/cds=(482,3112) /gb=AB040951	AD040931	1113.204200	NF_030300
		/gi=7959302 /ug=Hs.284208 /len=5370			
1057	0.04883	mRNA for KIAA1609 protein, partial cds.	AB046829	Hs.14449	
1037	0.04003	/cds=(1,1423) /gb=AB046829	AD040029	TS. 14449	- "
•	1	/gi=15425661 /ug=Hs.14449 /len=4683			
1111	0.010511		NIM OCCOS	110 0047	ND 000504
1114	0.012511	stromal antigen 2 (STAG2), mRNA	NM_006603	Hs.8217	NP_006594
		/cds=(405,3893) /gb=NM_006603		,	
4454	0.046364	/gi=27552767 /ug=Hs.8217 /len=4197	NIM COCOCC	11- 04040	ND 0000EC
1151	0.016261	RAD21 (S. pombe) (RAD21), mRNA	NM_006265	Hs.81848	NP_006256
	1	/cds=(185,2080) /gb=NM_006265			
4470	0.012000	/gi=5453993 /ug=Hs.81848 /len=3647	A16004004	11- 472022	ND 005500
1178	0.013668	cDNA: FLJ21311 fis, clone COL02167.	AK024964	Hs.173933	NP_005586
	·	/gb=AK024964 /gi=10437390			
4400	0.000000	/ug=Hs.173933 /len=3216	1111 04 4 5 4	70010	ND 055000
1190	0.036386	PTH-responsive osteosarcoma B1 protein	NM_014451	Hs.79340	NP_055266
	1	(B1), mRNA /cds=(81,2489)			
•		/gb=NM_014451 /gi=13929459	j	=	
1 THE!	0.010===	/ug=Hs.79340 /len=3331	<u> </u>		1.12
1192	0.013668	succinate dehydrogenase complex, subunit	NM_003002	Hs.168289	NP_002993
	1	D, integral membrane protein (SDHD),		}	
	* .	nuclear gene encoding mitochondrial			1
		protein, mRNA /cds=(12,491)	[ .	Į.	
		/gb=NM_003002 /gi=4506864			1
		/ug=Hs.168289 /len=1313	1.		I

Genes	Correspon	nding To Differentially Expressed Genes i	n Figure 14 - D	iabetes	
	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
· .			No.	No.	No.
1193	0.006524	CGI-100 protein (CGI-100), mRNA	NM_016040	Hs.348996	NP_057124
-		/cds=(113,802) /gb=NM_016040	*		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
	,	/gi=19923441 /ug=Hs.348996 /len=3635		*	
1196	0.04883	FK506 binding protein 14, 22 kDa	NM_017946	Hs.264636	NP 060416
		(FKBP14), mRNA /cds=(146,781)	·		_
	*.	/gb=NM_017946 /gi=8923658	- 1	· y · · · · ·	
		/ug=Hs.264636 /len=2248		- <del>-</del>	, O
1200	0.028884	hypothetical gene supported by	XM_000590		
		XM_000590 (LOC59176)			
1202	0.007185	leucyl-tRNA synthetase (LARS), mRNA	NM_020117	Hs.6762	NP_064502
		/cds=(73,3603) /gb=NM_020117			
		/gi=24496788 /ug=Hs.6762 /len=4248			* *
1203	0.022722	phosphoenolpyruvate carboxykinase 2	NM_004563	Hs.75812	NP_004554
		(mitochondrial) (PCK2), mRNA			
	7 4	/cds=(67,1989) /gb=NM_004563			,
-		/gi=4758885 /ug=Hs.75812 /len=2165			
1303	0.026691	imageqc_6_2001/snk86bdrr81.y1	BQ109159	Hs.433575	
		NIH_MGC_12 cDNA clone			
		IMAGE:5110111 5', mRNA sequence	T D	* **	\
		/clone=IMAGE:5110111 /clone_end=5'			
		/gb=BQ109159 /gi=20158813			]
		/ug=Hs.433575 /len=604	0.		
1305	0.016261	cytochrome c oxidase subunit VIIc	NM_001867	Hs.430075	NP 001858
		(COX7C), nuclear gene encoding	.)(-		
	,	mitochondrial protein, mRNA /cds=(90,281)		0	
		/gb=NM_001867 /gi=18105039			
		/ug=Hs.430075 /len=448			
1306	0.036799	poly(A) binding protein, cytoplasmic 1	NM_002568	Hs.172182	NP_002559
	*	(PABPC1), mRNA /cds=(503,2404)			_
		/gb=NM_002568 /gi=4505574	111		
-		/ug=Hs.172182 /len=2848			
1312	0.04883	endothelial zinc finger protein 2 (EZF-2),	NM_018337	Hs.24545	NP_060807
		mRNA /cds=(234,1214) /gb=NM_018337			
		/gi=8922893 /ug=Hs 24545 /len=1907			
1374	0.011439	likely ortholog of rat p47 (p47), mRNA	NM_016143	Hs.12865	0
	3.	/cds=(86,1198) /gb=NM_016143		•	1
	• 0	/gi=20149634 /ug=Hs.12865 /len=1450	·		,
1377	0.020932	procollagen (type III) N-endopeptidase	NM_002768	Hs.183138	NP_002759
		(PCOLN3), mRNA /cds=(41,997)	•	Y.	* -
	]	/gb=NM_002768 /gi=4506138		] .	
		/ug=Hs.183138 /len=2474			
1386	0.019241	AGENCOURT_6424254 NIH_MGC_67	BM479954	Hs.381243	
		cDNA clone IMAGE:5491531 5', mRNA			
		sequence /clone=IMAGE:5491531			
	1				
		/clone_end=5' /gb=BM479954			• •

Genes	Correspoi	nding To Diff r ntially Expressed Genes i	n Figure 14 - D	iabetes	
	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
		*	No	No.	No.
1401	0.029086	prosaposin (variant Gaucher disease and	NM_002778	Hs.406455	NP 002769
		variant metachromatic leukodystrophy)			]
	*	(PSAP), mRNA /cds=(39,1613)		ļ.,	/
		/gb=NM 002778 /gi=11386146			
		/ug=Hs.406455 /len=2767	* -	· .	
1414~	0.001319	thyroid hormone receptor interactor 11	NM_004239	Hs.85092	NP_004230
		(TRIP11), mRNA /cds=(357,6296)			. =
100		/gb=NM_004239 /gi=10863904			
		/ug=Hs.85092 /len=6452			
1420	0.042232	ribosomal protein L36a-like (RPL36AL),	NM_001001	Hs.419465	NP_000992
1.		mRNA /cds=(95,415) /gb=NM_001001	4. T	1	
		/gi=16306559 /ug=Hs.419465 /len=537		· ·	
1454	0.042232	Dmx-like 1 (DMXL1), mRNA	NM_005509	Hs.181042	NP_005500
*	*.	/cds=(81,9164) /gb=NM_005509	-		
		/gi=21536473 /ug=Hs.181042 /len=11072	4		*
1467	0.00953	SON DNA binding protein (SON), transcript	NM_058183	Hs.92909	NP_620305
		variant e, mRNA /cds=(50,6376)			
		/gb=NM_058183 /gi=21040317			
	*	/ug=Hs 92909 /len=8482			
1491	0:031226	KIAA0907 protein (KIAA0907), mRNA	NM_014949	Hs.24656	NP_055764
		/cds=(27,1721) /gb=NM_014949	1		-
4		/gi=7662371 /ug=Hs.24656 /len=4500			
1494	0.045433	basic leucine zipper and W2 domains 2	NM_014038	Hs.5216	NP_054757
}		(BZW2), mRNA /cds=(163,1422)			
		/gb=NM_014038 /gi=7661743 /ug=Hs.5216	i.e	7	0
		/len=1869		<u> </u>	
1504	0.033724	myeloid cell leukemia sequence 1 (BCL2-	NM_021960	Hs.86386	NP_068779
		related) (MCL1), mRNA /cds=(64,1116)			
1.5		/gb=NM_021960 /gi=19923213		¥ 1-	±.
		/ug=Hs.86386 /len=3953		·	
1522	0.007185	G protein-coupled receptor 64 (GPR64),	NM_005756	Hs.184942	NP_005747
		mRNA /cds=(73,3117) /gb=NM_005756			•
		/gi=5031732 /ug=Hs.184942 /len=4665			
1555		KIAA1573 mRNA protein	AB046793		
1567	0.042232	RAD21 (S. pombe) (RAD21), mRNA	NM_006265	Hs.81848	NP_006256
	1	/cds=(185,2080) /gb=NM_006265			
		/gi=5453993 /ug=Hs.81848 /len=3647			1
1575	0.033724	WW domain-containing adapter with a	NM_100264	Hs.70333	NP_567823
		coiled-coil region (WAC), transcript variant	50.0		1
ļ	1:	2, mRNA /cds=(332,2140) /gb=NM_100264	<b>,</b>	<b>\</b>	<u> </u>
		/gi=18379329 /ug=Hs.70333 /len=3088			*
1500	0.004000	Association of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Co	NIM COCCC	11- 04070	ND 0000=0
1598	0.024639	troponin I, skeletal, slow (TNNI1), mRNA	NM_003281	Hs.84673	NP_003272
1		/cds=(74,637) /gb=NM_003281	· ·		*
1010	0.044047	/gi=21361554 /ug=Hs.84673 /len=1108	NA 000070	11- 4740	ND GOODS:
1613	0.01491/	IQ motif containing GTPase activating	NM_003870	Hs.1742	NP_003861
l ·	2	protein 1 (IQGAP1), mRNA	1 * -		
		/cds=(468,5441) /gb=NM_003870			
L		/gi=4506786 /ug=Hs.1742 /len=7573	L	L	

<u>Gene</u> s	Correspon	nding To Differentially Expressed Genes i	in Figure 14 - [	Diabetes	1
	p-value	Description	Gene	Unigene	Prot in
			Accession	Accession	Accession
			No.	No.	No.
1652	0.042232	procollagen-lysine, 2-oxoglutarate 5-	NM_000302	Hs.75093	NP 00029
		dioxygenase (lysine hydroxylase, Ehlers-	· -	*	
		Danlos syndrome type VI) (PLOD), mRNA	'		
		/cds=(201,2384) /gb=NM_000302	<u>:</u>		
	,	/gi=4557836 /ug=Hs.75093 /len=3115			
1704	0.016261	zinc finger protein 9 (a cellular retroviral	NM_003418	Hs.2110	NP_00340
	3.3,523	nucleic acid binding protein) (ZNF9), mRNA		1,10.2 1 10	
	7	/cds=(103,636) /gb=NM_003418			
	, .	/gi=4827070 /ug=Hs.2110 /len=1500			
1750		protein phosphatase 1, regulatory (inhibitor)	NM 170781	Hs.82887	NP 74075
1750	0.04276	subunit 11 (PPP1R11), transcript variant 2,	170701	115.02001	1117_/40/3
		mRNA /cds=(200,343) /gb=NM_170781			
	_	/gi=25777672 /ug=Hs.82887 /len=1712	1.56		
		/gi-25///6/2/ug-HS.6266/ /ieii=1/12			
4707	0.04002	aDNA EL MACCO Sa alama	A1400.4400	11- 200005	<del>                                     </del>
1797	0.04883	cDNA FLJ14066 fis, clone	AK024128	Hs.306665	
		HEMBB1001197. /gb=AK024128	*		
· · · ·		/gi=10436433 /ug=Hs.306665 /len=2086			1
1832	0.022722	ubiquitin protein ligase (UBE3B), mRNA	NM_130466	Hs.17639	NP_56973
		/cds=(585,3791) /gb=NM_130466			]
		/gi=26080339 /ug=Hs.17639 /len=5731			
1858	0.03318	cDNA FLJ41000 fis, clone	AK098319	Hs.356310	. 7
	1	UTERU2016761, highly similar to ES/130	• • .		
		mRNA. /gb=AK098319 /gi=21758311	e y		
	<u> </u>	/ug=Hs.356310 /len=2196			
1859	0.046446	golgi reassembly stacking protein 1, 65kDa	NM_031899	Hs.4291	NP_11410
		(GORASP1), mRNA /cds=(99,1421)			
		/gb=NM_031899 /gi=13994252		•	
٠.		/ug=Hs.4291 /len=2998	·	*	
1952	0.022722	target of myb1 (chicken) (TOM1), mRNA	NM_005488	Hs.9482	NP_00547
		/cds=(62,1540) /gb=NM 005488			111
		/gi=4885636 /ug=Hs.9482 /len=2310			
1967	0.026691	CTL2 gene (CTL2), mRNA /cds=(1,2121)	NM_020428	Hs.105509	NP_06516
	ľ	/gb=NM_020428 /gi=9966908	* -	1	
	~	/ug=Hs.105509 /len=2121			
1987	0.004381		NM_016127	Hs.279921	NP_05721
		mRNA /cds=(17,1036) /gb=NM_016127			56721
		/gi=18252054 /ug=Hs.279921 /len=1840	Ì	1	1
		1 1020200 17dg 110.210021 11011 10.70	1	1	
2002	0.042232	ANG2 (ANG2)	AF024631		NP 00891
2005		class I histone deacetylase (HDAC8)	AF230097	<del>                                     </del>	NP_06095
2017		nephronophthisis 1 (juvenile) (NPHP1),	NM_000272	Hs.75474	NP 00033
2017	0.004049		[NIVI_000212	1715.73474	ואר_טטטאָס
	,	mRNA /cds=(34,2232) /gb=NM_000272	{	1 .	
2024	0.04000	/gi=4557804 /ug=Hs.75474 /len=3713	NIM 040055	11-05000	ND 05760
2024	0.04883	family with sequence similarity 8, member	NM_016255	Hs.95260	NP_05733
	-55-	A1 (FAM8A1), mRNA /cds=(56,1297)			
. '		/gb=NM_016255 /gi=7705267			1
		/ug=Hs.95260 /len=4695		1.	

		nding To Differentially Expressed Genes i			Protein
Shor	p-value	Description	Gene	Unigene	
			Accession	Accession	Accession
2022	0.004294	jalmadulin 4 (nhaanhandasa kiinasa dalta)	No.	No.	No.
2033	0.004381	calmodulin 1 (phosphorylase kinase, delta)	NM_006888	Hs.282410	NP_008819
	*	(CALM1), mRNA /cds=(200,649)	* * *		
		/gb=NM_006888 /gi=5901911		] .	
0047	0.040000	/ug=Hs.282410 /len=1526	1	10 10 10 10	1.5 0005
2047	0.042232	p8 protein (candidate of metastasis 1) (P8),	NM_012385	Hs.424279	NP_036517
		mRNA /cds=(103,351) /gb=NM_012385			1
		/gi=6912569 /ug=Hs.424279 /len=719	*		•
2040	0.000000		A D 04 4 C 04	450000	
2048	0.003208	mRNA for KIAA0701 protein, partial cds.	AB014601	Hs.153293	7
	*	/cds=(1,4065) /gb=AB014601			
0050	0.000000	/gi=20521136 /ug=Hs.153293 /len=4625			N.D. 000046
2059	0.008683	hypothetical protein FLJ20337 (FLJ20337),	NM_017772	Hs.26898	NP_060242
*		mRNA /cds=(148,639) /gb=NM_017772	:	<i>:</i> -	
-		/gi=8923313 /ug=Hs.26898 /len=2491		*	
2000	0.046064		NIM COCACA	211-04004	NID 2000 446
2080	0.016261	brefeldin A-inhibited guanine nucleotide-	NM_006421	Hs.94631	NP_006412
		exchange protein 1 (BIG1), mRNA	*		
		/cds=(142,5691) /gb=NM_006421		l	
2139	0.042660	/gi=6715588 /ug=Hs.94631 /len=6969 KIAA0916 protein (KIAA0916), mRNA	NIM O45057	115 45444	ND OFFOR
2139	0.013000		NM_015057	Hs.151411	NP_055872
		/cds=(147,14072) /gb=NM_015057			
2144	0.004940	/gi=7662379 /ug=Hs.151411 /len=14807 quiescin Q6 (QSCN6), mRNA	NIM OCCOS	115 77266	ND 00204
2 144	0.004049	/cds=(76,2319) /gb=NM_002826	NM_002826	Hs.77266	NP_002817
•					100
2152	0.031336	/gi=13325074 /ug=Hs.77266 /len=3314 CGI-72 protein (LOC51105), mRNA	NM_016018	Hs.318725	NP_057102
2 (32	0.031220	/cds=(70,1401) /gb=NM_016018	NIVI_0 100 10	I	INF_05/ 102
-		/gi=7705782 /ug=Hs.318725 /len=1763		200	- 7
2170	0.026601	splicing factor 3b, subunit 1, 155kDa	NM 012433	Hs.334826	NP. 036565
2170	0.020031	(SF3B1), mRNA /cds=(1,3915)	[NIVI_012433 :	115.554620	INF_03030
		/gb=NM_012433 /gi=6912653			
		/ug=Hs.334826 /len=4259		0	
2200	0.012511	mRNA, cDNA DKFZp667O2119 (from	AL832314	Hs.180789	
2203	0.012311	clone DKFZp667O2119) /gb=AL832314	AL632314	JUS. 1001 03	
	<u>.</u>	/gi=21732861 /ug=Hs.180789 /len=6868			
2228	0.039219	clone_MGC:15451 IMAGE:2960796,	BC014640	Hs.403836	<del> </del>
2220	0.000210	mRNA, complete cds /cds=(381,2660)	DC014040	11 13.40,5000	
	,	/gb=BC014640 /gi=15779149			1.
	_	/ug=Hs.403836 /len=3479			
2271	0.006524	transcription factor IGHM enhancer 3,	AF196779	<del> </del>	
	3.000024	JM11 protein, JM4 protein, JM5 protein,	1,11 190770	*	
		T54 protein, JM10 protein, A4		*	· . '
		differentiation-dependent protein, triple LIM	· ·		
	- 1	domain protein 6, and synaptophysin			
		genes, complete cds, and L-type calcium	<u> </u>		
*		channel a>			

		nding To Differentially Expressed Genes i	n Figure 14 - D	iabetes	
Spot	p-value	Description	G ne	Unigene	Protein
	,		Acc ssion	Accession	Accession
	}	. ,	No.	No.	No.
2278	0.045433	latent transforming growth factor beta	NM 000627	Hs.241257	NP_000618
*		binding protein 1 (LTBP1), mRNA			
		/cds=(91,4275) /gb=NM_000627			
		/gi=4557730 /ug=Hs.241257 /len=5075			
2326	0.006524	formin binding protein 4 (FNBP4), mRNA	NM_015308	Hs.6834	NP_056123
		/cds=(28,3075) /gb=NM_015308			
		/gi=24308032 /ug=Hs.6834 /len=3995			
2334	0.010447	androgen induced protein (AIG-1), mRNA	NM_016108	Hs.107528	NP_057192
	0.0.0	/cds=(28,744) /gb=NM_016108	0.0.00		-007 102
	_, ,	/gi=7705269 /ug=Hs.107528 /len=1398		*	
2348	0.039219	neuropilin-2 (a5)	AF022861		·
2402		aldo-keto reductase family 7, member A2	NM_003689	Hs.6980	NP_003680
2702	0.040400	(aflatoxin aldehyde reductase) (AKR7A2),	14141_000003	113.0300	141005000
	*	mRNA /cds=(78,1070) /gb=NM_003689			ļ
		/gi=4502020 /ug=Hs.6980 /len=1331			
2414	0.011430	metaxin 1 (MTX1), mRNA /cds=(1,954)	NM 002455	Hs.247551	NP_002446
2414	0.011439	/gb=NM 002455 /gi=4505280	14141_002455	IDS.247551	INP_002440
		/ug=Hs.247551 /len=1065	*	1	
2444	0.045422	germ line gene homologous to bladder	V00574		<del> </del>
2444	0.045455	( -			*
		carcinoma oncogene T24 (Gene code c-Ha			1
2540	0.040004	ras-1)with four exons	A)A/40CC00		ND 004050
2510	0.016261	EST (xm35g05.x1 NCI_CGAP_GC6 cDNA	AW196683	×	NP_004958
0544	0.000000	clone IMAGE:2686232 3')	104 00000	11. 000544	NE 00000
.2511	0.020932	ribosomal protein L35a (RPL35A), mRNA	NM_000996	Hs.288544	NP_000987
		/cds=(74,406) /gb=NM_000996	1		
0500	0.04000	/gi=16117790 /ug=Hs.288544 /len=511			1.15 2.2272
2536	0.04883	H3 histone, family 3B (H3.3B) (H3F3B),	NM_005324	Hs.180877	NP_005315
		mRNA /cds=(118,528) /gb=NM_005324			
		/gi=21264598 /ug=Hs.180877 /len=1662			ļ.,
2539	0.024639	Similar to hypothetical protein	BC039372	Hs.439358	
		DKFZp547l224, clone IMAGE:5271326,			<b>J</b> .
	}	mRNA /gb=BC039372 /gi=25058800	24	1	Ì
		/ug=Hs.439358 /len=2494		<u> </u>	
2564		mitochondrion, complete genome	NC_001807		
2577	0.024639	NADH dehydrogenase (ubiquinone) 1 beta	NM_004547	Hs.227750	NP_004538
	1	subcomplex, 4, 15kDa (NDUFB4), mRNA			· ·
		/cds=(9,398) /gb=NM_004547 /gi=6041668			
		/ug=Hs.227750 /len=464			
2620	0.04883	pleckstrin domain containing, family A	NM_020904	Hs.9469	NP_065955
		(phosphoinositide binding specific) member			
		4 (PLEKHA4), mRNA /cds=(526,2865)			
	1	/gb=NM_020904 /gi=10190743		1	1
		/ug=Hs.9469 /len=3056			(3)
2625	0.010447	hypothetical protein (KIAA0714)	AB018257		-
2629		similar to S. pombe dim1 (DIM1), mRNA	NM_006701	Hs.433683	NP_006692
٠.	1	/cds=(141,569) /gb=NM_006701	-		· -
1	I .	/gi=20070233 /ug=Hs.433683 /len=1415	·	1	] .

		nding To Differ ntially Expressed G nes i			<u></u>
Spot	p-value	Description	Gene	Unigene	Protein
	:		Accession	Accession	Accession
			No.	No.	No.
2704	0.007185	angiomotin like 2 (AMOTL2), mRNA	NM_016201	Hs.92186	
		/cds=(1,1712) /gb=NM_016201			
		/gi=7705577 /ug=Hs.92186 /len=3542	- 1		
2705	0.039219	H3 histone, family 3B (H3.3B) (H3F3B),	NM 005324	Hs.180877	NP_005315
		mRNA /cds=(118,528) /gb=NM_005324			
	0,0	/gi=21264598 /ug=Hs.180877 /len=1662			
2706	0.019262	nuclear receptor interacting protein 1	NM_003489	Hs.155017	NP 003480
2700	0.013232	(NRIP1), mRNA /cds=(288,3764)	11111_000403	113.100017	141 - 000-
		/gb=NM 003489 /gi=4505454		_	
2744	0.047700	/ug=Hs.155017 /len=7247	NINA 004074	11- 0000	ND GO 4000
2741	0.017708	golgi SNAP receptor complex member 1	NM_004871	Hs.8868	NP_004862
	[	(GOSR1), mRNA /cds=(13,765)		•	. 7
		/gb=NM_004871 /gi=4758455 /ug=Hs.8868	h.m	*	
•		/len=999	*		10
2743	0.04883	clone MGC:9947 IMAGE:3876105, mRNA,	BC013590	Hs.2437	
		complete cds /cds=(51,2216)			
		/gb=BC013590 /gi=15488925 /ug=Hs.2437		X-	9
		/len=2651		, 9	
2791	0.028884	hypothetical protein FLJ10283 (FLJ10283),	NM_018046	Hs.284216	NP_060516
	•	mRNA /cds=(218,1039) /gb=NM_018046			_
	· ·	/gi=8922325 /ug=Hs.284216 /len=1876			
			·		
2815	0.039219	proteasome (prosome, macropain) subunit,	NM 002791	Hs.410276	NP_002782
2		alpha type, 6 (PSMA6), mRNA			<del>-</del>
	. "	/cds=(110,850) /gb=NM_002791	1		•
		/gi=23110943 /ug=Hs.410276 /len=1035		1	
2816	0.04883	CD109 (CD109), mRNA /cds=(113,4450)	NM 133493	Hs.55964	NP_598000
-	0.04000	/gb=NM_133493 /gi=19424129	11111_100400	113.00004	
		/ug=Hs.55964 /len=5883	•		
2862	0.000693	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM 001356	Hs.380774	NP_076829
2002	0.006663		MM_001336	IUS:300114	INP_0/6058
		polypeptide 3 (DDX3), transcript variant 2,		,	
		mRNA /cds=(857,2845) /gb=NM_001356		3	1
0070	0.000704	/gi=13514812 /ug=Hs.380774 /len=5322	1114 600044	11 100001	ND 005000
2872	0.033724	oxysterol binding protein-like 8 (OSBPL8),	NM_020841	Hs.109694	NP_065892
	Ì.	mRNA /cds=(481,3150) /gb=NM_020841	*		
		/gi=22035617 /ug=Hs.109694 /len=7239			
					ļ
2883	0.033724	thymosin, beta 10 (TMSB10), mRNA	NM_021103	Hs.76293	NP_066926
		/cds=(66,200) /gb=NM_021103		*	
-		/gi=10863894 /ug=Hs.76293 /len=453	·		*
2887	0.019262	RNA binding motif protein 12 (RBM12),	NM_006047	Hs.180895	NP_690051
		transcript variant 1, mRNA /cds=(275,3073)	*		=
				I	
		/gb=NM_006047 /gi=23510460		I .	
		/gb=NM_006047 /gi=23510460 /ug=Hs 180895 /len=6650			1
2891	0.036386	/ug=Hs 180895 /len=6650	NM 007218	Hs.28285	NP 009149
	0.036386	/ug=Hs 180895 /len=6650 patched related protein translocated in	NM_007218	Hs.28285	NP_009149
	0.036386	/ug=Hs 180895 /len=6650	NM_007218	Hs.28285	NP_009149

	p-value	nding T Differentially Expressed Genes in Description	Gene	Unigene	Protein
Opol	P value	Description	Accession	Accession	Accession
	1		No.	No.	No.
2948	0.042232	endothelial differentiation-related factor 1	NM_003792	Hs.174050	NP_694880
2370	0.042202	(EDF1), transcript variant alpha, mRNA	14141_0037.92	115.174050	147_094000
•		/cds=(29,475) /gb=NM_003792		a * ·	
					1 2
2950	0.008683	/gi=24497592 /ug=Hs.174050 /len=658 cytochrome c oxidase subunit IV isoform 1	NM_001861	Hs.433419	NP 001852
2930	0.000000	(COX4I1), nuclear gene encoding	14141-00 100 1	I	NP_00 1052
		mitochondrial protein, mRNA		•	
	· · ·	1	*		Ì
		/cds=(165,674) /gb=NM_001861	* *		
2978	0.047700	/gi=17017985 /ug=Hs.433419 /len=802	NIM 000000	LIS FCOC	NID 0000C
2970	0.017708	RAB6A, member RAS oncogene family	NM_002869	Hs.5636	NP_002860
. 1		(RAB6A), mRNA /cds=(427,1053)			
		/gb=NM_002869 /gi=19923230	* ,		
0007	0.045400	/ug=Hs.5636 /len=3079	NA 000455	110150	NID 000 (46
2987	0.045433	nucleolar autoantigen (55kD) similar to rat	NM_006455	Hs.446459	NP_006446
		synaptonemal complex protein (SC65),			
• =		mRNA /cds=(12,1325) /gb=NM_006455		0 6	
		/gi=5454037 /ug=Hs.446459 /len=2347			
2989	0.039219	hypothetical protein DKFZp434B195	NM_031284	Hs.10748	NP_11257
		(DKFZP434B195), mRNA /cds=(514,1290)	1.		
		/gb=NM_031284 /gi=21361960		37.	
J 201	X-1	/ug=Hs.10748 /len=2262			
2993	0.017708	integrin beta 4 binding protein (ITGB4BP),	NM_002212	Hs.406444	NP_002203
	٠.	mRNA /cds=(71,808) /gb=NM_002212			*
		/gi=4504770 /ug=Hs.406444 /len=1112	4		
3011		mitochondrion, complete genome	NC_001807		
3060	0.028884	1	NM_005732	Hs.41587	NP_59781
		variant 1, mRNA /cds=(388,4326)	*		
	18	/gb=NM_005732 /gi=19924128			
<u> </u>		/ug=Hs.41587 /len=5891			
3068	0.00953	deiodinase, iodothyronine, type II (DIO2),	NM_013989	Hs.154424	NP_054644
		transcript variant 1, mRNA /cds=(707,1528)			
		/gb=NM_013989 /gi=7549802			
		/ug=Hs.154424 /len=6735			
3071	0.020932	endothelin receptor type A (EDNRA),	NM_001957	Hs.76252	NP_001948
		mRNA /cds=(485,1768) /gb=NM_001957	1		
	-1	/gi=4503464 /ug=Hs.76252 /len=4105		*	
3077	0.013668	mRNA; cDNA DKFZp586E1120 (from	AL049437	Hs.351178	
	7	clone DKFZp586E1120) /gb=AL049437			
	<u> </u>	/gi=4500220 /ug=Hs.351178 /len=2141			
3085	0.022722	PEF protein with a long N-terminal	NM_012392	Hs.241531	NP_036524
	. , ;	hydrophobic domain (peflin) (PEF), mRNA	· -		
* -	œ.	/cds=(13,867) /gb=NM_012392		*-	
		/gi=6912581 /ug=Hs.241531 /len=1641	* *	:	· · · ·
3088	0.026691	sulfotransferase family, cytosolic, 1C,	NM_006588	Hs.312644	NP 006579
		member 2 (SULT1C2), mRNA			-
	′ :	/cds=(330,1238) /gb=NM_006588			, ,
	Į.	/gi=5730070 /ug=Hs.312644 /len=2143			1 ' ' '

		nding To Differentially Expressed Genes i			
Spot	p-valu	Description	Gene Accession	Unigene Accession	Protein Accession
			No.	No.	No.
3090	0.04883	Similar to kinesin family member C1, clone MGC:1202 IMAGE:3506669, mRNA,	BC000712	Hs.20830	NP_002254
		complete cds /cds=(168,2189)			
· .		/gb=BC000712 /gi=12653842			
		/ug=Hs.20830 /len=2400		}	
3094	0.033724	SON DNA binding protein (SON), transcript	NM 058183	Hs.92909	NP 620305
		variant e, mRNA /cds=(50,6376)			
		/gb=NM_058183 /gi=21040317			
		/ug=Hs.92909 /len=8482	-		
3102	0.036386	deoxyribonuclease I-like 3 (DNASE1L3),	NM 004944	Hs.88646	NP 004935
		mRNA /cds=(71,988) /gb=NM_004944	· ·		_
		/gi=4826697 /ug=Hs.88646 /len=1079			
3113	0.04883	phosphodiesterase 4D interacting protein	NM_014644	Hs.265848	NP_055459
•		(myomegalin) (PDE4DIP), mRNA			
	*	/cds=(658,4056) /gb=NM_014644		0	
		/gi=11036643 /ug=Hs.265848 /len=5676	*		
3137	0.028884	yp24c06.s1 Soares breast 3NbHBst cDNA	H43642	Hs.418241	
		clone IMAGE:188362 3' similar to			
		gb:M10942_cds1 metallothionein-le gene			100
	*	mRNA sequence /clone=IMAGE:188362			ļ. ·
		/clone_end=3' /gb=H43642 /gi=919694			- 0
		/ug=Hs.418241 /len=452		1 - 2 - 2	
3151	0.028884	hypothetical protein FLJ37440 (FLJ37440),	NM_153214	Hs.355577	NP_694946
		mRNA /cds=(272,1591) /gb=NM_153214			- The
		/gi=23397470 /ug=Hs.355577 /len=2299	3		
3164	0.039219	adenylyl cyclase-associated protein 2	NM_006366	Hs.296341	NP_006357
		(CAP2), mRNA /cds=(84,1517)			
		/gb=NM_006366 /gi=5453592 /			
	<u> </u>	/ug=Hs.296341 /len=1517	Ý · · ·		
3166	0.022722		NM_023079	Hs.168232	NP_075567
		mRNA /cds=(328,1068) /gb=NM_023079	*	* *	
		/gi=20149671 /ug=Hs.168232 /len=3053			
				<u> </u>	
3187	0.00208	clone IMAGE:5229459, mRNA	BC044229	Hs.266263	
·		/gb=BC044229 /gi=28277403	Y.		1
	0.000040	/ug=Hs.266263 /len=2044	416005044	11-444000	
3198	0.039219	cDNA: FLJ21691 fis, clone COL09555.	AK025344	Hs.141003	
	į	/gb=AK025344 /gi=10437842	1	-	
2204	F 625 04	/ug=Hs.141003 /len=1824	BC027740	Hs.18016	<del> </del>
3204	0.03⊏-04	clone IMAGE:5263531, mRNA	BC037740	IUS' 100 10	)
	-	/gb=BC037740 /gi=22902216	* * * * * * * * * * * * * * * * * * * *		1
3336	0.017700	/ug=Hs.18016 /len=5036 stromal antigen 2 (STAG2), mRNA	NM_006603	Hs.8217	NP_006594
3330	0.017708	/cds=(405,3893) /gb=NM_006603	14141_000003	115.021/	1145_000094
		//gi=27552767 /ug=Hs.8217 /len=4197	Į.		la .
	<u> </u>	1/91-21002101 /ug-115.021/ /lell-419/	<u> </u>	<del></del>	1

Genes	C rrespoi	nding To Differentially Expressed Gen si	n Figur 14 - D	iabetes	
		Description	Gene Accession	Unigene Accession	Protein Accession
			No.	No.	No.
3367	0.033724	nuclear receptor subfamily 3, group C,	NM_000176	Hs.75772	NP_000167
	00	member 1 (glucocorticoid receptor)			
	,	(NR3C1), mRNA /cds=(133,2466)	6		
		/gb=NM_000176 /gi=4504132			
0070	0.004000	/ug=Hs.75772 /len=4788	N. 2 - 2 - 4 - 4 - 2		115 05 1001
3376	0.031226	trichorhinophalangeal syndrome I (TRPS1),	NM_014112	Hs.26102	NP_054831
90	50 100	mRNA /cds=(639,4484) /gb=NM_014112 /gi=7657658 /ug=Hs.26102 /len=10011		** "	
		/gi=/05/050/ug=Hs.20102/lefi=10011		5	
3392	0.039219	NADH dehydrogenase (ubiquinone) 1 alpha	NM 002490	Hs.274416	NP_002481
		subcomplex, 6, 14kDa (NDUFA6), mRNA	<del>-</del>		
		/cds=(2,388) /gb=NM_002490	* .		
		/gi=20070136 /ug=Hs.274416 /len=1063			
3397	0.036386	chromosome 20 open reading frame 6.	NM_016649	Hs.88820	NP_057733
	. * >	(C20orf6), mRNA /cds=(109,2664)			*
		/gb=NM_016649 /gi=22507381	* :		
		/ug=Hs.88820 /len=3216			
3400	0.028884	KH domain containing, RNA binding, signal	NM_006559	Hs.119537	NP_006550
		transduction associated 1 (KHDRBS1);			-3.0
* :. :		mRNA /cds=(107,1438) /gb=NM_006559 /gi=5730026 /ug=Hs.119537 /len=2685			
		/gi=3/30020/ug=ris.//1955/,/left=2005	*		
3407	0.017708	BCL2/adenovirus E1B 19kD-interacting	XM_048077		· · · · · · · · · · · · · · · · · · ·
,		protein 3-like (BNIP3L)			ß.
3429	0.039219	family with sequence similarity 13, member	NM_014883	Hs.177664	NP_055698
	٠.	A1 (FAM13A1), mRNA /cds=(227,2320)			
}		/gb=NM_014883 /gi=7662375	, ,		]
0.440	0.004000	/ug=Hs.177664 /len=4491	NIN 040404	11. 3553	ND 000500
3440	0.031226	TERF1 (TRF1)-interacting nuclear factor 2	NM_012461	Hs.7797	NP_036593
		(TINF2), mRNA /cds=(263,1327) /gb=NM_012461 /gi=6912715 /ug=Hs.7797			» ·
-		/len=2095		. ,	
3482	0.039219	proteasome (prosome, macropain) 26S	NM_002805	Hs.79387	NP_002796
ţ-		subunit, ATPase, 5 (PSMC5), mRNA			
		/cds=(42,1262) /gb=NM_002805	* *		*
		/gi=24497434 /ug=Hs.79387 /len=1332		*	
3491	0.020932	cDNA: FLJ22071 fis, clone HEP11691.	AK025724	Hs.422407	
	1.	/gb=AK025724 /gi=10438333			
ļ	0.0/2222	/ug=Hs.422407 /len=2047			
3518	0.012381	hypothetical protein FLJ23548 (FLJ23548),	NM_024590	Hs.22895	NP_078866
		mRNA /cds=(204,713) /gb=NM_024590			
{		/gi=13375780 /ug=Hs.22895 /len=1871			
3521	0.026691	ubiquitin-like, containing PHD and RING	NM_152306	Hs.348602	NP 690856
		finger domains 2 (URF2), transcript variant			
	•	1, mRNA /cds=(341,1852) /gb=NM_152306			
"	[	/gi=23312361 /ug=Hs.348602 /len=3720	!		
	L		<u> </u>	<u> </u>	

Genes	Correspoi	nding To Differentially Express d Genes i	n Figure 14 - D	iabetes	
Spot	p-value	Description	Gene	Unigene	Protein
	7.	*	Accession -	Accession	Accession
1			No.	No.	No.
3535	0.003954	mRNA, cDNA DKFZp761C169 (from clone	AL161991	Hs.71252	NP 075064
	* *	DKFZp761C169); partial cds	,		
		/cds=(997,2475) /gb=AL161991			
		/gi=7328122 /ug=Hs.71252 /len=3324		. *	
3536	0.045433	mRNA for KIAA1367 protein, partial cds.	AB037788	Hs.224961	
		/cds=(1,1741) /gb=AB037788 /gi=7243114		1,5,22,55	
		/ug=Hs.224961 /len=4196		,	
3539	0.042232	ubiquitin C (UBC), mRNA /cds=(136,2193)	NM 021009	Hs.183704	NP_066289
) ()	0.5.2202	/gb=NM_021009 /gi=20149305	02 1000	110.100701	-000200
		/ug=Hs.183704 /len=2309		*	
3540	0.012511	nucleoporin 155kDa (NUP155), transcript	NM_153485	Hs.23255	NP 705618
3370	0,012911	variant 1, mRNA /cds=(119,4294)	14141_133403		141 _700010
•		/gb=NM_153485 /gi=24430148		•	
l ·	o. de	/ug=Hs.23255 /len=4355	* '		÷
3544	0.031336	mRNA for KIAA1999 protein. /cds=(1,3829)	A D002520	Hs.9343	
3344	0.031220		Apriozaan	ITS.9343	* * *
		/gb=AB082530 /gi=21693143 /ug=Hs.9343		* * * * * * * * * * * * * * * * * * * *	
0550	0.040000	/len=8213	NN 450000	11 050705	ND 000540
3550	0.019262	chromosome 14 open reading frame 31	NM_152330	Hs.250705	NP_689543
		(C14orf31), mRNA /cds=(246,2090)		H	
	. 1	/gb=NM_152330 /gi=22748720			
2-21		/ug=Hs.250705 /len=4528			
3572		KIAA0171 gene product (KIAA0171)	NM_014666	100	NP_055481
3578	0.00208	DKFZp586D2322 (from clone	AL049455		NP_001928
		DKFZp586D2322)			
3619	0.042232		NM_001861	Hs.433419	NP_001852
ļ .,		(COX4I1), nuclear gene encoding			*
		mitochondrial protein, mRNA			
		/cds=(165,674) /gb=NM_001861	• •		· ·
<u> </u>		/gi=17017985 /ug=Hs.433419 /len=802			
3626	0.017708	paired basic amino acid cleaving system 4	NM_002570	Hs.170414	NP_612198
41.	-	(PACE4), transcript variant 1, mRNA			· ·
Y		/cds=(315,3224) /gb=NM_002570			•
L		/gi=20336178 /ug=Hs.170414 /len=4553		(F) +	
3633	0.026691	DiGeorge syndrome critical region gene 6-	NM_033257	Hs.347285	NP_150282
		like (DGCR6L), mRNA /cds=(98,760)			
	0,3,0	/gb=NM_033257 /gi=15718677			.55
		/ug=Hs.347285 /len=1182		·	
3634	0.026691	FLJ13067 fis, clone NT2RP3001712, highly	AK023129	Hs.142442	NP_057371
		similar to Homo sapiens HP1-BP74 protein			_
		mRNA /cds=UNKNOWN /gb=AK023129	*		
1.		/gi=10434909 /ug=Hs.142442 /len=3913		٠ إ	` ·
3640	0.031226	PTD015 protein (PTD015), mRNA	NM_014040	Hs.95870	NP_054759
		/cds=(148,504) /gb=NM_014040			
-		/gi=7662642 /ug=Hs.95870 /len=620			
3678	0.045433	immunoglobulin superfamily, member 9	NM_020789	Hs.38002	NP_065840
30,0	0.545455	(IGSF9), mRNA /cds=(208,3699)	. 1111_020703	1.10.00002	
	,	/gb=NM_020789 /gi=21357326			<u> </u>
		/ug=Hs.38002 /len=4024			
		rug-ria.Jouuz ricji+40Z#	L	<u> </u>	

		nding To Differentially Expressed Genes i			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No	No	No.
3726	0.008683	phosphofructokinase, liver (PFKL), mRNA	NM_002626	Hs.155455	NP_002617
	* *	/cds=(356,2839) /gb=NM_002626	-		
		/gi=21361069 /ug=Hs.155455 /len=3385			ļ
3769	0.042232	signal transducer and activator of	NM_139276	Hs.321677	NP 644805
		transcription 3 (acute-phase response	_ , , , ,		<u></u>
		factor) (STAT3), transcript variant 1, mRNA		*	
		/cds=(241,2553) /gb=NM_139276		*	
0.0		/gi=21618339 /ug=Hs.321677 /len=3455	, .		
3796	0.016261	immunoglobulin light chain	D87000		
3809		DiGeorge syndrome critical region gene 6-	NM 033257	Hs.347285	NP_150282
,	0.000.2	like (DGCR6L), mRNA /cds=(98,760)	11000207	110.047.200.	111 _100202
		/gb=NM_033257 /gi=15718677			
		/ug=Hs.347285 /len=1182	1		
3833	0.039219	linker for activation of T cells (LAT), mRNA	NIM 014387	Hs.83496	NP_055202
0000	0.000210	/cds=(79,867) /gb=NM 014387	14141_014301	1113.03430	14055202
		/gi=24475949 /ug=Hs.83496 /len=1460	*	,	
3883	0.04883	Meis1, myeloid ecotropic viral integration	NM_002398	Hs.170177	NP_002389
3003	0.04003	site 1 (mouse) (MEIS1), mRNA	UVIVI_UU2390	П5. 170177	1117_002369
	1.0	/cds=(66,1238) /gb=NM 002398	* .		•
3907	0.005350	/gi=4505150 /ug=Hs.170177 /len=2511	NIM 007000	115 0004	ND 000400
3907	0.005359	lg superfamily protein (Z39IG), mRNA	NM_007268	Hs.8904	NP_009199
		/cds=(46,1245) /gb=NM_007268			
2040	0.044420	/gi=6005957 /ug=Hs 8904 /len=1787	NN 044040	7050	NID 055404
3916	0.011439	integral inner nuclear membrane protein	NM_014319	Hs.7256	NP_055134
		(MAN1), mRNA /cds=(7,2742)	**		1
ę		/gb=NM_014319 /gi=7706606 /ug=Hs.7256			}
20.40	0.000004	/len=4703		<del></del>	
3940	0.026691	calpain 2, (m/II) large subunit (CAPN2),	NM_001748	Hs.76288	NP_001739
-		mRNA /cds=(143,2245) /gb=NM_001748		<b>!</b>	-
2050	2 2 1 2 2	/gi=12408645 /ug=Hs.76288 /len=3419			ļ. <u></u>
3950	0.045433	B-cell translocation gene 1, anti-	NM_001731		NP_001722
1		proliferative (BTG1)			*
3982	0.016261	ORF2 consensus sequence encoding	AAB41224	}	
		endonuclease and reverse transcriptase			
0000	2 2 1 2 2 2 2	minus RNaseH			
3990	0.019262	hypothetical protein HSPC155 (HSPC155),	NM_016406	Hs.177507	NP_057490
		mRNA /cds=(241,744) /gb=NM_016406			
		/gi=7705480 /ug=Hs.177507 /len=1137	, ·		
3993	0.033724	fatty acid binding protein 4, adipocyte	NM_001442	Hs.391561	NP_001433
į	*	(FABP4), mRNA /cds=(48,446)	}		ł
	٠,	/gb=NM_001442 /gi=4557578			
	<u>.</u>	/ug=Hs.391561 /len=619	·		
4001	0.042232	BCL2-like 13 (apoptosis facilitator)	NM_015367	Hs.10267	NP_056182
		(BCL2L13), nuclear gene encoding		* *	
		mitochondrial protein, mRNA			"
•		/cds=(72,1232) /gb=NM_015367			*
		/gi=7662505 /ug=Hs.10267 /len=3024		Ì	]

		nding To Diff rentially Expressed Genes			Director
Spot	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
4006	0.036386	protein kinase D2 (PRKD2), mRNA	NM_016457	Hs.91146	NP_05754
		/cds=(40,2676) /gb=NM_016457			
		/gi=19923467 /ug=Hs.91146 /len=2900			
4019	0.028884	BCG-induced gene in monocytes, clone	NM_022154	Hs.284205	NP_07143
		103 (BIGM103), mRNA /cds=(478,1860)			
•		/gb=NM_022154 /gi=24586664			
		/ug=Hs.284205 /len=3246		* 7	
4056	0.004849	Gene 33/Mig-6 (MIG-6), mRNA	NM_018948	Hs.11169	NP_06182
		/cds=(213,1601) /gb=NM_018948			
•	:	/gi=21314673 /ug=Hs.11169 /len=3099			
4069	0.012511	mRNA for KIAA0256 protein, partial cds.	D87445	Hs.432934	
		/cds=(136,3468) /gb=D87445 /gi=6634006			
	İ	/ug=Hs.432934 /len=7071			
4111	0.022722	estrogen related receptor alpha (ESTRRA)	U85258		
		pseudogene		1	
4112	0.028884	hypothetical protein FLJ22555 (FLJ22555),	NM 024520	Hs.3592	NP 07879
•	1	mRNA /cds=(323,1198) /gb=NM_024520		•	7-1
	0	/gi=13375659 /ug=Hs.3592 /len=1530			(X)
		, , , , , , , , , , , , , , , , , , ,			1.
4118	0.005359	HSPC154 protein (HSPC154), mRNA	NM_014177	Hs.7922	NP_05489
	0.555555	/cds=(200,946) /gb=NM_014177		110.7022	
	i i	/gi=7661809 /ug=Hs.7922 /len=1343	100		- 1
4126	0.019262	TAF7 RNA polymerase II, TATA box	NM 005642	Hs.155188	NP_00563
1120	1 0.010202	binding protein (TBP)-associated factor,	14141_0000-12	113.100100	1111 _00000
		55kDa (TAF7), mRNA /cds=(741,1790)			
	1	/gb=NM_005642 /gi=14717406			~ ,
	*	/ug=Hs.155188 /len=2310	;		
4159	0.042232	suppressor of Ty 3 (S. cerevisiae)	NM_003599	Hs.304173	NP 00359
4139	0.042232	(SUPT3H), mRNA /cds=(72,1025)	MM_002599	III8.3041/3	NP_00359
	1	1'		*	
		/gb=NM_003599 /gi=4507308			
1160	0.000504	/ug=Hs.304173 /len=1165	A E 4 C E 4 O 4	<del></del>	ND 00540
4160		BPAG1n3 (BPAG1)	AF165191	11. 47000	NP_06512
4181	0.045433	KIAA0663 gene product (KIAA0663),	NM_014827	Hs.17969	NP_05564
	7	mRNA /cds=(214,2646) /gb=NM_014827			
1405	0.040004	/gi=7662231 /ug=Hs.17969 /len=4365	1111	1110000	
4185	0.016261	APR-1 protein (MAGEH1), mRNA	NM_014061	Hs.279819	NP_05478
		/cds=(271,930) /gb=NM_014061	1 .		
1122		/gi=18105051 /ug=Hs.279819 /len=1475			
4188	0.039219	secreted protein of unknown function	NM_013349	Hs.109494	NP_03748
		(SPUF), mRNA /cds=(16,534)			
		/gb=NM_013349 /gi=20127529			
		/ug=Hs.109494 /len=953		*	
4201	0.014917	cytochrome c oxidase subunit VIb	NM_001863	Hs.431668	NP_00185
		(COX6B), nuclear gene encoding			<u>;</u> ,
		mitochondrial protein, mRNA			
	:	/cds=(163,423) /gb=NM_001863			
	*	/gi=17999530 /ug=Hs.431668 /len=578		4	1

		nding To Differentially Expressed Gen s			Ducto
Spot	p-value	Description	Gene	Unigene	Protein
	:		Accession	Accession	Accession
			No.	No.	No.
4206	0.017708	ring finger protein 4 (RNF4), mRNA	NM_002938	Hs.66394	NP_002929
		/cds=(271,843) /gb=NM_002938	1		*
		/gi=4506560 /ug=Hs.66394 /len=2918	, ,		
4246	0.013553	hypothetical protein MGC10471	NM_030818	Hs.24998	NP_11044
		(MGC10471), mRNA /cds=(227,1417)			
		/gb=NM_030818 /gi=13540613			
		/ug=Hs.24998 /len=1688	0		+
4254	0.020932	PA28 gamma subunit (Psme3)	AB007139		
4300		hypothetical protein MBC3205 (MBC3205),	NM_033408	Hs.43621	
<b>-1000</b>	0.020332	mRNA /cds=(215,784) /gb=NM_033408	114101_033400	113.43021	
10	- 0	/gi=15529965 /ug=Hs.43621 /len=961			*
		/gi=15529905 /ug=H\$.4502   /lefi=90			.*
4000	0.040544	aib a de a a a la carta de COC (DDCCC) a a DMA	AUA 004000	11- 000405	ND 00400
4383	0.012511	ribosomal protein S26 (RPS26), mRNA	NM_001029	Hs.299465	NP_00102
: '		/cds=(26,373) /gb=NM_001029			
		/gi=15011935 /ug=Hs.299465 /len=459			
4392	0.024639	hypothetical protein MGC14697	NM_032747	Hs.171625	NP_11613
		(MGC14697), mRNA /cds=(264,440)			,:
		/gb=NM_032747 /gi=14249375	*		3
	0	/ug=Hs.171625 /len=581			
4394	0.014917	Likely ortholog of mouse tumor necrosis-	AK027807	Hs.44208	NP 07891
		alpha-induced adipose-related protein,			
		cDNA FLJ14901 fis, clone PLACE1005409		*	· ·
		(AK027807.1)		-	4
4407	0.007185	15 kDa selenoprotein (SEP15), mRNA	NM_004261	Hs.90606	NP_00425
4401	0.007 103		14141_004201	113.30000	NF_00425
	1 ·	/cds=(5,493) /gb=NM_004261	1		
1110	0.000704	/gi=20127464 /ug=Hs.90606 /len=1519	10040005		ND 00000
4419		KIAA0742	AB018285	11 00504	NP_06090
4420	0.011439	Machado-Joseph disease (spinocerebellar	NM_004993	Hs.66521	NP_109376
•	•	ataxia 3, olivopontocerebellar ataxia 3,	· · · · · ·		
:		autosomal dominant, ataxin 3) (MJD),	1	0.0	9
٠.,		transcript variant 1, mRNA /cds=(59,1144)			1
		/gb=NM_004993 /gi=13518018		*	
	1	/ug=Hs.66521 /len=1900	* *		
			3		
4435	0.020932	clone IMAGE:3633225, mRNA	BC012758	Hs.356377	1.
,		/gb=BC012758 /gi=15706478		* * * * * * * * * * * * * * * * * * * *	
		/ug=Hs.356377 /len=1914	Ì		
4439	0.007185	retinoblastoma binding protein 6 (RBBP6),	NM_006910	Hs.91065	NP_00884
7703	0.007 103	mRNA /cds=(92,2938) /gb=NM_006910	14141_000310	113.31003	_00004
	' '			, in	
		/gi=5902043 /ug=Hs.91065 /len=2994	· .		
4.655	0.01055		NII 00000	490555	No see
4462	0.042232	collagen, type I, alpha 2 (COL1A2), mRNA	NM_000089	Hs.179573	NP_00008
	· .	/cds=(138,4238) /gb=NM_000089			
		/gi=21536289 /ug=Hs.179573 /len=5084	.,		
4496	0.00953	proteasome (prosome, macropain) subunit,	NM_002797	Hs.261927	NP_00278
		beta type, 5 (PSMB5), mRNA		}	
		/cds=(20,811) /gb=NM_002797			
	1	/gi=22538468 /ug=Hs.261927 /len=1050	1	,	1

		nding To Diff rentially Expressed Genes i			<u> </u>
Spot	p-value	Description	Gene	Unigen	Protein
			Accession	Accession	Accession
	L		No.	No.	No.
4507	0.018462	prostaglandin-endoperoxide synthase 2	NM_000963	Hs.196384	NP_00095
		(prostaglandin G/H synthase and			
		cyclooxygenase) (PTGS2), mRNA			*
,		/cds=(135,1949) /gb=NM_000963		•	
		/gi=4506264 /ug=Hs.196384 /len=4465	- <del>*</del>	4. 1	
4510	0.014917	integrin, alpha 6 (ITGA6), mRNA	NM 000210	Hs.227730	NP 00020
		/cds=(147,3368) /gb=NM_000210		1	
		/gi=4557674 /ug=Hs.227730 /len=5611			<b>!</b> ·
4572	0.005359	neuroligin 3	AF217413		<del>                                     </del>
4577		biliverdin reductase A (BLVRA), mRNA	NM 000712	Hs.81029	NP 00070
4011	0.013000	/cds=(61,951) /gb=NM_000712	14141_0007.12	115.01025	141-00016
	·	/gi=4502416 /ug=Hs.81029 /len=1070			
4600	0.000000	hypothetical protein FLJ11756 (FLJ11756),	NM 024606	LI- 07407	ND 07000
4622	0.020932		[NIVI_U246U6	Hs.27497	NP_07888
		mRNA /cds=(375,2795) /gb=NM_024606	*		ľ
1.3		/gi=24431999 /ug=Hs.27497 /len=3167			.*
	2 - 1000		1	7	
4626	0.04883	nuclear receptor coactivator 4 (NCOA4),	NM_005437	Hs.99908	NP_00542
	*	mRNA /cds=(141,1985) /gb=NM_005437			
		/gi=14149616 /ug=Hs.99908 /len=3506			
4631	0.036386	chemokine (C-X-C motif) ligand 9 (CXCL9),	NM_002416	Hs:77367	NP_00240
	*	mRNA /cds=(40,417) /gb=NM_002416			* 1
•		/gi=4505186 /ug=Hs.77367 /len=2545	e		
4639	0.036386	ym45h08.s1 Soares infant brain 1NIB	H18675	Hs.314777	
	,	cDNA clone IMAGE:51273 3', mRNA			
		sequence /clone=IMAGE:51273	l de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de l		
		/clone_end=3' /gb=H18675 /gi=884915		.,	
		/ug=Hs.314777 /len=191			ĺ
4693	0.036386	H3 histone, family 3B (H3.3B) (H3F3B),	NM_005324	Hs.180877	NP_0053
,000	1 0.00000	mRNA /cds=(118,528) /gb=NM 005324	1111_000021	110.100077	
		/gi=21264598 /ug=Hs.180877 /len=1662			
4694	0.034630	hypoxia-inducible factor 1, alpha subunit	NM 001530	Hs.197540	NP_85139
4034	0.024039		14141_001930	1113.137340	11VF_00138
		(basic helix-loop-helix transcription factor)		1)	
		(HIF1A), mRNA /cds=(265,2745)	4-	1	
		/gb=NM_001530 /gi=4504384			
		/ug=Hs.197540 /len=3933			
4701	0.017708	ubiquitin-like 5 (UBL5), mRNA	NM_024292	Hs.13836	NP_07726
	10.7	/cds=(66,287) /gb=NM_024292			
	L	/gi=13236509 /ug=Hs.13836 /len=413		<del> </del>	
4710	0.04883	vinculin (VCL), transcript variant meta-VCL,	NM_014000	Hs.75350	NP_05470
		mRNA /cds=(86,3490) /gb=NM_014000	1		
	-	/gi=7669549 /ug=Hs.75350 /len=5341			
	<u> </u>				
4736	0.026691	E74-like factor 1 (ets domain transcription	NM_172373	Hs.154365	NP_75896
•.		factor) (ELF1), mRNA /cds=(256,2115)	= ,		
•	1.	/gb=NM_172373 /gi=27363483		}	
	1	/ug=Hs.154365 /len=3526		I	i

Genes	Correspoi	nding To Diff rentially Expressed Genes i	n Figure 14 - D	iabetes	THE 27 M 87 PM 1 TO 1
Spot	p-value	Description	Gene	Unigene	Protein
*	,		Accession	Accession	Accession
*	0.91		No.	No.	No.
4747	0.036386	leucine zipper transcription factor-like 1	NM_020347	Hs.30824	NP 065080
		(LZTFL1), mRNA /cds=(125,1024)	_		_
		/gb=NM_020347 /gi=9966792			. :
		/ug=Hs.30824 /len=3384			
4751	0.031226	hypothetical protein (HSPC117), mRNA	NM 014306	Hs.10729	NP 055121
	1	/cds=(76,1593) /gb=NM 014306		.,	
		/gi=7657014 /ug=Hs.10729 /len=2005			
4779	0.045433	signal sequence receptor, alpha	NM_003144	Hs.250773	NP 003135
	0.010.00	(translocon-associated protein alpha)	000111	110.200770	
·		(SSR1), mRNA /cds=(112,972)			
		/gb=NM_003144 /gi=6552340			
		/ug=Hs.250773 /len=3285	. *		
4781	0.036386	ARP2 actin-related protein 2 (yeast)	NM 005722	Hs.393201	NP 005713
	0.000000	(ACTR2), mRNA /cds=(75,1259)	11111 0007 22	113.000201	_000710
		/gb=NM 005722 /gi=5031570			*
		/ug=Hs.393201 /len=2704			j
4805	0.036386	high-mobility group box 1 (HMGB1), mRNA	NM 002128	Hs.6727	NP 002119
4000	0.000000	/cds=(77,724) /gb=NM_002128	14141_002 120	113.0727	INF_002113
	' '	/gi=20149538 /ug=Hs.6727 /len=1207			*) ×
4910	0.021226		NM 000991	Un 256274	ND 000000
4819	0.031220	ribosomal protein L28 (RPL28), mRNA	14141_000991	Hs.356371	NP_000982
	] .	/cds=(43,456) /gb=NM_000991		1	
4020	0.000004	/gi=13904865 /ug=Hs.356371 /len=500	NIM 000044	115 70005	ND 000005
4838	0.020004	protein tyrosine phosphatase, receptor	NM_002844	Hs.79005	NP_002835
		type, K (PTPRK), mRNA /cds=(221,4543)	* *		·. ·
	Ì	/gb=NM_002844 /gi=18860901		_	
4000	0.040363	/ug=Hs.79005 /len=5982	NIM COCCAO	110 404000	ND 000004
4868	0.019262	MLL septin-like fusion (MSF), mRNA	NM_006640	Hs.181002	NP_006631
ie.		/cds=(258,1964) /gb=NM_006640			. ,
4070	0.000004	/gi=19923366 /ug=Hs.181002 /len=3929	NIM 040404	11- 447005	ND COCECC
4876	0.026691	solute carrier family 17 (anion/sugar	NM_012434	Hs.117865	NP_036566
		transporter), member 5 (SLC17A5), mRNA			
		/cds=(125,1612) /gb=NM_012434		. 10	
1077	0.045400	/gi=21314648 /ug=Hs.117865 /len=3329	NI	111100074	115 00005
4877	0.045433	chromosome 20 open reading frame 31	NM_018217	Hs.93871	NP_060687
		(C20orf31), mRNA /cds=(83,1819)	***		-
		/gb=NM_018217 /gi=8922666		( )	<u>.</u>
1000	0.000704	/ug=Hs.93871 /len=1885	1111 000700	00575	1107 00000
4886	0.033724	proteasome (prosome, macropain) subunit,	NM_002796	Hs.89545	NP_002787
		beta type, 4 (PSMB4), mRNA			-33
		/cds=(24,818) /gb=NM_002796		ļ	. '
		/gi=22538466 /ug=Hs.89545 /len=925			
4893	0.026691	growth arrest and DNA-damage-inducible,	NM_015675	Hs.110571	NP_056490
		beta (GADD45B), mRNA /cds=(101,586)			}
		/gb=NM_015675 /gi=9945331	1	1	
		/ug=Hs.110571 /len=1121		<u> </u>	
4905	0.022722	cytoskeleton associated protein 2 (CKAP2),	NM_018204	Hs.24641	NP_060674
		mRNA /cds=(97,2145) /gb=NM_018204	[	*	
	1	/gi=19923520 /ug=Hs.24641 /len=3626			
			1	I	

		nding To Differentially Expressed Genes i			7,44
Spot	p-valu	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No
4919	0.04883	KIAA0436 mRNA, partial cds.	AB007896	Hs.110	
		/cds=(1,2070) /gb=AB007896 /gi=2662152			-00
	,	/ug=Hs.110 /len=4661		*	
4921	0.00953	cDNA FLJ10423 fis, clone NT2RP1000259.	AK001285	Hs.106909	
		/gb=AK001285 /gi=7022444	4:	.\	
- 3.		/ug=Hs.106909 /len=1837			
4944	0.04883	hypothetical protein FLJ20452 (FLJ20452),	NM 017828	Hs.351327	NP 060298
		mRNA /cds=(15,614) /gb=NM_017828	· ·		
		/gi=21361660 /ug=Hs 351327 /len=1948			
٠.					-
4945	0.04883	eukaryotic translation initiation factor 3,	NM 003754	Hs.7811	NP_003745
		subunit 5 epsilon, 47kDa (EIF3S5), mRNA			
	-	/cds=(7,1080) /gb=NM_003754	*10		
	,	/gi=4503518 /ug=Hs.7811 /len=1231			
4949	0.007903	carboxypeptidase A3 (mast cell) (CPA3),	NM 001870	Hs.646	NP_001861
	* * *	mRNA /cds=(12,1265) /gb=NM_001870			T - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 -
		/gi=4503000 /ug=Hs.646 /len=1633			
4952	0.026691	os44g10.s1 NCI_CGAP_Br2 cDNA clone	AI000954	Hs.408052	
		IMAGE:1608258 3' similar to			
		gb:J00272 rna1 metallothionein-II		* *	
		pseudogene mRNA sequence		1	
		/clone=IMAGE:1608258 /clone_end=3'			
		/gb=Al000954 /gi=3191508 /ug=Hs.408052	**		
		/len=259			
4966	0.002322	vav 3 oncogene (VAV3), mRNA	NM 006113	Hs.267659	NP 006104
.000	9.002022	/cds=(48,2591) /gb=NM_006113	000110	110.201.000	
		/gi=21614495 /ug=Hs.267659 /len=4768			
4975	0.039219	hypothetical protein MGC2747 (MGC2747),	NM 024104	Hs.194017	NP 077009
	0.0002.0	mRNA /cds=(93,248) /gb=NM_024104		110.1017	111 _077000
	Y	/gi=13129111 /ug=Hs.194017 /len=1171	0		-00
		1			•
4997	0.031226	hypothetical protein FLJ20489 (RefSeq aa	NP 060312		,
70,01	0.001220	3e-31)	141 _000012		
5027	0.04883	nucleobindin 1 (NUCB1), mRNA	NM_006184	Hs.172609	NP_006175
JUZ1,	0.04000	/cds=(27,1412) /gb=NM_006184	14141_000104	113.172009	111 -000 173
	- 170	/gi=20070227 /ug=Hs.172609 /len=2311		a	4.5
5036	0.007185	peptidylprolyl isomerase B (cyclophilin B)	NM_000942	Hs.394389	NP_000933
3030	0.007 103	(PPIB), mRNA /cds=(150,800)	14141_000942	115.354305	INF_000933
		/gb=NM_000942 /gi=20149505		3.	
		/ug=Hs.394389 /len=1028		}.	
5044	0.04002		NM 002061	Hs.81256	ND 062427
JU44	0.04003	\$100 calcium binding protein A4 (calcium	NM_002961	175.01230	NP_062427
		protein, calvasculin, metastasin, murine			
	*	placental (S100A4), transcript variant 1,			· ·
		mRNA /cds=(70,375) /gb=NM_002961			
5000	0.00.1005	/gi=9845514 /ug=Hs.81256 /len=512	111111111111111111111111111111111111111	11 50500	NE SEE
5069	0.024639	hsp70-interacting protein (HSPBP1),	NM_012267	Hs.53066	NP_036399
		mRNA /cds=(312,1400) /gb=NM_012267		* * * * * * * * * * * * * * * * * * * *	
		/gi=21361406 /ug=Hs.53066 /len=1795	I	ī	1

Genes	Correspon	nding To Differentially Expressed Genes i	n Figure 14 - D	iabetes	
	p-value	Description	Gene	Unigene	Protein
	0.0		Accession	Accession	Accession
			No	No.	No.
5070	0.045433	cDNA FLJ12776 fis, clone NT2RP2001678.		Hs.372558	
·		/gb=AK022838 /gi=10434465			]
		/ug=Hs.372558 /len=2629			
5099	0.045433	ATPase, Na /K transporting, alpha 1	NM_000701	Hs.76549	NP_000692
		polypeptide (ATP1A1), mRNA	<del>-</del> .	1	-
		/cds=(262,3333) /gb=NM 000701	*.		ļ !
		/gi=21361180 /ug=Hs.76549 /len=3680			
5104	0.045433	T-cell activation leucine repeat-rich protein	NM_015350	Hs.199243	NP 056165
		(TA-LRRP), mRNA /cds=(565,2976)			
		/gb=NM_015350 /gi=21245133			
	1	/ug=Hs.199243 /len=3588		1	
5105	0.00186	hypothetical protein FLJ20312 (FLJ20312),	NM 017761	Hs.7862	NP_060231
		mRNA /cds=(384,803) /gb=NM 017761			7.00
-,		/gi=20127576 /ug=Hs.7862 /len=2382	,	*	1
	1	, g. 20 12, 0.0 rag (1.0., 002) 1011 2002			*
5111	0.004381	chromosome 14 open reading frame 94	NM 017815	Hs.8886	NP_060285
	1530	(C14orf94), mRNA /cds=(211,1302)	-		
0		/gb=NM 017815 /gi=8923395 /ug=Hs.8886		* '	
		/len=1618		*	] -
5153	0.022722	ATPase, H transporting, lysosomal 13kDa,	NM 004888	Hs.90336	NP_004879
		V1 subunit G isoform 1 (ATP6V1G1),	,,,,,,		
-	1	mRNA /cds=(94,450) /gb=NM_004888		<u> </u>	1
· .		/gi=20357534 /ug=Hs.90336 /len=1110			1
		, g,,,,,,,		į.	
5157	0.039219	Kallmann syndrome 1 sequence (KAL1),	NM_000216	Hs.89591	NP_000207
	*	mRNA /cds=(151,2193) /gb=NM_000216			_
	·	/gi=4557682 /ug=Hs.89591 /len=6314			
5167	0.042232	chromosome 1 open reading frame 8	NM 004872	Hs.416495	NP_004863
		(C1orf8), mRNA /cds=(251,1222)	_		<del>-</del>
	1	/gb=NM_004872 /gi=27545320			ĺ
		/ug=Hs.416495 /len=1709			
5236	0.042232	mitochondrial ribosomal protein L20	NM_017971	Hs.182698	NP_060441
		(MRPL20), nuclear gene encoding	_		
}		mitochondrial protein, mRNA /cds=(65,514)			1
		/gb=NM_017971 /gi=26638656	l		
	*	/ug=Hs.182698 /len=705			
5238	0.020932	NRAS-related gene (D1S155E), mRNA	NM_007158	Hs.69855	NP_009089
:	·	/cds=(428,2824) /gb=NM_007158	_	, "	_
		/gi=20070240 /ug=Hs.69855 /len=4076			
5242	0.039219	CDK2-associated protein 1 (CDK2AP1),	NM_004642	Hs.433201	NP_004633
)		mRNA /cds=(523,870) /gb=NM_004642		1	
		/gi=17978492 /ug=Hs.433201 /len=1627			
5243	0.026691	chromosome 14 open reading frame 2	NM_004894	Hs.109052	NP_004885
		(C14orf2), mRNA /cds=(61,237)			
		/gb=NM_004894 /gi=4758939		1 .	1
	,	/ug=Hs.109052 /len=627			
	1 0 000 - 0 1	paternally expressed 10 (PEG10), mRNA	NM_015068	Hs.137476	NP_055883
5279	0.033724	paternally expressed to (PEG 10), minne	114141 0 1 2 0 0 0	1113.137470	1111000000
5279	0.033724	/cds=(118,1095) /gb=NM_015068	14141_013000	115.157470	

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gen	Unigene	Prot in
		1 ×	Accession	Accession	Accession
			No.	No.	No.
5293	0.033724	chromosome 6 open reading frame 48	NM_016947	Hs.109798	NP_058643
		(C6orf48), mRNA /cds=(42,422)	, ,	ļ	0
		/gb=NM_016947 /gi=8393383		i	
		/ug=Hs.109798 /len=711			
5318	0.019262	603021120F1 NIH_MGC_114 cDNA clone	BI488592	Hs.380956	
-	·	IMAGE:5191733 5, mRNA sequence			
•		/clone=IMAGE:5191733 /clone_end=5'			1
	,	/gb=BI488592 /gi=15327820	<b>\</b>	*	
		/ug=Hs.380956 /len=988	1 4 4		
5355	0.045433	quinolinate phosphoribosyltransferase	NM_014298	Hs.8935	NP_055113
-		(nicotinate-nucleotide pyrophosphorylase	101.1200	110.0000	1.11 _000110
	. *	(carboxylating)) (QPRT), mRNA		·	
		/cds=(45,938) /gb=NM 014298	*	× • •	J. Salar
		/gi=9257236 /ug=Hs.8935 /len=1182		1 4.1	
5410	0.016261	hypothetical protein FLJ21016 (FLJ21016).	NM_025160	Hs.289069	NP 079436
0.710	0.010201	mRNA /cds=(33,1136) /gb=NM_025160	14141_023100	115.209009	NF_0/ 9430
		/gi=24432014 /ug=Hs.289069 /len=3165		X-8-	
	. :	/gi=24432014/ug=115.205005/lef1=3103			= *
5411	0.036396	DKFZp566J2446 (from clone	AL050082		ND 000044
3 <del>4</del> 1 1	0.030300	l '	ALUSUU6Z		NP_008944
5415	0.006604	DKFZp566J2446)	NIM 000570	11- 400042	ND 000507
04 10	0.026691	serine/threonine kinase 24 (STE20 yeast)	NM_003576	Hs.168913	NP_003567
		(STK24), mRNA /cds=(146,1477)	1		
		/gb=NM_003576 /gi=20070157		Į.	
F 404	0.000704	/ug=Hs 168913 /len=2505	1111 000044	11 170004	NESSO
5431	0.033724	thymine-DNA glycosylase (TDG), mRNA	NM_003211	Hs.173824	NP_003202
	ė ·	/cds=(400,1632) /gb=NM_003211		ľ	* .
F 4 40	0.045400	/gi=4507422 /ug=Hs.173824 /len=3410	V. 12 . 2 . 2 . 2 . 2 . 2	-	
5446	0.045433	heme binding protein 2 (HEBP2), mRNA	NM_014320	Hs.111029	NP_055135
		/cds=(276,893) /gb=NM_014320			
	1 1 1 1 1 1	/gi=7657602 /ug=Hs.111029 /len=1137		<u> </u>	
5449	0.016261	mRNA, cDNA DKFZp667D2123 (from	AL832786	Hs.283643	
,		clone DKFZp667D2123) /gb=AL832786			
		/gi=21733368 /ug=Hs.283643 /len=3000			
5459	0.020932	transforming growth factor, beta-induced,	NM_000358	Hs.118787	NP_000349
		68kDa (TGFBI), mRNA /cds=(48,2099)	1		]
	· .	/gb=NM_000358 /gi=4507466	ļ		
		/ug=Hs.118787 /len=2691		- 1-	<u> </u>
5477	0.045433	lectin, galactoside-binding, soluble, 3	NM_002306	Hs.621	NP_002297
		(galectin 3) (LGALS3), mRNA			
	-	/cds=(19,771) /gb=NM_002306	1	-,	
	- 100	/gi=4504982 /ug=Hs.621 /len=914		L	
5503	0.019241	HSPC142 protein (HSPC142), mRNA	NM_014173	Hs.190722	NP_054892
		/cds=(127,1230) /gb=NM_014173	Ì		
		/gi=7661801 /ug=Hs.190722 /len=1432		<u> </u>	
5507	0.031226	hypothetical protein MGC13170	NM_032712	Hs.256301	NP_116101
		(MGC13170), mRNA /cds=(555,908)		,	
	·	/gb=NM_032712 /gi=14249313	-		, , , ,
	1	/ug=Hs.256301 /len=1316	1	i	

	p-value	orresponding To Differentially Expressed Genes in value Description			Protein
Spor	h-vairie	Description	Gene	Unigene	
		*	Accession	Accession	Accession
5500	b 0 5 5 6 6	<del></del>	No.	No.	No.
5508	0.005916	KIAA0185 mRNA, complete cds.	D80007	Hs.239499	
	* "	/cds=(1,5656) /gb=D80007 /gi=1136429			* _
		/ug=Hs.239499 /len=5823			
5509		brain protein 44-like (BRP44L), mRNA	NM_016098	Hs.108725	NP_057182
		/cds=(123,452) /gb=NM_016098		*	
·	*	/gi=7706368 /ug=Hs.108725 /len=988	·	<u> </u>	
5533	0.036386	upstream binding transcription factor, RNA	NM_014233	Hs.89781	NP_055048
,		polymerase I (UBTF), mRNA		i .	*
	ļ ·	/cds=(148,2442) /gb=NM_014233			•
-		/gi=7657670 /ug=Hs.89781 /len=3097			·
5569	0.026691	aurora-A kinase interacting protein (AKIP),	NM_017900	Hs.76239	NP_060370
		mRNA /cds=(82,681) /gb=NM_017900			
		/gi=8923564 /ug=Hs.76239 /len=794	, <u>(</u> , , )	100	
÷					
5577	0.042232	kangai 1 (suppression of tumorigenicity 6,	NM 002231	Hs:323949	NP_002222
	İ	prostate; CD82 antigen (R2 leukocyte			
		antigen, antigen detected by monoclonal		2	
		and antibody IA4)) (KAI1), mRNA		3	
		/cds=(182,985) /gb=NM_002231		*	
		/gi=13259537 /ug=Hs.323949 /len=1623		. *	-
5586	0.001481	Williams Beuren syndrome chromosome	NM_017528	Hs.155020	NP 059998
		region 22 (WBSCR22), mRNA	01,020		
		/cds=(59,904) /gb=NM_017528		0.0	
		/gi=23199994 /ug=Hs.155020 /len=1258			
5601	0.007185	hypothetical protein FLJ12443 (FLJ12443),	NM_024830	Hs.179882	NP 07910
	0.007 100	mRNA /cds=(475,1188) /gb=NM_024830	11111_02-1000	11 13. 17 5002	_0/5/00
		/gi=21314725 /ug=Hs.179882 /len=3476		-	į.
5616	0.022722	solute carrier family 31 (copper	NM 001859	Hs.380728	NP_001850
	0.022,22	transporters), member 1 (SLC31A1),	11111_001000	119.000720	111 _001001
		mRNA /cds=(153,725) /gb=NM_001859			*
		/gi=4507014 /ug=Hs.380728 /len=1804			
5645	0.022722	MAGE-E1 protein (MAGE-E1), mRNA	NM_030801	Hs.7457	NP_80388
3043	0.022122	/cds=(146,1390) /gb=NM_030801	14141_030001	1115.74,57	ME_00300
		/gi=13540587 /ug=Hs.7457 /len=2997			
5671	0.005350	EPC-1 (=M76979 PEDF;U29953;M90493)	U57446		
5692		mRNA for MEGF6 protein (KIAA0815),	AB011539	Hs.56186	-
	0.031220	partial cds. /cds=(153,3893) /gb=AB011539		115.50100	
	. 00	· · · · · · · · · · · · · · · · · · ·		·	. :
		/gi=20269128 /ug=Hs.56186 /len=4501		}	
5710	0.04992	UI-H-DF0-bes-i-11-0-UI.s1	C A 427702	Ho 420502	
3/10	0.04883	·	CA427703	Hs.428583	
		NCI_CGAP_DF0 cDNA clone UI-H-DF0-	,	l	- 50
		bes-i-11-0-UI 3', mRNA sequence	***	·	
	•	/clone=UI-H-DF0-bes-i-11-0-UI	1		}
		/clone_end=3' /gb=CA427703	1		
	1	/gi=24790429 /ug=Hs.428583 /len=1096		1	0.

		nding To Differentially Expressed Genes i			<u> </u>
Spot	p-value	Description	Gene	Unigene	Protein
	,	w .	Acc ssion	Accession	Acc ssion
			No.	No.	No.
5724	0.039219	proliferation-associated 2G4, 38kDa	NM_006191	Hs.374491	NP_006182
		(PA2G4), mRNA /cds=(98,1282)			
. 4	ļ ·	/gb=NM_006191 /gi=5453841	,	ļ	
	Š	/ug=Hs.374491 /len=1697			
5744	0.039219	DNA segment on chromosome X (unique)	NM_004699	Hs.54277	NP_004690
		9928 expressed sequence (DXS9928E),			
		mRNA /cds=(76,1095) /gb=NM_004699		,	
	·	/gi=4758219 /ug=Hs.54277 /len=1311			
5746	0.017708	glypican 1 (GPC1), mRNA /cds=(222,1898)	NM_002081	Hs.2699	NP_002072
		/gb=NM_002081 /gi=4504080 /ug=Hs.2699			
	·	/len=3692			
5760	0.017708	WD40 and FYVE domain containing 1	NM 020830	Hs.44743	NP 848127
		(WDFY1), mRNA /cds=(30,1262)			-
		/gb=NM_020830 /gi=18482372			
		/ug=Hs.44743 /len=4585		*	
5778	0.00953	abl-interactor 2 (ABI-2), mRNA	NM_005759	Hs.343575	NP_005750
	3.3333	/cds=(35,1462) /gb=NM_005759			
		/gi=20127476 /ug=Hs.343575 /len=1735			
5779	0.024639	3'-phosphoadenosine 5'-phosphosulfate	NM 005443	Hs.3833	NP 005434
0,,,,	0.02 1000	synthase 1 (PAPSS1), mRNA	11111_000 110	1.0.000	
	-	/cds=(27,1901) /gb=NM_005443	5 0.5%		
		/gi=20127474 /ug=Hs.3833 /len=2265			
5788	0.011439	aryl hydrocarbon receptor nuclear	NM 001178	Hs.74515	NP 001169
0,00	0.011300	translocator-like (ARNTL), mRNA	1.1.1001170	110.7-10.10	1001100
	ļ* ,	/cds=(370,2250) /gb=NM_001178			-00
		/gi=20127415 /ug=Hs.74515 /len=2776			
5795	0.039219	progestin induced protein (DD5), mRNA	NM_015902	Hs.278428	NP_056986
3193	0.039219	/cds=(34,8433) /gb=NM_015902	14141_0 13302	113.270420	_000900
	* *-	/gi=15147336 /ug=Hs.278428 /len=8838		:	
5834	0.022722	myosin IE (MYO1E), mRNA	NM_004998	Hs.82251	NP_004989
3034	0.022122	/cds=(376,3705) /gb=NM_004998	14141_004990	113.02231	NF_004909
			. 1		
EOEO	0.022724	/gi=4826843 /ug=Hs.82251 /len=4666 mRNA for KIAA1233 protein, partial cds.	AB033059	Hs.18705	<del> </del>
5850	0.033724		AB033039	ITIS. 10703	
		/cds=(1,3074) /gb=AB033059 /gi=6330728	ļ		
FOF7	0.046364	/ug=Hs.18705 /len=5107	NIM OUTOCO	Hs.343173	NP_057046
5857	0.016261	chromosome 14 open reading frame 111	NM_015962	П8.5451/3	INP_05/046
		(C14orf111), mRNA /cds=(1,597)			8:
:	1:	/gb=NM_015962 /gi=7705729			:
F0=2	0.000040	/ug=Hs.343173 /len=1021	NIM 445000	110 024570	ND CCCCCC
5872	0.039219	TL132 protein (LOC220594), mRNA	NM_145809	Hs.234573	NP_665808
		/cds=(1242,2306) /gb=NM_145809	0.		
-	6 6 / / / 6 =	/gi=21956646 /ug=Hs.234573 /len=4413	NI 000000	111- 400571	ND COCCE
5884	0.011439	polymerase (RNA) II (DNA directed)	NM_006232	Hs.432574	NP_006223
		polypeptide H (POLR2H), mRNA			
		/cds=(88,540) /gb=NM_006232			
	1	/gi=14589952 /ug=Hs.432574 /len=821	1	} .	1

		nding To Differentially Expressed Genes i			
Spot	p-value	Description	Gene	Unigene	Protein
	: 0		Accession	Accession	Accession
		7 · · · · · · · · · · · · · · · · · · ·	No.	No.	No.
5899	0.033724	Fas (TNFRSF6) associated factor 1	NM_007051	Hs.25821	NP_572051
:	*	(FAF1), transcript variant 1, mRNA			
		/cds=(454,2406) /gb=NM_007051	*		
		/gi=19528653 /ug=Hs.25821 /len=2610			
5909	0.045433	LIM domain containing preferred	NM_005578	Hs.180398	NP_005569
		translocation partner in lipoma (LPP),			[ -
		mRNA /cds=(247,2085) /gb=NM_005578			.9
		/gi=5031886 /ug=Hs.180398 /len=5656			
5959	0.007185	germline T-cell receptor beta chain	U66061		
5987		DAZ associated protein 2 (DAZAP2),	NM_014764	Hs.75416	NP_055579
		mRNA /cds=(70,576) /gb=NM_014764			_
		/gi=7661885 /ug=Hs.75416 /len=1897	* .		Y 3
6003	0.010447	tumor protein, translationally-controlled 1	NM 003295	Hs.401448	NP_003286
		(TPT1), mRNA /cds=(95,613)			
	8 \$-	/gb=NM_003295 /gi=4507668			
	* 10:2	/ug=Hs.401448 /len=830			
6004	0.020932	UDP-glucose pyrophosphorylase 2 (UGP2),	NM 006759	Hs.77837	NP 006750
ا دېد	0.02002	mRNA /cds=(85,1611) /gb=NM_006759	000700		
	9 9	/gi=13027637 /ug=Hs.77837 /len=1832	* 4		
		1002700774g=113.7700771cH=1032			
6009	0.020932	methylmalonyl Coenzyme A mutase (MUT),	NM 000255	Hs.155212	NP 000246
Q005	0.020002	nuclear gene encoding mitochondrial	14141_000233	113.133212	_000240
		protein, mRNA /cds=(77,2329)		****(**	
		/gb=NM_000255 /gi=4557766		ė.	1
•		/ug=Hs.155212 /len=2798	3.1		
6020	0.04883	cDNA FLJ37774 fis, clone BRHIP2026021,	AK095093	Hs.119533	
0020	0.04003	highly similar to Mus musculus formin	AKU95U93	ns.119555	
1		binding protein 30 mRNA. /gb=AK095093		** * *	- 00
الإ					
	0	/gi=21754285 /ug=Hs.119533 /len=2767			
cocó	0.000000		NIM 04445	11- 70000	ND OFFOCE
6069	0.003208	stress-associated endoplasmic reticulum	NM_014445	Hs.76698	NP_055260
	-	protein 1; ribosome associated membrane	0		
		protein 4 (SERP1), mRNA /cds=(316,516)			
		/gb=NM_014445 /gi=19923408		. (	
0070	0.000704	/ug=Hs.76698 /len=2488	1111		
6079	0.033724	extracellular matrix protein 2, female organ	NM_001393	Hs.35094	NP_001384
		and adipocyte specific (ECM2), mRNA			
		/cds=(74,2173) /gb=NM_001393			<b>1</b>
		/gi=4557542 /ug=Hs.35094 /len=3171			
6124	0.036386	prolyl endopeptidase (PREP), mRNA	NM_002726	Hs.86978	NP_002717
	1	/cds=(1,2133) /gb=NM_002726		-	
		/gi=20149544 /ug=Hs.86978 /len=2756			
6145	0.036386	replication factor C (activator 1) 2, 40kDa	NM_002914	Hs.139226	NP_002905
	4 &	(RFC2), mRNA /cds=(208,1272)			1
	-	/gb=NM_002914 /gi=4506486	*		<u>}</u>
		/ug=Hs.139226 /len=1709			· ·
6180	0.020932	mRNA for KIAA0774 protein, partial cds.	AB018317	Hs.22201	
		/cds=(1,3492) /gb=AB018317 /gi=3882268			
		/ug=Hs.22201 /len=4021	ſ	l '.	

		nding To Differentially Expr ssed Genes i			BAC
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Acc ssion	Accession
			No.	No.	No.
6231	0.040244	methylenetetrahydrofolate reductase	AF260233		
	<u> </u>	(MTHFR) gene, exon 11 and 3' UTR,		i	4.
		alternatively spliced			· ·
6268	0.014718	cDNA: FLJ22008 fis, clone HEP06934.	AK025661	Hs.193700	1
		/gb=AK025661 /gi=10438250		E ()	*
		/ug=Hs.193700 /len=2207	6.		*
6295	0.022722	Notch 2 (Drosophila) (NOTCH2), mRNA	NM_024408	Hs.8121	NP_077719
		/cds=(257,7672) /gb=NM_024408	<del>-</del>		
		/gi=24041034 /ug=Hs.8121 /len=11433		•	
6311	0.016261	peptidylprolyl isomerase A (cyclophilin A)	NM_021130	Hs.401787	NP 066953
00.,	0.010201	(PPIA), mRNA /cds=(45,542)	14111_021100	113.401707	111 _000333
		/gb=NM_021130 /gi=10863926			
		/ug=Hs.401787 /len=753			
6222	0.000603		VM 000EC2	- X = -X	
6322		ubiquitin specific protease 9 (USP9Y)	XM_000563	11 000404	
6408	0.04883	ir24c06.y1 HR85 islet cDNA clone	CA848700	Hs.389121	,
		IMAGE:6546227 5', mRNA sequence	ļ		
		/clone=IMAGE:6546227 /clone_end=5'	<i>t</i> (		
		/gb=CA848700 /gi=26999906		-	
		/ug=Hs.389121 /len=616		*	9.0
6410	0.007185	laminin, alpha 2 (merosin, congenital	NM_000426	Hs.75279	NP_000417
	:	muscular dystrophy) (LAMA2), mRNA	*		
		/cds=(50,9382) /gb=NM_000426			
• •		/gi=4557708 /ug=Hs.75279 /len=9534			
6411	0.042232	tubulin, gamma complex associated protein	NM_006322	Hs.9884	NP_006313
		3 (TUBGCP3), mRNA /cds=(85,2808)	_		
	00	/gb=NM_006322 /gi=5453659 /ug=Hs.9884			
	*	/len=3795	•	. 54 (	*
6415	0.00259	chromosome 20 open reading frame 36	NM 018257	Hs.184628	NP_060727
		(C20orf36), mRNA /cds=(128,1213)	T 7	, ,	· · · · · · · · · · · · · · · · · · ·
		/gb=NM_018257 /gi=8922738			
		/ug=Hs.184628 /len=3655		·	
6416	0.019262	MAD, mothers against decapentaplegic 5	NM_005903	Hs.37501	NP 005894
0110	0.010202	(Drosophila) (MADH5), mRNA	, · · · · · · · · · · · · · · · · · · ·	113.07001	1111 _00000
•		/cds=(193,1590) /gb=NM_005903			
		/gi=20070216 /ug=Hs.37501 /len=2049			
6485	0.003308	serologically defined colon cancer antigen 8	NM 006642	Hs.300642	NP 006633
0400	0.003200	(SDCCAG8), mRNA /cds=(1,2142)	14101_000042	IU2:200045	INF_000033
•			,		
	ļ	/gb=NM_006642 /gi=28269671		ļ	
CEOE	0.045400	/ug=Hs.300642 /len=2142	D0047500	75404	
6535	0.045433	Similar to cerebellar degeneration-related	BC017503	Hs.75124	*()
		2, clone MGC:23119 IMAGE:4873337,		-	
		mRNA, complete cds /cds=(324,1655)	. 967		Θ.
		/gb=BC017503 /gi=17028382			
		/ug=Hs.75124 /len=2713			
6564	0.022722	mitogen-activated protein kinase 1	NM_002745	Hs.324473	NP_620407
		(MAPK1), transcript variant 1, mRNA			
		/cds=(241,1323) /gb=NM_002745			
	I	/gi=20986528 /ug=Hs.324473 /len=2934	·		]

		nding To Differentially Expressed Genes i				
Spot p-value	p-value	ue Description	Gene	Unigen	Protein	
•	- 1	· · · · · · · · · · · · · · · · · · ·	Accession	Accession	Accession	
			No.	No.	No.	
6582	0.028884	mRNA for KIAA1028 protein, partial cds.	AB028951	Hs.129836	NP_055891	
		/cds=(1,1506) /gb=AB028951				
,		/gi=20521737 /ug=Hs.129836 /len=6063				
5591	0.036386	ribonuclease, RNase A family, 4	NM_002937	Hs.283749	NP_002928	
		(RNASE4), mRNA /cds=(173,616)		·		
		/gb=NM_002937 /gi=20070170				
		/ug=Hs.283749 /len=1414				
3594	0.039219	lactate dehydrogenase A (LDHA), mRNA	NM_005566	Hs.2795	NP_005557	
		/cds=(98,1096) /gb=NM_005566				
		/gi=5031856 /ug=Hs.2795 /len=1661				
650	0.04883	tetratricopeptide repeat domain 1 (TTC1),	NM_003314	Hs.7733	NP_003305	
		mRNA /cds=(51,929) /gb=NM_003314				
		/gi=4507710 /ug=Hs.7733 /len=1407				
6661	0.033724	stromal antigen 1 (STAG1), mRNA	NM_005862	Hs.286148	NP_005853	
		/cds=(401,4177) /gb=NM_005862		.*.	1	
		/gi=5032062 /ug=Hs.286148 /len=4337				
6691	0.04883	runt-related transcription factor 3 (RUNX3),	NM_004350	Hs.170019	NP_004341	
	**	mRNA /cds=(10,1257) /gb=NM_004350				
		/gi=4757917 /ug=Hs.170019 /len=3809		}		
			-			
693	0.014917	PHD finger protein 1 (PHF1), transcript	NM_024165	Hs.166204	NP_077084	
		variant 2, mRNA /cds=(216,1919)			l	
	.*	/gb=NM_024165 /gi=13435396				
		/ug=Hs.166204 /len=2260				
5711	0.031226	FXYD domain containing ion transport	NM_022003	Hs.3807	NP_071286	
		regulator 6 (FXYD6), mRNA /cds=(67,354)				
		/gb=NM_022003 /gi=11612654		}		
	;	/ug=Hs.3807 /len=1677				
728	0.004381	Kelch-like ECH-associated protein 1	NM_012289	Hs.57729	NP_036421	
		(KEAP1), mRNA /cds=(113,1987)	X	1	{	
		/gb=NM_012289 /gi=22027641	·			
		/ug=Hs.57729 /len=2513				
3734	0.028884	PAI-1 mRNA-binding protein (PAI-RBP1),	NM_015640	Hs.165998	NP_056455	
		mRNA /cds=(86,1249) /gb=NM_015640				
		/gi=7661625 /ug=Hs.165998 /len=2201	141		7	
735	0.007185	DKFZp586J021 (from clone	AL110197	Hs.6441	NP_003246	
		DKFZp586J021) /cds=UNKNOWN				
		/gb=AL110197 /gi=5817115 /ug=Hs.6441		}	-0.0	
		/len=1896		4 29		
3748	0.04883	UI-E-DX1-agw-i-20-0-UI r1 UI-E-DX1 cDNA	BM698866	Hs.356089		
	-	clone UI-E-DX1-agw-i-20-0-UI 5', mRNA			1	
		sequence /clone=UI-E-DX1-agw-i-20-0-UI	1			
		/clone_end=5' /gb=BM698866	1		ì	
		/gi=19012124 /ug=Hs.356089 /len=1231	·		(	
3758	0.008683	proteasome (prosome, macropain) 26S	NM_002803	Hs.61153	NP_002794	
		subunit, ATPase, 2 (PSMC2), mRNA	_			
•		/cds=(71,1372) /gb=NM_002803				
	1	/gi=24430152 /ug=Hs.61153 /len=1545	1	1	1	

		nding To Differentially Expressed Gen s i				
Spot	p-value	Description	Gene	Unigene	Protein	
			Accession	Accession	Acc ssion	
			No.	No	No.	
6769	0.031226	mRNA; cDNA DKFZp434E033 (from clone	AL080130	Hs.15740		
		DKFZp434E033) /gb=AL080130	: .			
		/gi=5262569 /ug=Hs.15740 /len=3990				
6795	0.039219	KIAA0438 gene product (KIAA0438),	NM_014819	Hs.279849	NP_055634	
		mRNA /cds=(118,2244) /gb=NM_014819	_			
		/gi=7662123 /ug=Hs.279849 /len=4765				
6813	0.00953	constitutive photomorphogenic protein	NM_022457	Hs.105737	NP_071902	
		(COP1), mRNA /cds=(1,2196)		,	-	
		/gb=NM 022457 /gi=21359962				
		/ug=Hs.105737 /len=2196			- ;	
6828	0.042232	proteasome (prosome, macropain) 26S	NM 002814	Hs.433559	NP 736606	
1	0.012202	subunit, non-ATPase, 10 (PSMD10),	7	110.40000		
		mRNA /cds=(99,779) /gb=NM_002814				
		/gi=4506216 /ug=Hs.433559 /len=1544				
6840	. 0 04883	FK506 binding protein 7 (FKBP7), mRNA	NM 016105	Hs.344379	NP_851939	
0040	0.04000	/cds=(96,875) /gb=NM_016105	1444_010100	1113.044070	141 _001000	
		/gi=23618828 /ug=Hs.344379 /len=1067				
6842	0.04883	protein phosphatase 1, regulatory (inhibitor)	NIM 002480	Hs.16533	NP_002471	
00-2	0.04803	subunit 12A (PPP1R12A), mRNA	11111_002400	118.10333	NF_00247 1	
	-	/cds=(1,3093) /gb=NM 002480		1	1	
		/gi=4505316 /ug=Hs.16533 /len=4613	ľ			
6861	0.010262		AL096752	Hs.306327	<del> </del>	
0001	0.019202	DKFZp434A012) /gb=AL096752	AL090732	JUS.20027		
		, -				
6863	0.00000	/gi=5419888 /ug=Hs.306327 /len=2248 Sm protein F (LSM6), mRNA /cds=(82,324)	NIM 007090	Ho 42429	ND 000011	
0003	0.000003		NN	Hs.42438	NP_009011	
	· · · · · · · · · · · · · · · · · · ·	/gb=NM_007080 /gi=5901997		i i	İ	
COEO	0.00004	/ug=Hs.42438 /len=596	NIM COSESS	H= 462420	ND 000544	
6958	0.028884	origin recognition complex, subunit 5-like	NM_002553	Hs.153138	NP_002544	
		(yeast) (ORC5L), mRNA /cds=(89,1396)	· ·			
•		/gb=NM_002553 /gi=4505524	4		1	
0007	0.000504	/ug=Hs.153138 /len=1901	1114 000000	11. 074000	110 00000	
6987	0.003564	carnitine palmitoyltransferase II (CPT2),	NM_000098	Hs.274336	NP_000089	
		nuclear gene encoding mitochondrial	-	1		
	1	protein, mRNA /cds=(517,2493)				
		/gb=NM_000098./gi=4503022				
	8 212211	/ug=Hs.274336 /len=3090		111 1		
7019	0.012511	hypothetical protein MGC10986	NM_030576	Hs.50601	NP_085053	
		(MGC10986), mRNA /cds=(145,528)				
ţ		/gb=NM_030576 /gi=22095372	ļ		_	
		/ug=Hs.50601 /len=3178		111		
7040	0.004381	PAK2 mRNA, complete cds	AF092132	Hs.284275		
		/cds=(218,1840) /gb=AF092132				
		/gi=5138913 /ug=Hs.284275 /len=4137				
7105		PRO0657	AAF24054			
7142	0.007185	eukaryotic translation elongation factor 1	NM_001402	Hs.422118	NP_001393	
	}	alpha 1 (EEF1A1), mRNA /cds=(63,1451)	}	1		
	1	/gb=NM_001402 /gi=25453469	l		-30	
	I	/ug=Hs.422118 /len=1837	1			

Genes	Correspo	nding To Differentially Expressed Genes	in Figure 14 - D	iabetes	
Spot	p-value	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
	"	(0.000)	No.	No.	No
7203	0.031226	KIAA1036 protein (KIAA1036), mRNA	NM_014909	Hs.155182	NP_055724
-		/cds=(386,1483) /gb=NM_014909			_
	·	/gi=7662453 /ug=Hs.155182 /len=5481			
7205	0.045433	ribosomal protein S20 (RPS20), mRNA	NM 001023	Hs.8102	NP 001014
		/cds=(128,487) /gb=NM 001023	00,020	1.0.0102	700,000
		/gi=14591915 /ug=Hs.8102 /len=539			*
7206	0.031226	hypothetical protein FLJ13081 (FLJ13081),	NM_024834	Hs.180638	NP 079110
, 200	0.001220	mRNA /cds=(171,2099) /gb=NM_024834	J. 1101 - 02 - 00 - 1	113.100000	141 _0/0/10
	. 1	/gi=13376242 /ug=Hs.180638 /len=4113	t the same	- 1	* •
		1007024274g=113.10003071611=41113			
7222	0.045433	REV3-like, catalytic subunit of DNA	NM_002912	Hs.115521	NP_002903
,	0.040100	polymerase zeta (yeast) (REV3L), mRNA	14141_002012.	1 (3, 1 (332 )	141 _002303
	. '	/cds=(823,9981) /gb=NM 002912	•		
		/gi=4506482 /ug=Hs.115521 /len=10919			<b></b>
7231	0.04883	clone MGC:29744 IMAGE:3347567,	BC021250	Hs.29645	NP 612373
1201	0.04003	mRNA, complete cds /cds=(1622,2545)	PC02 1230	115.23045	NF_0123/3
		/gb=BC021250 /gi=20987353	*		
,	, :	/ug=Hs.29645 /len=2712		•	
7264	0.007003	RNA polymerase I transcription factor	NM 018427	He 110102	ND 060907
1204	0.007903		NIVI_U 10427	Hs.110103	NP_060897
		RRN3 (RRN3), mRNA /cds=(23,1978)	2.75		4
		/gb=NM_018427 /gi=21361630			
7004	0.000004	/ug=Hs.110103 /len=3756	NINA 000400	11. 00040	110 004577
7284	0.028884	GK003 protein (GK003), mRNA	NM_020192	Hs.83313	NP_064577
		/cds=(10,690) /gb=NM_020192			*
7004	0.005750	/gi=21281666 /ug=Hs.83313 /len=901	1.500000	11 15-12	115 2522
7294	0.005753	mRNA for KIAA0823 protein, partial cds.	AB020630	Hs.45719	NP_056383
		/cds=(157,1893) /gb=AB020630	- A		
70.15	2 2 2 2 2 2 2	/gi=20521667 /ug=Hs.45719 /len=6250	1		
7315	0.036386	Hypothetical protein(cDNA: FLJ20994 fis,	AK024647		* *
	· · · · · · · · · · · · · · · · · · ·	clone CAE02453)			
7323	0.045433	mRNA for KIAA1327 protein, partial cds.	AB037748	Hs.106204	
	5-	/cds=(1,5417) /gb=AB037748		e ,	.:
		/gi=20521883 /ug=Hs.106204 /len=6687			
7324	0.020932	angiopoietin-like factor (CDT6), mRNA	NM_021146	Hs.146559	NP_066969
•		/cds=(240,1280) /gb=NM_021146			
		/gi=20127595 /ug=Hs.146559 /len=2255			
7340	0.036386	DKFZp586H2223 (from clone	AL117550		NP_057140
į.		DKFZp586H2223)			
7342	0.006524	KIAA0874 protein (KIAA0874), mRNA	NM_015208	Hs.27973	NP_056023
		/cds=(1,6189) /gb=NM_015208			8
	,	/gi=14140237 /ug=Hs.27973 /len=6189			
7368	0.022722	NADH-ubiquinone oxidoreductase subunit	NM_175614	Hs.406062	NP_783313
		B14.7 (NDUFA11), mRNA /cds=(1,426)	· .	7.1	•
	ļ	/gb=NM_175614 /gi=28269680	, , ,		
		/ug=Hs.406062 /len=426			
7372	0.036386	mRNA; cDNA DKFZp727I051 (from clone	AL117478	Hs.239370	NP_056412
•		DKFZp727l051); partial cds /cds=(1,2099)			_
	1	/gb=AL117478 /gi=5911952	1		= .
	1	/ug=Hs.239370 /len=2480	I	1 .	

		nding To Differentially Expressed Gen s i			Drotein
Spot	p-value	,	Gene	Unigene	Protein
			Accession	Accession	Accession
*.			No.	No.	No.
7385	0.013668	v-maf musculoaponeurotic fibrosarcoma	NM_005360	Hs.30250	NP_00535
		oncogene (avian) (MAF), mRNA			
	. ·	/cds=(808,2019) /gb=NM 005360	,		13.
	]	/gi=5453735 /ug=Hs.30250 /len=2145			
7392	0.028884	cDNA FLJ30250 fis, clone	AK054812	Hs.318977	
7002	0.020004	BRACE2002304. /gb=AK054812	17-11(00-1012	11,9.010977	1
*	]	/gi=16549424 /ug=Hs.318977 /len=2148			1
7422	0.000500		A DO 40700	115.40000	ND 00000
7433	0.008522	KIAA1579 protein, partial cds	AB046799	Hs.49933	NP_06068
	· · · · ·	/cds=UNKNOWN /gb=AB046799	* *		
		/gi=10047232 /ug=Hs.49933 /len=4352		00	1
		(=FLJ25300)			
7436	0.033724	hypothetical protein GL009 (GL009),	NM_032492	Hs.24054	NP_11588
		mRNA /cds=(78,629) /gb=NM_032492			
		/gi=14210501 /ug=Hs.24054 /len=1097		*	
7456	0.019262	lysyl-tRNA synthetase (KARS), mRNA	NM 005548	Hs.3100	NP_00553
		/cds=(41,1834) /gb=NM_005548		* * * * * * * * * * * * * * * * * * * *	-1
•	· ·	/gi=5031814 /ug=Hs.3100 /len=1997	1		
7466	0.031226	ret finger protein (RFP), transcript variant	NM 006510	Hs.142653	NP 11221
7400	0.031220	alpha, mRNA /cds=(359,1900)	114141_000210	1115. 142000	NF_! 122 1
	-			,	
		/gb=NM_006510 /gi=17105396	··-	` ` ·	1
		/ug=Hs.142653 /len=2984			
7520	0.010447	hypothetical protein FLJ10350 (FLJ10350),	NM_018067	Hs.177596	NP_06053
		mRNA /cds=(676,2340) /gb=NM_018067			
	· . ·	/gi=21361780 /ug=Hs.177596 /len=2811		ì	1
7536	0.039219	inhibitor of growth family, member 1	NM_005537	Hs.46700	NP 00552
		(ING1), mRNA /cds=(433,1701)		70	
1.4		/gb=NM_005537 /gi=19923770	.x. 0		
		/ug=Hs.46700 /len=2886		T.	
7554	0.028884	mRNA IRO40627 full length insert cDNA	AL109779	+	NP_07537
7004	0.020004	clone EUROIMAGE 40627	ALIOSTIS	•	_0,33,
7501	0.047700		NINA 045740	115 404007	ND OFCEO
7591	0.017708	glioma tumor suppressor candidate region	NM_015710	Hs.421907	NP_05652
÷	· ·	gene 2 (GLTSCR2), mRNA /cds=(53,1489)			
٠.	1	/gb=NM_015710 /gi=21359905			
		/ug=Hs.421907 /len=1610			
7635	0.026691	RAB4A, member RAS oncogene family	NM_004578	Hs.119007	NP_00456
	<b>,</b>	(RAB4A), mRNA /cds=(209,865)			
		/gb=NM_004578 /gi=19923259	*		
		/ug=Hs.119007 /len=1861	•		
7663	0.045433	cDNA FLJ10131 fis, clone	AK000993	Hs.274128	
, 000	1 0.0 10 100	HEMBA1003041. /gb=AK000993	,	1.0.2.7.7.20	}.
	,	/gi=7021996 /ug=Hs 274128 /len=2065		÷ *	
7666	0.010447		AK024164	Hs.301811	+
1000	0.010447	FLJ14102 fis, clone MAMMA1000940	ANUZ4 104	Lu8.301011	7
	<b>.</b> .	/cds=UNKNOWN /gb=AK024164	1	1	1
		/gi=10436477 /ug=Hs.301811 /len=1878		<b>_</b>	<del> </del>
7673	0.036386	hypothetical protein FLJ10970 (FLJ10970),	NM_018286	Hs.173233	NP_06075
		mRNA /cds=(229,633) /gb=NM_018286			
		/gi=8922795 /ug=Hs.173233 /len=1670			4
	1				- "

		nding To Differentially Expressed Genes i				
Spot	p-valu	•	Gene	Unigene	Protein Accession	
			Accession	Accession		
			No	No.	No.	
7685	0.022773	lymphocyte antigen 75 (LY75), mRNA	NM_002349	Hs 153563	NP_00234	
1-,		/cds=(54,5222) /gb=NM_002349		•		
	·	/gi=4505052 /ug=Hs.153563 /len=6928				
7699	0.028884	mRNA full length insert cDNA clone	AL109691	Hs.306330		
		EUROIMAGE 239714. /gb=AL109691			W	
		/gi=5689821 /ug=Hs.306330 /len=1453			*	
7710	0.039719	cDNA: FLJ21531 fis, clone COL06036.	AK025184	Hs.102941	1 % - 1 . X 1	
		/gb=AK025184 /gi=10437647			,	
		/ug=Hs.102941 /len=2671				
7716	0.019262	IFNAR gene (HSIFNAR) for interferon	X60459			
	0.010202	alpha/beta receptor	7.00 100			
7727	0.031226	hypothetical protein FLJ13081 (FLJ13081),	NM_024834	Hs.180638	NP 07911	
1121	0.001220	mRNA /cds=(171,2099) /gb=NM_024834	14141_02-100-1	113.100030	_0/3//	
		/gi=13376242 /ug=Hs.180638 /len=4113			• • •	
	1 .	1/gi- 15570242 /dg-115. 100050 /ieii-4 115.				
7839	0.020004	EST(xc43h04.x1 NCl_CGAP_Co20 clone	AW081723	4 - 4	NP 00325	
1039	0.020004		AVV001723		INP_00323	
	}	IMAGE:2587063 3' gb:M99436	**			
	· ,	TRANSDUCIN-LIKE ENHANCER				
70 40	0.00000	PROTEIN 2)	41004040			
7843	0.036386	EST(qu23h09.x1 NCI_CGAP_Br12 clone	AI284640			
	-	IMAGE:1965665 contains Alu repeat)		100 122 7 727		
7871.	0.011439	clone IMAGE:5267224, mRNA	BC045644	Hs.425116		
		/gb=BC045644 /gi=28279007		-00 ·	. *	
		/ug=Hs.425116 /len=4064		ļ.,		
7876	0.013668	BBP-like protein 1 (BLP1), transcript variant	NM_031940	Hs.7471	NP_51088	
		2, mRNA /cds=(47,304) /gb=NM_031940		•		
		/gi=17865794 /ug=Hs.7471 /len=1628	1 3 × 1		<u>.</u>	
			* 2			
7893	0.011439	EST(ba58h09.x1 NIH_MGC_10 clone	AW673893		NP_00514	
	7.	IMAGE:2900801 3')				
7895	0.031226	EST(zw54g08.r1	AA463590			
		Soares_total_fetus_Nb2HF8_9w clone			·	
	•	IMAGE:773918 5' contains Alu and MER22				
		repeat)				
7925	0.026691	EST(ng19d12.s1 NCI CGAP Lip2 cDNA	AA501823			
		clone IMAGE:929879 similar to contains			*	
		Alu repetitive element, contains element	20		1	
		MSR1 repetitive element)	N			
7931	0.036386	EST (nq43g05.s1 NCI_CGAP_Co10 cDNA	AA622008	1-1	NP 00292	
		clone IMAGE:1146680 3' similar to	1022000	*		
		gb:D26129 RIBONUCLEASE	÷ 5			
	1	PANCREATIC PRECURSOR)	*	2		
7933	0.012511	DKFZP564O1863 protein	NM_015633	Hs.406184	NP 05644	
, 500	0.012311	(DKFZP564O1863), mRNA	14141 0 15035	119.400104	NE_05044	
				*		
	1	/cds=(343,1104) /gb=NM_015633		*	-	
	1	/gi=24308110 /ug=Hs 406184 /len=2306	L .	· .	l	

		nding To Differentially Expressed Genes i			
Spot	p-value	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
7938	0.04883	UI-H-EU1-bai-b-07-0-UI.s1	BQ448117	Hs.8705	
		NCI CGAP_Ct1 cDNA clone UI-H-EU1-bai-	9		
		b-07-0-UI 3', mRNA sequence /clone=UI-H-			, y
•		EU1-bai-b-07-0-UI /clone_end=3'			i i
		/gb=BQ448117 /gi=21251229 /ug=Hs.8705			
	- '	/len=1171			i .
7939	0.012511	EST (IL-BT003-221198-003 BT003)	AI902209		- IA
7949		hypothetical protein PR01094 (PR01094),	NM_018575		
	1.	mRNA	11111_010070		
7955	0.026691	cDNA FLJ34394 fis, clone	AK091713	Hs.378859	
7 3 3 3	0.020031	HCHON2000676. /gb=AK091713	711051715	113.070000	
		/gi=21750150 /ug=Hs.378859 /len=1932			
7961	0.045433	FtsJ 2 (E. coli) (FTSJ2), mRNA	NM 013393	Hs.279877	NP 803191
1 90 1	0.040400	/cds=(30,770) /gb=NM_013393	11111 0 13383	113.2/30//	145 2003 191
				1	
7065	0.005040	/gi=7019376 /ug=Hs.279877 /len=1605	NIM 020440	Un 202527	ND 445404
7965	0.005916	hypothetical protein FLJ12953 similar to	NM_032118	Hs.323537	NP_115494
		Mus musculus D3Mm3e (FLJ12953),	× 1		
		mRNA /cds=(89,1093) /gb=NM_032118	*		
====		/gi=14149770 /ug=Hs.323537 /len=1146		10000	115 005000
7983	0.028884	proteasome (prosome, macropain) 26S	NM_005047	Hs.193725	NP_005038
. (		subunit, non-ATPase, 5 (PSMD5), mRNA			-
		/cds=(20,1534) /gb=NM_005047			· ,
		/gi=25777613 /ug=Hs.193725 /len=3411			<u> </u>
8020	0.012511	phosphoribosylglycinamide	NM_000819	Hs.82285	NP_780294
		formyltransferase,		,	
		phosphoribosylglycinamide synthetase,	1	- 3-	
		phosphoribosylaminoimidazole synthetase		10°	
		(GART), mRNA /cds=(79,3111)			0
	**	/gb=NM_000819 /gi=24475881			P P
		/ug=Hs.82285 /len=3291			
8054	0.04883	pyruvate dehydrogenase kinase 4 mRNA,	AF334710	Hs.8364	NP_002603
* ' '		3' untranslated region, partial sequence			
	-	/cds=UNKNOWN/gb=AF334710		* :	
	*	/gi=12658438 /ug=Hs.8364 /len=1819		20	- Y
8056	0.003954	ADP-ribosyltransferase (NAD; poly (ADP-	NM_001618	Hs.177766	NP_001609
		ribose) polymerase) (ADPRT), mRNA	_		
		/cds=(160,3204) /gb=NM_001618			1
	6	/gi=11496989 /ug=Hs.177766 /len=3859	,	*	
8059	0.04883	myotubularin related protein 2 (MTMR2),	NM_016156	Hs.181326	NP 057240
		mRNA /cds=(342,2273) /gb=NM_016156			
		/gi=20357517 /ug=Hs.181326 /len=4681		,	,
8068	0.012511	hypothetical protein FLJ10726 (FLJ10726),	NM_018195	Hs.268561	NP_060665
	3.312011	mRNA /cds=(176,622) /gb=NM_018195		10.20001	
	i	/gi=8922622 /ug=Hs.268561 /len=2800			10
8070	0.033724	similar to lung type-I cell membrane-	XM 048883	<del>                                     </del>	
OULU	0.000124	associated glycoprotein, isoform 2	VINI_040002		
	·		**		
		precursor; hT1a-1; hT1alpha-1; hT1alpha-2	w · · _ =		1
	1	(H. sapiens) (LOC126756), mRNA	I		

		nding To Differentially Expressed Genes i	n Figure 14 - D	liabet s	
Spot	p-value	Description	Gene	Unigene	Protein
		Acc ssion	Accession	Accession	
		30	No.	No.	No
8095	0.003954	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM_004728	Hs.169531	NP_004719
		polypeptide 21 (DDX21), mRNA		1	-
	Ì	/cds=(266,2413) /gb=NM_004728	ļ	Į.	1
	1	/gi=13787208 /ug=Hs.169531 /len=3319			0
8114	0.019262	URB mRNA, complete cds	AF506819	Hs.356289	
		/cds=(146,2998) /gb=AF506819			
		/gi=21039408 /ug=Hs.356289 /len=3320			
8115	0.014917	STRIN protein (STRIN), mRNA	NM_016271	Hs.180403	NP_057355
		/cds=(100,837) /gb=NM_016271			-
		/gi=21361538 /ug=Hs.180403 /len=3226			·
8116	0.011439	hypothetical protein FLJ21616 (FLJ21616),	NM 024567	Hs.23590	NP 078843
	i e	mRNA /cds=(120,1094) /gb=NM_024567	7		
-	. "	/gi=13375737 /ug=Hs 23590 /len=1858		· .	
8147	0.013668	hypothetical protein FLJ20003 (FLJ20003),	NM 017615	Hs.258798	NP_060085
		mRNA /cds=(31,1188) /gb=NM_017615	_		
	1	/gi=8923008 /ug=Hs.258798 /len=1387		*	
					1
8152	0.04883	COP9 constitutive photomorphogenic	NM_006837	Hs.380969	NP_006828
		subunit 5 (Arabidopsis) (COPS5), mRNA		,	<del>-</del>
	*	/cds=(121,1125) /gb=NM_006837	1.	•	
		/gi=5803045 /ug=Hs.380969 /len=1277			
8186	0.028884	Arkadia (ARK), mRNA /cds=(374,1486)	NM_017610	Hs.12504	NP_060080
-		/gb=NM_017610 /gi=24111229		1	,
·		/ug=Hs.12504 /len=3010			
8194	0.00953	mRNA for KIAA0876 protein, partial cds.	AB020683	Hs.301011	
		/cds=(150,3509) /gb=AB020683			1
		/gi=14133222 /ug=Hs.301011 /len=5595			
8198	0.022722	PHD zinc finger protein XAP135 (XAP135),	NM_133325	Hs.7759	NP_579866
		transcript variant 2, mRNA /cds=(222,1448)			
		/gb=NM_133325 /gi=19747275	. *		
	,	/ug=Hs.7759 /len=1583	•		*
8271	0.004381	EST (RC3-OT0091-170300-011-c12	AW887541		
		OT0091)			*
8296	0.045433	EST(zk44a11.r1 Soares pregnant uterus	AA040238		NP_057250
		NbHPU clone 485660 5')			
8308	0.014917	EST(ty24e09.x1 NCI_CGAP_Ut3 clone	AI758800		
		IMAGE:2280040 3' contains Alu repeat)			4
8337	0.045433	EST382184 MAGE resequences, MAGK	AW970103		
`		H.sapiens cDNA			
8340	0.026836	hypothetical protein MGC5306 (MGC5306),	NM_024116	Hs.301732	NP_077021
		mRNA /cds=(207,1043) /gb=NM_024116		·	, :
	1	/gi=13129135 /ug=Hs.301732 /len=2336		-)(- *	
	1		*		

		nding To Differentially Expressed Gen s			Dent-
Spot	p-value		Gene	Unigene	Protein
		4	Accession	Accession	Accession
		× × × × × × × × × × × × × × × × × × ×	No.	No.	No.
8346	0.022722	UI-H-BW1-and-h-10-0-UI.s1	BF514341	Hs.445663	
		NCI_CGAP_Sub7 cDNA clone	1		
		IMAGE:3082218 3', mRNA sequence			
		/clone=IMAGE:3082218 /clone end=3'			ĺ .
		/gb=BF514341 /gi=11599520		* *	
		/ug=Hs.445663 /len=613	· .		,
8375	0.04883	EST (oz69d09.x1	AI148288		
		Soares_senescent_fibroblasts_NbHSF	1		Ĭ
1		IMAGE:1680593 3')		·	
8395	0.008683	EST xp73h11.x1 NCI_CGAP_Ov40 cDNA	AW270457	<del> </del>	<del></del>
0393	0.000003	clone IMAGE:2746053 3' similar to	AVV210431		. 00
	١.			. 59	
٠	<b>[</b> .	contains Alu repetitive element; contains			
		element MER32 repetitive element;	11/20/20/20		
8404	0.013668	Hypothetical protein(cDNA sequence	AK001911	10.	NP_06587
		FLJ11049 fis, clone PLACE1004548)			
8420	0.036386	hypothetical protein FLJ10774 (FLJ10774),	NM_024662	Hs.71472	NP_07893
		mRNA /cds=(207,3284) /gb=NM_024662	,		
		/gi=13399321 /ug=Hs.71472 /len=4002			
			- (	·	
8432	0.012511	EST 7f59d09.x1	BE677740		24 24 24
-		Soares_NSF_F8_9W_OT_PA_P_S1			
		H.sapiens cDNA clone IMAGE:3298961 3'	:		5.
	1 `				
8436	0.016261	EST 7e76f05.x1 NCI_CGAP_Pr28 cDNA	BE645808		NP_06510
0-100	0.010201	clone IMAGE:3288417 3' similar to	DE0-10000		
		contains element MER36 repetitive			*
		element;	,		
8440	0.002054		NM_003663	Hs.86041	NP 00365
0440	0.003954	CGG triplet repeat binding protein 1	NN_003003	лs.0004 I	INP_00365
	*	(CGGBP1), mRNA /cds=(357,863)			
		/gb=NM_003663 /gi=21361098			s. 8
		/ug=Hs.86041 /len=4279		·	•
8450	0.031226	skeletal muscle HSB84A051	Z28721	*	
		STRATAGENE cDNA library, cat. #936215.			*
	. *	cDNA clone 84A05			
8451	0.020932	EST (PM1-HT0422-170100-005-c12	BE160711		
	*	HT0422)			
8458	0.042232	cDNA FLJ35666 fis, clone SPLEN2017781.	AK092985	Hs.233382	
		/gb=AK092985\/gi=21751702			
•		/ug=Hs.233382 /len=2153			Ì
8481	0.04883	yg34g10.s1 Soares infant brain 1NIB cDNA	R44308	Hs.242302	
0,401	0.04000	clone IMAGE:34476 3' similar to	11144300	113.242002	1
	' '	* 0		*	
		gb M87924 HUMALCE162 carcinoma cell-			* .
	:	derived Alu RNA transcript, (rRNA);	•		
		gb:M32315 TUMOR NECROSIS FACTOR			
		RECEPTOR 2 PRECURSOR mRNA			
		sequence /clone=IMAGE:34476	1		
		/clone_end=3' /gb=R44308 /gi=821279		1'	
	1	/ug=Hs.242302 /len=557	1		1

		nding To Differentially Expressed Genes i			<u></u>
Spot	p-value	Description	G n	Unigene	Protein
, .	•	, * <sub>X</sub>	Accession	Accession	Accession
			No	No.	No.
8500	0.045433	EST375644 MAGE resequences, MAGH	AW963571	Hs.182962	Va
		cDNA, mRNA sequence /gb=AW963571		*	
- 1		/gi=8153407 /ug=Hs.182962 /len=672			
8548	0.045433	EST (RC1-BN0413-041000-021-a09	BF748890		1 1 1
0,040	0.040400	BN0413)	DI 740000		, .
OFCC	0.040447	UI-H-BI1-aex-h-12-0-UI.s1	A1A/205452	LIS FORCE	**
8566	0.010447		AW205453	Hs.59368	
	* * * * * * * * * * * * * * * * * * * *	NCI_CGAP_Sub3 cDNA clone			
		IMAGE:2720903 3', mRNA sequence			* *
-		/clone=IMAGE:2720903 /clone_end=3'			
	• .	/gb=AW205453 /gi=6504925 /ug=Hs.59368			
· .		/len=665			
8569	0.039719	URB mRNA, complete cds	AF506819	Hs.356289	
		/cds=(146,2998) /gb=AF506819			•
	· · · · ·	/gi=21039408 /ug=Hs 356289 /len=3320			
8586	0.045433	UPF3 regulator of nonsense transcripts A	NM_023011	Hs.399740	NP 542418
		(yeast) (UPF3A), transcript variant 1,		200	
٠.		mRNA /cds=(38,1468) /gb=NM 023011		÷	
		/gi=18375523 /ug=Hs.399740 /len=2381			
0503	0.026296		CA392625	Hs.389253	<del> </del>
8593	0.030300	cs26g08.y1 Retinal pigment	CA392023	IUS 209523	. **
		epithelium/choroid cDNA (Un-normalized,		<i>*</i>	1 .
	1-	unamplified): cs cDNA clone cs26g08 5',			
	ì .	mRNA sequence /clone=cs26g08			
		/clone_end=5' /gb=CA392625			
	- 1	/gi=24725520 /ug=Hs.389253 /len=648			<u> </u>
8632	0.028884	cDNA clone IMAGE:4769918 5'	BG623330		NP_777568
8635	0.039219	ESTs, cDNA, 3' end /clone_end=3'	BI789108	Hs.304928	5.4
		/gb=BI789108 /gi=15816833	4		
		/ug=Hs.304928 /len=529	-	,	
8645	0.026691	cDNA FLJ37304 fis, clone	AK094623	Hs.249721	
	3.32333	BRAMY2016070. /gb=AK094623			. 👊 .
		/gi=21753716 /ug=Hs.249721 /len=2730	*		1
8647	0.04993	tm62d04.x1 NCI_CGAP_Brn25 cDNA	Al475033	Hs.36915	<del>                                     </del>
0047	0.04663		A1473033	118.30913	×
		clone IMAGE:2162695 3', mRNA sequence		-)(-	
•		/clone=IMAGE:2162695 /clone_end=3'			
	1	/gb=Al475033 /gi=4328078 /ug=Hs.36915			1.0
		/len=453		- 112	
8653	0.036386	EST, cDNA /clone=DKFZp586F2021	AL047579	Hs.310753	1
		/gb=AL047579 /gi=4728575			3.0
	·	/ug=Hs.310753 /len=431			
8660	0.045433	nk74h02.s1 NCI_CGAP_Sch1 cDNA clone	AA551072	Hs 368624	
		IMAGE:1019283 3' similar to contains Alu			1
	* .	repetitive element; contains element LTR5		1	
	***	repetitive element;, mRNA sequence			
10.11	7	/clone=IMAGE:1019283 /clone_end=3'			
	1.7	· · · · · · · · · · · · · · · · · · ·		1 .	1
4		/gb=AA551072 /gi=2321324 ,			
		/ug=Hs.368624 /len=477	-	1	<del> </del>
8699	0.039219	clone IMAGE:3909623, mRNA, partial cds	BC015894	Hs.33264	
	0	/cds=(1,178) /gb=BC015894 /gi=16198445			1
	1	/ug=Hs.33264 /len=2980	P.	1	1

		nding To Differentially Expressed Genes i			Ductoin
Spot	p-value	Description	G ne	Unigene	Protein
	f		Acc ssion	Accession	Accession
			No.	No.	No.
8719	0.008683	clone UWGC:y17c090 from 6p21,	AC004188		
	<u> </u>	complete sequence			1
8721	0.042232	UI-H-BI1-adn-e-07-0-UI.s1	AW136018	Hs.76704	
·		NCI_CGAP_Sub3 cDNA clone		. *	
		IMAGE:2717293 3', mRNA sequence		* *	·
		/clone=IMAGE:2717293 /clone_end=3'			
		/gb=AW136018 /gi=6140151 /ug=Hs.76704			
		/len=818		,	* *
8736	0.003421	clone RP11-45Q16, WORKING DRAFT	AC015641	1	* * ***
		SEQUENCE, 4 unordered pieces			1
8761	0.003954	UI-H-DT1-awb-g-11-0-UI.s1	BQ016101	Hs.438666	
		NCI_CGAP_DT1 cDNA clone		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
		IMAGE:5887138 3', mRNA sequence	*		
		/clone=IMAGE:5887138 /clone_end=3'			
		/gb=BQ016101 /gi=19751378			· .
		/ug=Hs.438666 /len=800		*	
8832	0.022722	yz39c12.s1 Morton Fetal Cochlea cDNA	N63237	Hs 269296	<del> </del>
00,52	0.022722	clone IMAGE:285430 3', mRNA sequence	1403237	113.203230	1
	ec 97	/clone=IMAGE:285430 /clone end=3'		1	
		/gb=N63237 /gi=1211066 /ug=Hs.269296			
000'5	0.004000	/len=444	4.0407000	y 2	
8835	0.031226	chromosome 4 clone RP11-731J8, ***	AC107398		* * * * * * * * * * * * * * * * * * * *
		SEQUENCING IN PROGRESS ***, 37	·		
		unordered pieces			<del> </del>
8917	0.026691	EST (hs96b03.x1 NCI_CGAP_Kid13	BE463624		
		IMAGE:3145037 3')			
8954	0.031491	nj20a07.s1 NCI_CGAP_AA1 cDNA clone	AA570674	Hs.162392	
		IMAGE:993012 3', mRNA sequence	* *		
		/clone=IMAGE:993012 /clone_end=3'			27
		/gb=AA570674 /gi=2344654	, .	-	-
		/ug=Hs.162392 /len=435	<u> </u>		
8955	0.039219		AK096708	Hs.120785	
		/gb=AK096708 /gi=21756262			*
		/ug=Hs.120785 /len=1350		·	
8962	0.024639	UI-H-BW0-ajq-g-03-0-UI.s1	AW298806	Hs.438211	2
		NCI_CGAP_Sub6 cDNA clone			
	1 1	IMAGE:2732740 3', mRNA sequence	ł	<b>\</b>	
* . *		/clone=IMAGE:2732740 /clone_end=3'			1
•		/gb=AW298806 /gi=6705442	* %		
		/ug=Hs.438211 /len=615		*	
8966	0.005035	EST (AV764100 MDS cDNA clone	AV764100		
		MDSBAE09 5')			
8969	0.039219	EST(AV730379 HTF cDNA clone	AV730379		1 10 10 1
5555	0.0002 10	HTFAAA05 5')	1.100070	¥	
8985	0.034630	EST (RC3-BT0316-270400-016-a02	BE065650		NP_0089
دېږي	0.024039	BT0316)	10500000		_0009
	<del></del>	[D10010] . /	·	1	<u> </u>

		nding To Differentially Expressed Genes i			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
9000	0.013668	hd05h05.y1 Retina cDNA (Un-normalized,	BQ636204	Hs.135613	*
	*	unamplified): hd/he cDNA clone hd05h05			
-		5', mRNA sequence /clone=hd05h05	*		
		/clone_end=5"/gb=BQ636204	` .*		
2.44		/gi=21760663 /ug=Hs.135613 /len=544			[
9011	0.042232	EST(yb62b08.r1 Stratagene ovary	T58561	, , ,	NP 002088
		(#937217) cDNA clone IMAGE:75735 5')			
9038	0.012511	protein phosphatase 1, regulatory (inhibitor)	NM 005398	Hs.303090	NP 005389
		subunit 3C (PPP1R3C), mRNA	7		_
		/cds=(58,1011) /gb=NM_005398	9		*
	7.	/gi=21314622 /ug=Hs.303090 /len=2524		1,11	
9041	0.007903	7140g01.x1	BF112131	Hs.288083	1:-
50-11	0.007500	Soares_NSF_F8_9W_OT_PA_P_S1 cDNA	5. 112101	113.20000	
		clone IMAGE:3524136 3', mRNA sequence			
-00		/clone=IMAGE:3524136 /clone_end=3'			
		/gb=BF112131 /gi=10941821	0		*
• •		7			
9054	0.000700	/ug=Hs.288083 /len=620 cDNA FLJ37995 fis, clone	AK095314	Hs.99624	
9054	J U.ŲZZ1ZZ		AKU90314	I	
		CTONG2011825, moderately similar to	r		
		CARBONIC ANHYDRASE (EC 4.2.1.1).	*	1	1
		/cds=(52,840) /gb=AK095314			,
2001	2 2 4 2 4 2	/gi=21754548 /ug=Hs.99624 /len=3564	41/00/1070	11 100105	
9061	0.014819	cDNA FLJ33960 fis, clone	AK091279	Hs.126465	
•		CTONG2018843. /gb=AK091279		** **	x *
		/gi=21749612 /ug=Hs.126465 /len=2849			
9107		EST(cDNA clone IMAGE:6102185 5'.)	BQ438639		
9143	0.031491	mRNA; cDNA DKFZp434N185 (from clone	AL117645	Hs.33032	NP_07948
		DKFZp434N185) /gb=AL117645		*.	
· ·	· .	/gi=5912235 /ug=Hs.33032 /len=1641			
9148	0.024639	DKFZp434M2216 (from clone	AL137295	Hs.199429	NP_004632
	<b>!</b>	DKFZp434M2216) /cds=UNKNOWN			Ţ
		/gb=AL137295 /gi=6807756		•	
		/ug=Hs.199429 /len=1035	* -		
9173	0.04883	EST381780 MAGE resequences, MAGK	AW969703	Hs.142074	
		cDNA, mRNA sequence /gb=AW969703	• :	0.1	
		/gi=8159547 /ug=Hs.142074 /len=651			*
9179	0.04883	UI-E-EJ1-ajf-o-07-0-UI.r1 UI-E-EJ1 cDNA	BM718282	Hs.439477	
		clone UI-E-EJ1-ajf-o-07-0-UI 5', mRNA			-
•	ł	sequence /clone=UI-E-EJ1-ajf-o-07-0-UI	•		* -
		/clone_end=5' /gb=BM718282	6	**	
	\ .	/gi=19036470 /ug=Hs.439477 /len=1095		· .	
9197	0.033724	EST(603060869F1 NIH MGC 122 cDNA	BI767635		NP 68960
5 101	3.300727	clone IMAGE:5210201 5')			
	0.031226	qf54h05.x1 Soares_testis NHT cDNA	Al198847	Hs.368422	. 100-
9100	T U.UU IZZU	I '		113.300422	
9199	1	ICIONO IVIDICE: I /E 1881 1. WOKIN COMPANY			
9199		clone IMAGE:1753881 3', mRNA sequence			
9199	,	/clone=IMAGE:1753881 /clone_end=3'			
9199					

		nding To Differentially Expr ssed Genes	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon		<u></u>
Spot	p-value	Description	Gene	Unigene	Protein
		* * "	Accession	Accession	Accession
			No.	No.	No.
9225	0.00953	UI-H-DT0-atx-c-08-0-UI.s1	BM992885	Hs.436581	
		NCI_CGAP_DT0 cDNA clone			<b>)</b>
		IMAGE:5865535 3', mRNA sequence	,	İ .	
		/clone=IMAGE:5865535 /clone end=3'	· .	1	
		/gb=BM992885 /gi=19712274			
		/ug=Hs.436581 /len=1301			
9230	0.022722	hn49c02.x1 NCI_CGAP_Co17 cDNA clone	AW770800	Hs.371969	
	]	IMAGE:3026978 3' similar to contains		10.07	
	1	MER5.b1 MER5 repetitive element;			
-		mRNA sequence /clone=IMAGE:3026978			
	Į.	/clone_end=3' /gb=AW770800 /gi=7702847			
9.11				-	
		/ug=Hs.371969 /len=463			
00.10	0.00000			<u> </u>	
9246	0.028884	EST(T-cells V Homo sapiens cDNA 5' end	AA355092	[:	
<u> </u>	a with a real	)			
9252	0.039219	cDNA FLJ31169 fis, clone KIDNE2000026	AK055731		
9255		EST(cDNA clone IMAGE:5248188 5')	BI915287		NP_079330
9257	0.008683	602246637F1 NIH_MGC_62 cDNA clone	BF690692	Hs.442332	
		IMAGE:4331985 5', mRNA sequence			
0.5		/clone=IMAGE:4331985 /clone_end=5'			
-		/gb=BF690692 /gi=11976100	٠.	(i)	
		/ug=Hs.442332 /len=929	· · · · · · · · · · · · · · · · · · ·		
9289	0.024639	UI-CF-EC1-abq-b-24-0-UI.s1 UI-CF-EC1	BM972502	Hs.366185	
		cDNA clone UI-CF-EC1-abq-b-24-0-UI 3',			
		mRNA sequence /clone=UI-CF-EC1-abq-b-			
• •		24-0-UI /clone_end=3' /gb=BM972502			.1
		/gi=19590088 /ug=Hs.366185 /len=718	• 1		1
9302	0.024639	No significant match, ORF-		*** ** ** ******	
3302	0.024039	1(1~102,214~317)	SEQ.ID.No.11	*	· .
9320	0.042232	No significant match	SEG.ID.NO.11		
9320	0.042232		SEO ID No 62		
0000	0.005040	(ORF:+1:208~366[159])	SEQ.ID.No.62	11- 044500	ND 005046
9383	0.005916	phosphoinositide-3-kinase, regulatory	NM_005027	Hs.211586	NP_005018
		subunit, polypeptide 2 (p85 beta) (PIK3R2),		v.*	
	,	mRNA /cds=(242,2428) /gb=NM_005027		*	•
,		/gi=4826907 /ug=Hs.211586 /len=3201			•
5'					
9385	0.011439	ATP-binding cassette, sub-family F	NM_001090	Hs.9573	NP_001081
		(GCN20), member 1 (ABCF1), mRNA	¥ ,	*.	
	(i)	/cds=(95,2518) /gb=NM_001090	1		
		/gi=10947134 /ug=Hs.9573 /len=3141	(4) (4)	·	34
9419	0.026691	cDNA FLJ36429 fis, clone	AK093748	Hs.378821	
		THYMU2011573. /gb=AK093748			1
•		/gi=21752675 /ug=Hs.378821 /len=1901			* .
9442	0.019262	GTP binding protein overexpressed in	NM_005261	Hs.79022	NP_005252
J-774	0.010202	skeletal muscle (GEM), mRNA	1.1101_000201		-000232
		/cds=(214,1104) /gb=NM_005261	]	1	
					1
	1	/gi=4885262 /ug=Hs.79022 /len=2156	<u> </u>	1	<u> </u>

		nding To Differentially Expressed Genes			Protein
Spot	p-valu	Description	Gene	Unigene	
		* *	Acc ssion	Accession	Accession
011101	0.00004		No.	No.	No.
9443	0.026691	synapse associated protein 1, SAP47	NM_032796	Hs.47334	NP_116185
	-	(Drosophila) (SYAP1), mRNA	• • •	ļ	
	i I	/cds=(94,1152) /gb=NM_032796			
-		/gi=19923854 /ug=Hs.47334 /len=2030			
9455	0.019262	likely ortholog of mouse tumor differentially	NM_020755	Hs.146668	NP_065806
		expressed 1, like (TDE1L), mRNA			<b>.</b>
•		/cds=(76,1437) /gb=NM_020755			
	4	/gi=24308212 /ug=Hs.146668 /len=3149			1
9457	0.004381	serine/threonine kinase 17a (apoptosis-	NM_004760	Hs.9075	NP_004751
		inducing) (STK17A), mRNA			*
		/cds=(118,1362) /gb=NM_004760	<b>!</b> .		
1		/gi=4758191 /ug=Hs.9075 /len=2641			
9490	0.013668	pleckstrin domain interacting protein	NM 017934	Hs.10177	NP_060404
		(PHIP), mRNA /cds=(306,2429)			
		/gb=NM_017934 /gi=20149647		1	
	-	/ug=Hs.10177 /len=2573			1
9510	0.039355	chromosome 3 open reading frame 4	NM_019895	Hs:107393	NP_063948
0010	0.000000	(C3orf4), mRNA /cds=(881,1642)	11111_010000	1113.107330	141, _0000
		/gb=NM_019895 /gi=11096339			1.
	+ 1	/ug=Hs.107393 /len=2820	*		-
9511	0.04279	emopamil binding related protein, delta8-	NM 032565	Hs.433278	ND 11505
9011	0.04276		14141_032365	ПS,453216	NP_11595
		delta7 sterol isomerase related protein		7.	1
•		(EBRP), mRNA /cds=(53,673)			
		/gb=NM_032565 /gi=14211872			
0540	0.000704	/ug=Hs.433278 /len=931	1400007	11. 600770	<b>-</b>
9518	0.033724	kpni repeat mrna (cdna clone pcd-kpni-8),	K00627	Hs.203776	
		3' end. /gb=K00627 /gi=337653			1
	21	/ug=Hs.203776 /len=2126			
9532	0.011439	likely ortholog of rat V-1 protein (V-1),	NM_145808	Hs.21321	NP_66580
	1	mRNA /cds=(229,585) /gb=NM_145808		- ():-	
	-	/gi=21956644 /ug=Hs.21321 /len=3770			
9534	0.024639	codanin I mRNA, partial cds. /cds=(1,3798)	AF525398	Hs.334834	
7		/gb=AF525398 /gi=27451597			
<u> </u>	<u>.</u>	/ug=Hs.334834 /len=4725			
9570	0.024639	ERO1-like (S. cerevisiae) (ERO1L), mRNA	NM_014584	Hs.25740	NP_055399
		/cds=(227,1633) /gb=NM_014584			
		/gi=7657068 /ug=Hs.25740 /len=3334		1	
9584	0.022722	hypothetical protein FLJ20522 (FLJ20522),	NM_017861	Hs.35406	NP_06033
		mRNA /cds=(213,866) /gb=NM_017861	<del>-</del>		_
	1	/gi=23680884 /ug=Hs 35406 /len=1876			
9598	0.029086	mRNA; cDNA DKFZp761C169 (from clone	AL161991	Hs.71252	NP 075064
	1	DKFZp761C169); partial cds			
	]	/cds=(997,2475) /gb=AL161991	- 2		1
	1	/gi=7328122 /ug=Hs.71252 /len=3324			<b>]</b> .
9612	0.042232	ubiquitin-conjugating enzyme E2G 1 (UBC7	NM 003342	Hs.78563	NP_00333
00 1 <u>2</u>	0.072234	C. elegans) (UBE2G1), mRNA	14101_003042	113.7 0000	1.11,_003,33
					}
		/cds=(167,679) /gb=NM_003342	- 8-		
	1	/gi=21314607 /ug=Hs.78563 /len=2430	i	1	1

		nding To Differentially Expressed Genes i			Distair
Spot	p-value	Description	Gene	Unigene	Protein
	- 3		Accession	Accession	Accession
	2 2 2 2 2 2 2		No.	No.	No.
9617	0.00953	mRNA, cDNA DKFZp761B0823 (from	AL157462	Hs.306484	
		clone DKFZp761B0823) /gb=AL157462		,	
		/gi=7018477 /ug=Hs.306484 /len=5085			
9618	0.028884	protein phosphatase 1A (formerly 2C),	NM_021003	Hs.57764	NP_808821
	-	magnesium-dependent, alpha isoform			30
		(PPM1A), mRNA /cds=(358,1506)			
	₹	/gb=NM_021003 /gi=10337594		. ••	
	·	/ug=Hs.57764 /len=2346	* *		*
9661	0.042232	EST(ty69h03.x1 NCI_CGAP_Kid11 clone	Al613080	T	NP 659411
		IMAGE:2284373 3')		1	-
9665	0.017708	EST(df64h05.y1 Morton Fetal Cochlea	AW024055		
•		clone IMAGE:2488569 5') (5e-06 match)			
9677	0.004381	EST(QV3-NN1023-260400-168-a04	AW902143		NP 065960
		NN1023)			
9682	0.002322	BX091044 Soares retina N2b4HR cDNA	BX091044	Hs.435655	-
0002	0.002022	clone IMAGp998D18828 ; IMAGE:360161,	, p, 100 10-14	113.400000	*
		mRNA sequence	X-		· .
-		/clone=IMAGp998D18828_;_IMAGE:36016			
		1 /gb=BX091044 /gi=27826224			100
٠.		/ug=Hs.435655 /len=644		. 1	
0002	0.004600		AK022200	11- 400052	
9683	0.024639	cDNA FLJ12246 fis, clone	AK022308	Hs.188853	
		MAMMA1001343. /gb=AK022308			
0007	0.040447	/gi=10433677 /ug=Hs.188853 /len=1766		ļ	·
9697	0.010447	EST(wc77f09.x1 NCI_CGAP_Pan1 clone	Al674873		
	201000	IMAGE:2324681 3' contains Alu repeat)			9=
9723	0.019262	yx53g06.s1 Soares melanocyte 2NbHM	N21311	Hs.433011	
		cDNA clone IMAGE:265498 3', mRNA	9		Į.
		sequence /clone=IMAGE:265498	000	*	· ·
	i ·	/clone_end=3' /gb=N21311 /gi=1126481		9	. 7
		/ug=Hs.433011 /len=570			
9728	0.036386	EST(ow54e12.s1	AI022887	- 32 -	
	•	Soares_parathyroid_tumor_NbHPA clone ~		:	·
		IMAGE:1650670 3')			
9743	0.045433	hypothetical protein FLJ20507 (FLJ20507),	NM_017849	Hs.202955	NP_060319
		mRNA /cds=(258,974) /gb=NM_017849			
		/gi=8923465 /ug=Hs.202955 /len=4223			
9772	0.042232	hypothetical protein FLJ30596 (FLJ30596),	NM_153013	Hs.81907	NP_694558
		mRNA /cds=(223,1062) /gb=NM_153013	-		
	100	/gi=23308514 /ug=Hs.81907 /len=1978		-	
•	1		1		
9785	0.039219	hypothetical protein FLJ11184 (FLJ11184),	NM_018352	Hs.267446	NP_060822
2.00		mRNA /cds=(113,724) /gb=NM_018352		1	
		/gi=8922922 /ug=Hs.267446 /len=1748	1		,
	1	0022022 /dg=13.207440 /ieii=1740	1 .		4.0

		nding To Diff rentially Express d Genes i	n Figure 14 - D		
Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
-			No	No.	No.
9786	0.017708	UI-1-BC1p-auz-c-09-0-UI.s1	BQ012740	Hs.172844	
		NCI_CGAP_PI3 cDNA clone UI-1-BC1p-			)
		auz-c-09-0-UI 3', mRNA sequence			
		/clone=UI-1-BC1p-auz-c-09-0-UI			• •
		/clone_end=3' /gb=BQ012740	0		
		/gi=19737641 /ug=Hs.172844 /len=1046			
9812	0.031226	mRNA; cDNA DKFZp313C1042 (from	AL833436	Hs.376859	34 3 1 3 1
	*	clone DKFZp313C1042) /gb=AL833436			
		/gi=21734078 /ug=Hs.376859 /len=2103	- 1		
9818	0.026691	EST (zn89e09.s1 Stratagene lung	AA127265		
		carcinoma 937218 cDNA clone			
		IMAGE:565384 3')			
9823	0.045433	hypothetical protein MGC2560 (MGC2560),	NM_031452	Hs.80624	NP_113640
		mRNA /cds=(195,551) /gb=NM_031452		**	
		/gi=13899288 /ug=Hs.80624 /len=1229	1		
			r <sub>i</sub> S		
9827	0.004849	EST CB H sapiens cDNA clone	AV743921		
		CBCCHD05 5'			
9888	0.011439	hypothetical protein MGC5508 (MGC5508),	NM_024092	Hs.13662	NP_07699
		mRNA /cds=(73,804) /gb=NM_024092		-	
		/gi=13129091 /ug=Hs.13662 /len=2097			1
111 1 1					
9890	0.045433	FKSG64 (FKSG64) mRNA, complete cds	AF338199	Hs.143740	
		/cds=(66,440) /gb=AF338199 /gi=12802898			
2222	2 22 1222	/ug=Hs.143740 /len=916			
9928	0.024639	LIM domain containing preferred	NM_005578	Hs.180398	NP_00556
		translocation partner in lipoma (LPP),			
		mRNA /cds=(247,2085) /gb=NM_005578	}		D 1
00.47	0.000000	/gi=5031886 /ug=Hs.180398 /len=5656	4503475		-
9947	0.020932	PNAS-138 mRNA, complete cds	AF277175	Hs.326790	*
		/cds=(12,161) /gb=AF277175 /gi=12751080			90.
0070	0.00050	/ug=Hs.326790 /len=199	NINA 020400	110 205 474	ND 44004
9972	0.00953	caldesmon 1 (CALD1), transcript variant 1,	NM_033138	Hs.325474	NP_14934
	1.	mRNA /cds=(230,2611) /gb=NM_033138			
	Ĭ .	/gi=15149460 /ug=Hs.325474 /len=3610		`.	
0005	0.047700	mDNA from obromonomic Fe24 22	AB002449	Hs.182723	
9985	0.017708	mRNA from chromosome 5q21-22,	AB002449	ITIS. 102/23	
		clone:843Ex. /gb=AB002449 /gi=2943812 /ug=Hs.182723 /len=1228			T .
10039	0.007195	keratinocytes associated protein 2 (KCP2),	NM_173852	Hs.374854	NP_77625
10039	0.007 100	mRNA /cds=(1,489) /gb=NM_173852	1/300Z	1115,574004	NF_/ / 029
	No.	/gi=27777660 /ug=Hs.374854 /len=489			
10049	0.026601	FLJ12209 fis, clone MAMMA1000962	AK022271	Hs.366548	
10043	0.020031	/cds=UNKNOWN /gb=AK022271	1,11044211	11 19.000040	
		/gi=10433630 /ug=Hs.366548 /len=1239	. *		
,	1	1/gi- 10400000 rug-1 18.000040 rieti- 1208	1	1 .	1

		nding To Differentially Expressed Genes i			<u></u>
Spot	p-value	Description	Gene	Unigene	Protein
	,		Accession	Accession	Accession
			No.	No.	No.
10054	0.024639	similar to hypothetical protein FLJ10883	NM_052937	Hs.60293	NP_443169
		(LOC115294), mRNA /cds=(98,1171)		-	
	٠,	/gb=NM_052937 /gi=24308385			· · ·
	· .	/ug=Hs.60293 /len=3967		]	
10064	0.028884	KIAA0570 gene product (KIAA0570),	XM 002692	1177 - F	1111-11
•	:	mRNA			
10068	0.039219	mitochondrial ribosomal protein L10	NM_148887	Hs.347535	NP 683685
-		(MRPL10), nuclear gene encoding			, <del>, , , , , , , , , , , , , , , , , , </del>
		mitochondrial protein, transcript variant 2,			
		mRNA /cds=(95,910) /gb=NM_148887			
		/gi=22547124 /ug=Hs.347535 /len=1848			
10079	0.04883	UI-H-FL1-bfz-f-13-0-UI.s1 NCI CGAP_FL1	BU621287	Hs.96028	NP_004463
.00,0	0.01000	cDNA clone UI-H-FL1-bfz-f-13-0-UI 3',	D0021207	113.00020	_004400
-30.	6	mRNA sequence /clone=UI-H-FL1-bfz-f-13-			
	-	0-UI /clone_end=3' /gb=BU621287	:	*	
		/gi=23287502 /ug=Hs.96028 /len=1108		• • • •	*
10105	0.004840	programmed cell death 2 (PDCD2),	NM 144781	Hs.367900	NP 659005
,10105	0.004649	transcript variant 2, mRNA /cds=(80,766)	144701	IDS.307900	INF_059005
			0	:	
		/gb=NM_144781 /gi=21735593		170	
40440	0.040000	/ug=Hs.367900 /len=2066	NINA 04 400 4	11- 00477	ND 055740
10110	0.013668	zinc-finger protein DZIP1 (DZIP1), mRNA	NM_014934	Hs.60177	NP_055749
	-	/cds=(839,3385) /gb=NM_014934			
10100	2 244 422	/gi=7662435 /ug=Hs.60177 /len=4502	1111 000101		115 021000
10133	0.011439	hypothetical protein FLJ13576 (FLJ13576),	NM_022484	Hs.334335	NP_071929
	<b>l</b> ' .	mRNA /cds=(365,2458) /gb=NM_022484			200
		/gi=21362101 /ug=Hs.334335 /len=3973			
10110	10.01000				115 00 100
10143	0.04883	phospholipase A2 receptor 1, 180kDa	NM_007366	Hs.171945	NP_031392
		(PLA2R1), mRNA /cds=(207,4604)			
1	-	/gb=NM_007366 /gi=19923388		2	
		/ug=Hs.171945 /len=5633			
10145	0.016261	EST(fi21a05.x1 Sugano Kawakami	AW116880		
		zebrafish DRA clone 2601776 3')			
10146	0.011439	EST qz90a06.x1	Al493872		NP_008878
		Soares_pregnant_uterus_NbHPU cDNA		* 10	
-00		clone IMAGE:2041810 3'	* • -		
10170	0.016261	EST (ts95a10.x1 NCI_CGAP_GC6 cDNA	AI635513		
-	100	clone IMAGE:2239002 3')			
10179	0.039219	EST (wq27e08.x1 NCI_CGAP_Kid11	AI953360		NP_620149
		IMAGE:2472518 3')			*
10195	0.033724	mRNA for KIAA1586 protein, partial cds.	AB046806	Hs.180663	
		/cds=(1481,3700) /gb=AB046806			:
		/gi=10047246 /ug=Hs.180663 /len=4061		1	
10196	0.04883	UI-CF-DU1-aav-k-08-0-UI.s1 UI-CF-DU1	BM983293	Hs.424609	
		cDNA clone UI-CF-DU1-aav-k-08-0-UI 3',			
		mRNA sequence /clone=UI-CF-DU1-aav-k-	l		
		08-0-UI /clone_end=3' /gb=BM983293	S +	1	,
	ļ · .	/gi=19607660 /ug=Hs.424609 /len=684			
	<u> </u>	1/91 10001000 rug-113.424003 /(cit-004	<del></del>	<del>1</del>	

		nding To Differentially Expressed Genes i			(3)
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
10197	0.020932	CDA02 protein (CDA02), mRNA	NM_032025	Hs.332404	NP_114414
		/cds=(3,1832) /gb=NM_032025	* .		
		/gi=14042940 /ug=Hs.332404 /len=2179			
10198	0.007185	ze65h12.s1 Soares retina N2b4HR cDNA	AA021186	Hs.226306	
	1	clone IMAGE:363911 3', mRNA sequence	:		
		/clone=IMAGE:363911 /clone_end=3'		*	(
		/gb=AA021186 /gi=1484920		1	
	i	/ug=Hs.226306 /len=422		*	
10232	0.039219		BX094256	Hs.407356	
		cDNA clone IMAGp998B20783, mRNA	-		· ·
		sequence			
		/clone=IMAGp998B20783_;_IMAGE:34283	*	1	
		5 /gb=BX094256 /gi=27841884	· .	·	9 4 1
•		/ug=Hs.407356 /len=477		*	
10241	0.017708	EST (nc21a04.r1 NCI_CGAP_Pr1 cDNA	AA225070		
102 !!	0.517755	clone IMAGE:1008750)	7 1220070		
10251	0.045433	cDNA: FLJ21778 fis, clone HEP00201.	AK025431	Hs.283378	
10201	0.040400	/gb=AK025431 /gi=10437942	1711020401	113.200070	
		/ug=Hs.283378 /len=2117		*	1
10252	0.046131	EST wi39b12.x1 NCI CGAP Ut1 cDNA	AI858495		, , , .
10232	0.040131	clone IMAGE:2427263 3'	71050495	*	
10276	0.04002	Hypothetical protein(cDNA sequence	AK002173	<del>                                     </del>	NP_68997
10270	0.04003	FLJ11311 fis, clone PLACE1010102)	AK002173		ME_00991
				į	ļ
10277	0.007105	(=cDNA sequence DKFZp566J2146) likely ortholog of mouse embryonic	NM_017611	Hs.274453	NP 06008
10277	0.007.165	epithelial gene 1 (EEG1), mRNA	11/10/17/01/1	ITIS.274433	ΙΝΕ_ΟΘΌΟΘ
	,				[
		/cds=(319,1794) /gb=NM_017611			-
40004	0.040000	/gi=18252046 /ug=Hs.274453 /len=2630	ALECOEO1		- 3
10284	0.013008	EST (tn41b12.x1 NCI_CGAP_Brn25	Al568591	6	
40004	0.040004	IMAGE:2170175 3')	A14000400	<del>                                     </del>	ND OCCE
10294		unnamed protein product [Homo sapiens]	AK002129	<del> </del>	NP_06255
10296	0.011439	cDNA sequence (cDNA sequence	AK021665		
40007	0.010514	FLJ11603 fis, clone HEMBA1003926)	41.45000		
10307	0.012511	EST(ti95f04.x1 NCI_CGAP_Gas4 cDNA	Al445690		· .
40005	0.044400	clone IMAGE:2139775 3')	414/000004	<del> </del>	<del>                                     </del>
10325	0.011439	EST IL2-UM0076-130500-084-A01	AW802834	}	
7.20.		UM0076 cDNA			ļ
10330	0.002322	EST xa58b09.x1 NCI_CGAP_HSC2 cDNA	AW073612	Ì	1
		clone IMAGE:2570969 3' similar to	*		
	<u></u>	contains Alu repetitive element;			· · · · · · · · · · · · · · · · · · ·
10331	0.039219	EST QV4-UM0094-060400-159-f11	AW804948		NP_11218
	18	UM0094	L	1	
10335	0.01928	hypothetical protein MGC13024	NM_152288	Hs.333488	NP_68950
		(MGC13024), mRNA /cds=(196,1083)			
	·	/gb=NM_152288 /gi=22748650			1.
	<u> </u>	/ug=Hs.333488 /len=2239		1	100
10361	0.031226	Est (zf66a10.s1 Soares retina N2b4HR	AA058771		
	1 .	IMAGE:381882 3')		1	I '

		nding To Differentially Expr ssed Gen s i			
Spot	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
	,		No.	No.	No.
10367	0.033724	hypothetical protein BC009518	NM_138363	Hs.135265	NP 612372
		(LOC90799), mRNA /cds=(59,2524)			_
		/gb=NM_138363 /gi=19923898		~	-
	4.5	/ug=Hs.135265 /len=2705		6	
10375	0.016261	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM 018180	Hs.171835	NP 060650
		polypeptide 32 (DDX32), mRNA	, ,		
1		/cds=(492,2723) /gb=NM_018180	٠ ,		
		/gi=20336299 /ug=Hs.171835 /len=3070			
10381	0.016261	RST10553 Athersys RAGE Library cDNA,	BG191459	Hs.45070	
	0.0.00	mRNA sequence /gb=BG191459	[20.000		
		/gi=13713146 /ug=Hs.45070 /len=1258			
10401	0.00208	EST (Clontech human aorta polyA mRNA	C14262		
	0.00200	(#6572) cDNA clone GEN-041E02 5')	014202	,	
		(#0012) CD147 CIONE OEN-041E02 0 )			
10404	0.028884	mRNA for KIAA1993 protein. /cds=(1,1600)	ΔB082524	Hs.177633	. · · · · · · · · · · · ·
10404	0,020004	/gb=AB082524 /gi=21693131	1	1115.177055	
	* = 3* =	/ug=Hs.177633 /len=6545		•	1 (*
10406	0.031226	collagen, type V, alpha 2 (COL5A2), mRNA	NIM 000303	Hs.82985	NP_000384
10400	0.031220	/cds=(158,4648) /gb=NM_000393	14141_000393	IU2.05502	NP_000364
		/gi=16554580 /ug=Hs.82985 /len=6217			
10412	0.005350	EST(IL3-HT0618-060500-125-A10	BE179404		
10412	0.005559	HT0618)	DE179404		·
10433	0.010262	clone IMAGE:5275753, mRNA	BC044623	Hs.418416	1.5
10433	0.019202	/gb=BC044623 /gi=27882398	0044023	1115.410410	
		/ug=Hs.418416 /len=1997			
10488	0.007003	FLJ11842 fis, clone HEMBA1006652,	AK021904	Hs.26966	
10400	0.007903	weakly similar to 60S RIBOSOMAL	AKU21904	IU2.50900	
		PROTEIN L7 /cds=UNKNOWN			11.5
					- 18 · · · · · · · · · · · · · · · · · ·
	, 1 X	/gb=AK021904 /gi=10433196			
40405	0.004600	/ug=Hs.26966 /len=1861	DE 470000	11-05000	
10495	0.024639	7q35h07.x1 NCI_CGAP_GC6 cDNA clone	BF478238	Hs.356203	
		IMAGE:3700476 3' similar to contains	18		
		element MER4 MER4 repetitive element ;,	* 1		
. *		mRNA sequence /clone=IMAGE:3700476			
* .	1.0	/clone_end=3' /gb=BF478238		*	sys
	,	/gi=11549065 /ug=Hs.356203 /len=400	·	10	· ·
<del>1010=</del>	0.000000	LULL DECLARACIONE CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONT	0.4.400000	11 00555	
10497	0.029086	UI-H-DF0-bek-n-06-0-UI.s1	CA426336	Hs.20300	
		NCI_CGAP_DF0 cDNA clone UI-H-DF0-		*	
		bek-n-06-0-UI 3', mRNA sequence	" e		[
	1	/clone=UI-H-DF0-bek-n-06-0-UI			,
	. * '	/clone_end=3' /gb=CA426336		2	
		/gi=24789062 /ug=Hs.20300 /len=1060		<b>1</b> .	

		nding To Differentially Expressed Genes i			1
Spot	p-value	Description	G ne	Unig ne	Protein
			Accession	Accession	Accession
	rediction to the control		No.	No.	No.
10498	0.049642	wo45d05.x1 NCI_CGAP_Gas4 cDNA clone	Al926493	Hs.213840	[ .
141		IMAGE:2458281 3' similar to contains		1 .	
	,	element XTR repetitive element ;, mRNA			
		sequence /clone=IMAGE:2458281	and the second		0.
· e		/clone_end=3' /gb=Al926493 /gi=5662457	· .	1	1
		/ug=Hs.213840 /len=509			1
			3		
10506	0.024639	K-EST0187941 L14ChoiCK0 cDNA clone	CB135678	Hs.435110	
		L14ChoiCK0-30-C05 5', mRNA sequence	· .		1
	-0	/clone=L14ChoiCK0-30-C05 /clone_end=5'		·	
		/gb=CB135678 /gi=28102621			
		/ug=Hs.435110 /len=419			İ
10511	0.007019	cDNA FLJ34603 fis, clone KIDNE2013388.	AK091922	Hs.304130	
	, ,	/gb=AK091922 /gi=21750400			
ı		/ug=Hs.304130 /len=1992			
10542	0.003208	mRNA; cDNA DKFZp564F112 (from clone	AL049987	Hs.166361	7 0 mg
		DKFZp564F112) /gb=AL049987			
		/gi=4884238 /ug=Hs.166361 /len=1215			
10545	0.037777	yj71g12.s1 Soares breast 2NbHBst cDNA	R52072	Hs.411221	
4	,	clone IMAGE:154246 3', mRNA sequence			
		/clone=IMAGE:154246 /clone end=3'			
•		/gb=R52072 /gi=813974 /ug=Hs.411221	*	1	•
		/len=458	. e		
10547	0.005916	mRNA; cDNA DKFZp564B032 (from clone	AL049975	Hs.274510	
		DKFZp564B032) /gb=AL049975			1
•		/gi=4884225 /ug=Hs.274510 /len=1943			
10562	0.019262	twisted gastrulation 1 (Drosophila)	NM_020648	Hs.247302	NP 06569
		(TWSG1), mRNA /cds=(106,777)			
		/gb=NM_020648 /gi=21314788	. *		
		/ug=Hs.247302 /len=3693	0		1
10591	0.04883		BI492586		NP 00310
•		clone IMAGE:2484509 3' )			
10597	0.028884	BX106681	BX106681	Hs.293334	- 1
		Soares_parathyroid_tumor_NbHPA cDNA			
	<b> </b>	clone IMAGp998F054235, mRNA		1	10.0
		sequence			
		/clone=IMAGp998F054235_;_IMAGE:1668	,		
		484 /gb=BX106681 /gi=27847079			1
		/ug=Hs.293334 /len=605			_
10620	0.019262	UI-E-EJ0-ahk-c-20-0-UI.r1 UI-E-EJ0 cDNA	BM701368	Hs.356108	+
.0020	0.0 10202	clone UI-E-EJ0-ahk-c-20-0-UI 5', mRNA	)	110.000100	}
	. ,	sequence /clone=UI-E-EJ0-ahk-c-20-0-UI			
		/clone_end=5' /gb=BM701368			
	n · .	/gi=19014626 /ug=Hs.356108 /len=1532		***	
10624	0.014917	AGENCOURT_6417307 NIH_MGC_67	BM799896	Hs.304926	<del> </del>
.0024	0.014317	cDNA clone IMAGE:5492062 5', mRNA	5111, 00000	113.004320	
	·	sequence /clone=IMAGE:5492062	]	Х-	
		/clone_end=5' /gb=BM799896			1
					1
	<u></u>	/gi=19116719 /ug=Hs.304926 /len=913	<u></u>	ــــــــــــــــــــــــــــــــــــــ	

		nding To Differentially Expressed Genes i			
Spot	p-value	D scription	Gene	Unigene	Protein
	,		Accession	Accession	Accession
			No.	No.	No
0628	0.007185	ESTs, cDNA, 3' end /clone=IMAGE:565677	Al732470	Hs.191157	
		/clone end=3' /gb=Al732470 /gi=5053583			
		/ug=Hs.191157 /len=596	*		
	100	3	,	4.2	
0629	0.005359	ac74b05.x5 Stratagene lung (#937210)	AI791153	Hs.444952	
00-0		cDNA clone IMAGE:868305 3' similar to	,		
		contains Alu repetitive element;, mRNA			
	<b>]</b> · ·	sequence /clone=IMAGE:868305			. *
		/clone_end=3' /gb=Al791153 /gi=5338869	00		
	ŀ	/ug=Hs.444952 /len=498		•	
10020	0.000004		DUC2C204	11- 440400	<del></del>
0630	0.028884	UI-H-DF0-bet-j-17-0-UI.s1	BU626301	Hs.443120	a S
	'	NCI_CGAP_DF0 cDNA clone UI-H-DF0-			Į
		bet-j-17-0-UI 3', mRNA sequence /clone=UI			
	[ ·	H-DF0-bet-j-17-0-UI /clone_end=3'	3		
	140	/gb=BU626301 /gi=23292516			
		/ug=Hs.443120 /len=1130			
0631	0.026836	EST380924 cDNA	AW968848	Hs.268326	
		/gb=AW968848/gi=8158689		•	
		/ug=Hs.268326 /len=746			
10643	0.033724	UI-E-EJ0-ahu-o-12-0-UI.r1 UI-E-EJ0 cDNA	BM720005	Hs.132743	
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	clone UI-E-EJ0-ahu-o-12-0-UI 5', mRNA			
		sequence /clone=UI-E-EJ0-ahu-o-12-0-UI			
		/clone_end=5' /gb=BM720005		6 j	
	67	/gi=19038955 /ug=Hs.132743 /len=1441	* *		
10647	0.016185	UI-H-EU1-bad-b-17-0-UI.s1	BQ447217	Hs.435088	<del> </del>
10047	0.010103	NCI CGAP_Ct1 cDNA clone UI-H-EU1-	DQ447217	115.433000	
				ļ	-
	*	bad-b-17-0-UI 3', mRNA sequence	ļ		3.5
	- 37	/clone=UI-H-EU1-bad-b-17-0-UI	*		Ī
		/clone_end=3' /gb=BQ447217			
		/gi=21250329 /ug=Hs.435088 /len=1045	27-27-5		·
10648	0.020932	EST, cDNA, 3' end /clone=IMAGE:5843665	BQ002644	Hs.364307	
		/clone_end=3' /gb=BQ002644	٠.		1
		/gi=19727544 /ug=Hs.364307 /len=762			
· · · .					
10657	0.014917	cDNA FLJ34771 fis, clone NT2NE2003150.	AK092090	Hs.433010	
		/gb=AK092090 /gi=21750599		.:	
		/ug=Hs.433010 /len=2424			•
10658	0.028884	hypothetical protein MGC10233	NM_152715	Hs.29041	NP 689928
		(MGC10233), mRNA /cds=(547,1389)			
		/gb=NM_152715 /gi=22749416	*	•	,
	,	/ug=Hs.29041 /len=3915	1		*. '
10661	0.010447	ip18c02.y1 HR85 islet cDNA clone	CA777576	Hs.115779	
10001	0.010447		CAITIBIO	1113.113/13	
		IMAGE:6217706 5', mRNA sequence			÷
		/clone=IMAGE:6217706 /clone_end=5'		<b>,</b>	}
		/gb=CA777576 /gi=26015451		1	
``	<u> </u>	/ug=Hs.115779 /len=700			
10714		No significant match, ORF-1(226~461)	SEQ.ID.No.69		<u> </u>
10715	10010511	No significant match, low complexity	SEQ.ID.No.73	l i	1.

Gen s Corresponding To Diff rentially Express d Genes in Figure 14 - Diabetes  Spot   p-value   Description   Gene   Unigene					B 4.
Spot	p-value	Description	Gene	Unigene	Protein
	·		Accession	Accession	Accession
			No.	No.	No.
10733	0.042232	DKFZp434O0813_s1 434 (synonym: htes3)	AL040360	Hs.162203	
		cDNA clone DKFZp434O0813 3', mRNA		-)(-	
		sequence /clone=DKFZp434O0813	.* #	* * *	
	· .	/clone_end=3' /gb=AL040360 /gi=5409314	1	* * *	* .
		/ug=Hs.162203 /len=772			8.1
		*			
10777	0.007903	EST (wm51f05.x1 NCI CGAP Ut2	Al871724	<del></del>	· · · · · · · · · · · · · · · · · · ·
		IMAGE:2439489 3')			
10780	0.008683	hypothetical protein FLJ10300 (FLJ10300),	NM_018051	Hs.42233	NP 06052
,0,00	0.00000	mRNA /cds=(1710,3359) /gb=NM_018051	11111_010001	113.42200	-00002
		/gi=21361686 /ug=Hs.42233 /len=3785			4
		/g =21301000/ug=113.422337lef1=3703	. · ·		· · · ·
10782	0.010447	EST (cDNA clone IMAGE:120476 3' similar	TOFACO		
10702	0.010447		195469		
10787	0.016261	to cDNA FLJ37147 fis, clone	A14004400	11- 400000	-
10707	0.016261		AK094466	Hs.420088	
	**	BRACE2025316, weakly similar to tRNA-	***		
		splicing endonuclease subunit.			-
		/cds=(26,559) /gb=AK094466			- 20
		/gi=21753534 /ug=Hs.420088 /len=1738			
10792	0.036386	EST (hb87e12.x1 NCI_CGAP_Ut2 cDNA	AW439703		
		clone IMAGE:2890222 3' similar to			
	<u></u>	contains Alu repetitive element)		<u> </u>	
10794	0.00259		NM_004477	Hs.203772	NP_00446
	1	/cds=(192,968) /gb=NM_004477	,		
		/gi=4758403 /ug=Hs.203772 /len=1042			
10795	0.001481	UI-H-EU1-azy-n-05-0-UI.s1	BQ446028	Hs.444589	
		NCI_CGAP_Ct1 cDNA clone UI-H-EU1-azy			
	1	n-05-0-UI 3', mRNA sequence /clone=UI-H-		·	<b>i</b>
		EU1-azy-n-05-0-UI /clone_end=3'			
		/gb=BQ446028 /gi=21249140	1		V 19
		/ug=Hs.444589 /len=1059			
10848	0.010447	EST(yu63g11.r1 clone 238532 5')	H65434		
10870	0.042232	EST(601463665F1 NIH_MGC_67 cDNA	BE777895		NP_06765
		clone IMAGE:3866801 5')			
10884	0.024639	EST(wm68e05.x1 NCI_CGAP_Ut2 cDNA	AI888258		NP 00187
. 4 0,5	0.0=	clone IMAGE:2441120 3')			
10887	0.022722	EST(CIT-HSP-2366122.TF CIT-HSP	AQ078010		<del></del>
10001	0.022,22	genomic clone 2366l22)	110010010	,	,
10888	0.012511	UI-H-DH0-aul-j-10-0-UI.s1	BM994461	Hs.434057	
10000	0.012311	NCI CGAP DH0 cDNA clone	PINISSTAGI	113.404007	
		IMAGE:5871081 3', mRNA sequence			
		/clone=IMAGE:5871081 /clone_end=3'			
		/gb=BM994461 /gi=19719362			
10000	001555	/ug=Hs.434057 /len=2059	D0045050	11: 0000:10	
10925	0.019262	clone IMAGE:4401491, mRNA	BC015388	Hs.380349	
	}	/gb=BC015388 /gi=21955390			<b>.</b>
	1.	/ug=Hs 380349 /len=1881		<u> </u>	1 '

		nding To Differentially Expressed Genes i			2
Spot	p-value	Description	Gene	Unigene	Protein
*			Accession	Accession	Accession
			No.	No.	No.
10931	0.012511	MR2-CI0186-291100-010-a06 CI0186	BF814502	Hs.446594	
		cDNA, mRNA sequence /gb=BF814502			
		/gi=12147047 /ug=Hs.446594 /len=530			
10941	0.017708	BX100947 NCI_CGAP_Ut2 cDNA clone	BX100947	Hs.169099	1 11 12 18
		IMAGp998J035383, mRNA sequence		1	
		/clone=IMAGp998J035383_;_IMAGE:2178			, ,
		914 /gb=BX100947 /gi=27830924		Ĭ,	
,		/ug=Hs.169099 /len=471			
10947	0.04883	ESTs, cDNA /gb=AW959468 /gi=8149152	AW959468	Hs.188738	1. 10.
* * *	1	/ug=Hs.188738 /len=767			
10966	0.031226	mRNA; cDNA DKFZp586C1723 (from	AL050192	Hs.80285	**
		clone DKFZp586C1723) /gb=AL050192			i
		/gi=4884408 /ug=Hs.80285 /len=1797			1.
10967	0.002322	cDNA /clone=cD622 /gb=AF107454	AF107454	Hs.107537	NP 071903
4 - :	1,57	/gi=5052209 /ug=Hs.107537 /len=4850		. 15. 157 557	
10970	0.04883	BX098252 Soares fetal liver spleen 1NFLS	BX098252	Hs.32171	7
	9.0.1000	cDNA clone IMAGp998P03536, mRNA	D/1000202	110.02111	
	ī *	sequence			
		/clone=IMAGp998P03536_;_IMAGE:24830		Î	1 .
	*	6 /gb=BX098252 /gi=27829319		-	. *
	· ·	/ug=Hs.32171 /len=626	0.0		
10973	0.033724	IL3-HT0619-280600-191-F06 HT0619	BQ357271	Hs.232093	1 Tr. ;
,00.0	0.000724	cDNA, mRNA sequence /gb=BQ357271	DQ007271	1113.202000	
		/gi=21022994 /ug=Hs.232093 /len=580	and the second		
10978	0.042232	cDNA FLJ31827 fis, clone NT2RP6000100,	AK056389	Hs.378531	1
10070	0.042202	moderately similar to ZINC FINGER	711000000	113.576551	
		PROTEIN 41. /cds=(474,1694)			0.00
		/gb=AK056389 /gi=16551782		:	
•		/ug=Hs.378531 /len=3180		1 -	
10987	0.022722	IMAGE:20075 Soares infant brain 1NIB	W18186	Hs.117688	<del> </del>
10301	0.022122	cDNA clone IMAGE:20075, mRNA	VV 10 100	1113.117000	-
		sequence /clone=IMAGE:20075	. 00*		1 1
		/gb=W18186 /gi=1293860 /ug=Hs.117688	*.		
		/len=1232	· ***	*	
11000	0.020004		AA461279		<del>                                     </del>
1 1000	0.020004		AA401219		
		to contains L1.t1 L1 repetitive element;)		1	L
14040	0.047700	CCT- aDNA 21 and	A1400500	11- 400500	ND OCCOOL
11010	0.017708	ESTs, cDNA, 3' end	AI123563	Hs. 166593	NP_060035
	* ***	/clone=IMAGE:1690154 /clone_end=3'			
-		/gb=AI123563 /gi=3539329 /ug=Hs.166593	*	ļ	1
14040	0.044400	/len=530	144000407	11 400504	1
11012	J U.U11439	cDNA FLJ12135 fis, clone	AK022197	Hs.130581	
		MAMMA1000307. /gb=AK022197	. 1	1	1 .
		/gi=10433541 /ug=Hs.130581 /len=2356			

Genes	Correspon	nding To Diff rentially Expressed Genes i	n Figure 14 - D	iabetes	
		Description	Gen	Unigen	Protein
			Accession	Accession	Accession
	. ***		No	No.	No.
11013	0.04883	UI-H-FH0-bcl-g-09-0-UI.s1	CA419491	Hs.293327	
		NCI_CGAP_FH0 cDNA clone UI-H-FH0-bcl			- 0
		g-09-0-UI 3', mRNA sequence /clone=UI-H-		*	
	0	FH0-bcl-g-09-0-UI /clone_end=3'			
		/gb=CA419491 /gi=24782146	٠.	7	
		/ug=Hs.293327 /len=693		*	
11014	0.013668	cDNA FLJ14135 fis, clone	AK024197	Hs.289037	
		MAMMA1002728. /gb=AK024197			
	· ·	/gi=10436518 /ug=Hs.289037 /len=1784	101		·
11015	0.020932	unidentified mRNA, partial sequence.	U43604	Hs 159901	
		/gb=U43604 /gi=1171236 /ug=Hs.159901			*
•••	1.5	/len=1677			
11031	0.026691	cDNA: FLJ21228 fis, clone COL00739.	AK024881	Hs.306716	1
•		/gb=AK024881 /gi=10437293			
		/ug=Hs.306716 /len=1869			
11049	0.042232	cs69c03.y2 Retinal pigment	CA395789	Hs.446106	
		epithelium/choroid cDNA (Un-normalized,			*
		unamplified): cs cDNA clone cs69c03 5',			
	٠, ٠	mRNA sequence /clone=cs69c03			
		/clone_end=5' /gb=CA395789			
		/gi=24731580 /ug=Hs.446106 /len=585			8
11059	0.024639	UI-E-CQ1-aew-e-07-0-UI.s1 UI-E-CQ1	BU728934	Hs.436272	
	*.	cDNA clone UI-E-CQ1-aew-e-07-0-UI 3',			1
.00		mRNA sequence /clone=UI-E-CQ1-aew-e-		*	
		07-0-UI /clone_end=3' /gb=BU728934		· ·	
		/gi=23651308 /ug=Hs.436272 /len=1132		J	
11070	0.014917	cDNA FLJ34585 fis, clone KIDNE2008758.	AK091904	Hs.104627	
		/gb=AK091904 /gi=21750379		-	
		/ug=Hs.104627 /len=2438			
11097	0.031491	ESTs, cDNA, 3' end /clone=UI-E-EJ0-ahj-f-	BM674241	Hs.354662	
	. • •	02-0-UI /clone_end=3' /gb=BM674241			
		/gi=18984139 /ug=Hs.354662 /len=684			(0)
11099	0.031491	UI-H-DT1-avz-g-14-0-UI.s1	BQ015869	Hs.353471	
		NCI_CGAP_DT1 cDNA clone			
		IMAGE:5886373 3', mRNA sequence	ω · · · · · · · · · · · · · · · · · · ·	3	
	-8-	/clone=IMAGE:5886373 /clone_end=3'			
. ***		/gb=BQ015869 /gi=19751146		1	** .
		/ug=Hs.353471 /len=1192		1	*
11100	0.033724	EST(cDNA clone IMAGE:2267085 3')	Al609617	30.4	NP_776252
11135		UI-1-BC1p-asx-h-02-0-UI.s1	BQ012708	Hs.191900	
	:	NCI_CGAP_PI3 cDNA clone UI-1-BC1p-			
·		asx-h-02-0-UI 3', mRNA sequence			
		/clone=UI-1-BC1p-asx-h-02-0-UI	- (0		
		/clone_end=3' /gb=BQ012708		3	
		/gi=19737609 /ug=Hs.191900 /len=590			
11142	0.010447	cDNA: FLJ22447 fis, clone HRC09479.	AK026100	Hs.344000	
	,	/gb=AK026100 /gi=10438841		-	
		/ug=Hs.344000 /len=1659	1	1	1

		nding To Differentially Expressed Genes i			
Spot	p-value	D scription	G ne	Unigene	Protein
	·		Accession	Accession	Accession
			No.	No.	No.
11160	0.013668	Similar to LOC168246, clone MGC:40162	BC027989	Hs.180059	
		IMAGE:4995539, mRNA, complete cds		,	
. 141	,	/cds=(214,402) /gb=BC027989		٠., .	*
		/gi=20380198 /ug=Hs.180059 /len=1748			
11162	0.019262	cDNA FLJ33072 fis, clone	AK057634	Hs.348724	
:	,	TRACH2000243. /gb=AK057634		·	
-	1	/gi=16553392 /ug=Hs.348724 /len=2552			
11181	0.014917	No significant match	SEQ.ID.No.68		-
11192	0.036386	RC4-HT0277-160200-013-d07 HT0277	BE151126	Hs.158600	
		cDNA, mRNA sequence /gb=BE151126			())
		/gi=8613847 /ug=Hs.158600 /len=571	- * · · · · · ·		<b>.</b>
11202	0.042232	AV699513 GKC cDNA clone GKCDLA08	AV699513	Hs.131366	
		3', mRNA sequence /clone=GKCDLA08			
7 e	× 1.	/clone_end=3' /gb=AV699513	8		
		/gi=10301484 /ug=Hs.131366 /len=793			
11214	0.019262	No significant match (ORF:+1:1~147[147],			
		+2:68~193[126])	SEQ.ID.No.25		
11237	0.019262	vesicle-associated membrane protein 2	NM 014232	Hs.25348	NP 055047
. •		(synaptobrevin 2) (VAMP2), mRNA	_		<del>-</del>
*		/cds=(95,445) /gb=NM_014232			
		/gi=7657674 /ug=Hs.25348 /len=2159			
11256	0.004381	cDNA FLJ31919 fis, clone NT2RP7004964.	AK056481	Hs.400872	
		/gb=AK056481 /gi=16551895			1.
	1 -	/ug=Hs.400872 /len=4013		. :	
11292	0.033724	DNA sequence from clone RP11-151F5 on	AL158823		
		chromosome 9 Contains 2 isoforms for part		**	
	0,	of the AKAP2 gene for A kinase (PRKA)			
	, .	anchor protein 2, a ribosomal protein L21			
	-	pseudogene and a CpG island, complete			
0.		sequence [Homo sapiens]	g	-82	
. 3					
11293	0.011439	hypothetical protein (FLJ20485), mRNA	NM 019042	Hs.98806	NP_061915
		/cds=(112,729) /gb=NM_019042			
		/gi=9506680 /ug=Hs.98806 /len=2021	Y ,		*
11316	0.017657	KIAA1721 protein, partial cds	AB051508	Hs:117102	NP 071904
		/cds=UNKNOWN /gb=AB051508			
•		/gi=12697986 /ug=Hs.117102 /len=8047	<i>.</i>		
11337	0.033724	dihydropyrimidine dehydrogenase (DPYD),	NM_000110	Hs.1602	NP 000101
. , 501	3.000,27	mRNA /cds=(102,3179) /gb=NM_000110			
*		/gi=4557874 /ug=Hs.1602 /len=4407			
		100/0/4/49=110.1002/1611=440/	3		
11343	0.007185	chromosome 1 open reading frame 33	NM 016183	Hs.274201	NP_057267
. 10-70	0.00, 100	(C1orf33), mRNA /cds=(32,751)	1.4141_0.10.103	13.214201	131 -03/20/
	<b>]</b> ·	/gb=NM_016183 /gi=18490986			

		nding To Differentially Expressed Genes i			
Spot	p-value	Description	Gene	Unigene	Protein
	*		Accession	Accession	Accession
-		* <u>*</u>	No.	No.	No
11351	0.005916	type V preprocollagen alpha 2 chain	AY016295		
		(COL5A2) gene, exons 34 through 52 and	1.	<b>\</b>	1
٠.		partial cds; and type III preprocollagen			
		alpha 1 chain (COL3A1) gene, exons 2	1		•
44050	0.040000	through 52			1
11358	0.013668	v-raf-1 murine leukemia viral oncogene 1	NM_002880	Hs.349650	NP_002871
	ă.	(RAF1), mRNA /cds=(130,2076)			
		/gb=NM_002880 /gi=4506400			
		/ug=Hs.349650 /len=2977			
11365	0.011297	Rho-specific guanine-nucleotide exchange	NM_014786	Hs.45180	NP_055601
		factor 164 kDa (P164RHOGEF), mRNA	_		7
	· ·	/cds=(16,6207) /gb=NM_014786			
	<b>,</b>	/gi=21361457 /ug=Hs.45180 /len=7540	,	1	
		1.			
11384	0.031336	steroid sulfatase (microsomal),	NM 000351	Hs.79876	ND 000242
11504	0.031220		ININI_000351	ns./96/6	NP_000342
1	÷.	arylsulfatase C, isozyme S (STS), mRNA		Į.	
	·	/cds=(221,1972) /gb=NM_000351	1		
		/gi=13162281 /ug=Hs.79876 /len=6520			
11442	0.04883	cDNA FLJ23640 fis, clone COL00187.	AK074220	Hs.241869	
		/gb=AK074220 /gi=18676763			
	. 3	/ug=Hs.241869 /len=2875		. `	
11445	0.042232	hbc647 mRNA sequence. /gb=U68494	U68494	Hs.24385	
	7,0 1,202	/gi=1546096 /ug=Hs.24385 /len=1843			ľ
11467	0.019262	SMT3 suppressor of mif two 3 1 (yeast)	NM_006936	Hs.85119	NP 008867
11491	0.010202	(SMT3H1), mRNA /cds=(95,406)	14141_000300	113.00113	111 _000007
•	<b>[</b>	/gb=NM_006936 /gi=5902095	ļ		' '
	*			*	
44400	0.04000	/ug=Hs.85119 /len=1733	1114 450000	07440	ND 000 105
11480	0.04883	hypothetical protein FLJ23751 (FLJ23751),	NM_152282	Hs.37443	NP_689495
		mRNA /cds=(121,1563) /gb=NM_152282			
		/gi=22748648 /ug=Hs.37443 /len=2994			
11495	0.007903	leukocyte membrane antigen, clone	BC032352	Hs.9688	
•		MGC:40393 IMAGE:5218501, mRNA,	0	9	
		complete cds /cds=(287,1186)			**
	ľ	/gb=BC032352 /gi=21595376 /ug=Hs.9688	Į.	- ) -	
		/len=1876		ļ	
11496	0.010262	leucyl-tRNA synthetase (LARS), mRNA	NM_020117	Hs.6762	NP_064502
11450	0.019202		NIVI_020117	IDS.0762	INF_004502
		/cds=(73,3603) /gb=NM_020117		سر	
		/gi=24496788 /ug=Hs.6762 /len=4248		ļ., <u> </u>	
11502	0.042232	mRNA for KIAA1229 protein, partial cds	AB033055	Hs.71109	
		/cds=UNKNOWN /gb=AB033055			, *
		/gi=6330699 /ug=Hs.71109/len=5654			
11554	0.00953	EST(df27f12.y1 Morton Fetal Cochlea	AW021741		NP 057485
		clone IMAGE:2484646 5')			
11556	0.04883	hypothetical protein FLJ36812 (FLJ36812),	NM_153260	Hs.194071	NP_694992
	1 0.04000	mRNA /cds=(369,1088) /gb=NM_153260	1	1.10.10.10	
			ı		. ,
		/gi=23397553 /ug=Hs.194071 /len=2647		Ì	

Genes	Correspo	nding To Differentially Expr ssed Genes i	in Figure 14 - D	iabetes	V - 1
	p-valu	Description	Gene	Unigene	Protein
		*	Accession	Accession	Accession
		* * * * * * * * * * * * * * * * * * * *	No.	No.	No.
11594	0.033724	unnamed protein product (=IDH gamma	BAA91131	110.	140.
		gene and TRAP delta gene)			Ter.
11605	0.036386	hypothetical protein PRO1051 (PRO1051),	NM 018572	Hs.326548	NP 061042
		mRNA /cds=(756,1004) /gb=NM 018572		,0200,10	
		/gi=8924004 /ug=Hs.326548 /len=1393		9	14
,		,			
11615	0.04883	mRNA for KIAA0261 gene, partial cds.	D87450	Hs.154978	
		/cds=(1,3866) /gb=D87450 /gi=1665788			-0
		/ug=Hs.154978 /len=6155	,		*
11635	0.042232	EST(nk29g12.s1 NCI_CGAP_Co11 cDNA	AA553765	7.7	***
	,,	clone IMAGE:1014982 3')			
11726	0.00259	survival of motor neuron 2, centromeric	NM_017411	Hs.367729	NP_075015
		(SMN2), transcript variant d, mRNA		1.0.00.120	, ii _ y , y o , o
•	*,	/cds=(164,1048) /gb=NM_017411	8 0	*	
		/gi=13259525 /ug=Hs.367729 /len=1623		İ	
11745	0.006524	FLJ23172 fis, clone LNG10005	AK026825	Hs.306885 :	
		/cds=UNKNOWN /gb=AK026825			
		/gi=10439771 /ug=Hs.306885 /len=1882	*		
11762	0.04883	CDC45 cell division cycle 45-like (S.	NM 003504	Hs.114311	NP_003495
,		cerevisiae) (CDC45L), mRNA			
		/cds=(71,1771) /gb=NM_003504	• 1		-00
	Y	/gi=16357475 /ug=Hs.114311 /len=1932		., + .	
11780	0.014917	mRNA for KIAA1559 protein, partial cds.	AB046779	Hs.35524	
-		/cds=(61,1695) /gb=AB046779	,		
*		/gi=10047182 /ug=Hs.35524 /len=5659			
11781	0.045433	serum/glucocorticoid regulated kinase-like	NM_013257	Hs.380877	NP 733827
		(SGKL), transcript variant 1, mRNA			;
		/cds=(416,1705) /gb=NM 013257		•	
		/gi=25168264 /ug=Hs.380877 /len=4155	. 3		
11783	0.020932	cDNA FLJ20709 fis, clone KAIA1124,	AK000716	Hs.24697'	2.6
		highly similar to D86324 mRNA for CMP-N-			
	١	acetylneuraminic acid. /gb=AK000716			*
		/gi=7020978 /ug=Hs.24697 /len=3488		n <del>-</del>	- 4
11788	0.026691	Bardet-Biedl syndrome 2 (BBS2), mRNA	NM 031885	Hs.332633	NP_114091
		/cds=(422,2587) /gb=NM_031885		·	
		/gi=22208996 /ug=Hs.332633 /len=2978		4.0	
11796	0.013668	mannose-6-phosphate receptor (cation	NM_002355	Hs.134084	NP_002346
	•	dependent) (M6PR), mRNA	<b>-</b> ,		
		/cds=(171,1004) /gb=NM_002355	. ()		
		/gi=10947032 /ug=Hs.134084 /len=2454	·	. *.	L
11816	0.045433	likely ortholog of rat V-1 protein (V-1),	NM_145808	Hs.21321	NP_665807
		mRNA /cds=(229,585) /gb=NM_145808	_		
		/gi=21956644 /ug=Hs.21321 /len=3770			*
11817	0.013668	hypothetical protein FLJ12994 (FLJ12994),	NM 022841	Hs.126908	NP_073752
		mRNA /cds=(120,2678) /gb=NM_022841	_	,	
		/gi=12383091 /ug=Hs.126908 /len=3473		1	ļ
		to the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contrac		• • • • • • • • • • • • • • • • • • • •	

		nding To Differentially Expressed Genes i			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
11912	0.007185	hypothetical protein MGC40157	NM_152350	Hs.295362	NP_689563
		(MGC40157), mRNA /cds=(106,498)	- <del>-</del>		_
•	·	/gb=NM_152350 /gi=22748758			
		/ug=Hs.295362 /len=1250	*		-
11923	0.039219	unidentified mRNA, partial sequence.	U43604	Hs.159901	* * * * * * * * * * * * * * * * * * * *
11020	0.000210	/gb=U43604 /gi=1171236 /ug=Hs.159901	0 (000.)	110.100001	
		/len=1677		. ,	
11940	0.038884	sorting nexin 14 (SNX14), transcript variant	NIM 153916	Hs.375181	NP 722523
11340	0.020004	1, mRNA /cds=(182,3022) /gb=NM_153816	14141 122010	118.973101	NF_122323
				.] ,	],
	-	/gi=24797144 /ug=Hs.375181 /len=3490	1-	*	
44055	0.000004	DNA 6 1814 4 0005	A D000450	11. 40400	
11955	0.028884	mRNA for KIAA0935 protein, partial cds.	AB023152	Hs.12183	
		/cds=(1,2472) /gb=AB023152 /gi=4589513			
		/ug=Hs.12183 /len=6189		1	
11964	0.013668	golgi reassembly stacking protein 2, 55kDa	NM_015530	Hs.6880	NP_056345
*-		(GORASP2), mRNA /cds=(52,1524)			- A
		/gb=NM_015530 /gi=20127538			
		/ug=Hs.6880 /len=2424			
11970	0.017708	mRNA for KIAA1728 protein, partial cds.	AB051515	Hs.252748	
		/cds=(1,4937) /gb=AB051515	*		
•		/gi=12698000 /ug=Hs.252748 /len=6585			0.0
11979	0.020944	chromosome 20 open reading frame 6	NM 016649	Hs.88820	NP 057733
	0.0200	(C20orf6), mRNA /cds=(109,2664)			
		/gb=NM_016649 /gi=22507381			
		/ug=Hs.88820 /len=3216			4.0
12003	0.00053	EST(zi39c11.s1 Soares fetal liver spleen	AA680133	1	NP_660208
12005	0.00933	1NFLS S1 cDNA clone 433172 3')	777000 133		_000200
12007	0.040447		AL 022201	Uo 17767	1
12007	0.010447	mRNA; cDNA DKFZp667E236 (from clone	AL833201	Hs.17767	
	1.5	DKFZp667E236) /gb=AL833201			
	2 2 2 2 2 2 2	/gi=21733831 /ug=Hs.17767 /len=5949	1114 00 1700	1	NB 00 (B00
12022		kinesin family protein 3B (KIF3B)	NM_004798	<u> </u>	NP_004789
12051	0.042232	EST (wn37h08.x1 NCI_CGAP_Gas4	A1888883		
		IMAGE:2447679 3')			
12060	0.00953	mRNA for KIAA1387 protein, partial cds.	AB037808	Hs.301434	
	1	/cds=(1,2853) /gb=AB037808 /gi=7243154	• • • • • • • • • • • • • • • • • • • •		
		/ug=Hs.301434 /len=4385_	<u> </u>		· .
12062	0.010447	EST(wc78g04.x1 NCI_CGAP_Pan1 clone	AI701086		
		IMAGE:2324790 3')			
12150	0.014917	hypothetical protein FLJ35382 (FLJ35382),	NM_152608	Hs.99210	NP 689821
••		mRNA /cds=(165,1235) /gb=NM_152608	_	*	
	1	/gi=22749244 /ug=Hs.99210 /len=1349			-
		):			
12151	0.013668	topoisomerase (DNA) II binding protein	NM 007027	Hs.91417	NP_008958
12 101	0.010000	(TOPBP1), mRNA /cds=(347,4654)	1.1111_007027	113.51717	
		1,			-
	-	/gb=NM_007027 /gi=20143948			
10455	0.000700	/ug=Hs.91417 /len=5261	A) /72 4004		+
12155	0.022722	EST AV734861 cdA H sapiens cDNA clone	AV/34861		
		cdAAPC07 5'		1 '	1

		nding To Differentially Expressed Genes i			D:::2 - 5
Spot	p-value	Description	Gene	Unigene	Protein
: •			Accession	Accession	Accession
			No.	No.	No.
12157	0.011439	EST 9MR2-CN0038-170200-102-c02	AW843260		
		CN0038)			
12160	0.019241	DKFZp564P1871_s1 564 (synonym: hfbr2)	AL037446	Hs.208747	
		cDNA clone DKFZp564P1871 3', mRNA			4
		sequence /clone=DKFZp564P1871			
r		/clone_end=3' /gb=AL037446 /gi=5406837		•	
:	-	/ug=Hs.208747 /len=556			
١.		1 10.2007-17 /1CH 2000			
12178	0.010262	EST (of53c02.s1 NCI_CGAP_CNS1	AA836671		
12110	0.019202	IMAGE:1427906)	77030071		
12180	0.016261	cDNA FLJ13877 fis, clone	AK023939	He 247000	
12100	0.010201		AVOSSASA	Hs.317080	· · · · · · ·
		THYRO1001403. /gb=AK023939			
40400	0.044047	/gi=10436034 /ug=Hs.317080 /len=3065	1111 745045	11. 400000	NID GOOGG
12182	0.014917	Williams-Beuren Syndrome critical region	NM_145645	Hs.406306	NP_66362
		protein 20 copy B (WBSCR20B), mRNA	*	3-6	*
•		/cds=(984,1448) /gb=NM_145645		*	
	* :	/gi=21717802 /ug=Hs.406306 /len=1634		<u>.</u>	
12185	0.017708	hypothetical protein FLJ37318 (FLJ37318),	NM_152586	Hs.130184	NP_68979
		mRNA /cds=(226,2025) /gb=NM_152586			(
		/gi=22749206 /ug=Hs.130184 /len=3114			
			. ()	- ,	
12190	0.024639	oxysterol binding protein-like 11	NM 022776	Hs.61260.	NP_07361
	χ.	(OSBPL11), mRNA /cds=(306,2549)			
	*	/gb=NM_022776 /gi=23111058			
	-	/ug=Hs.61260 /len=4206	,		*
12193	0.020932	EST (yd68e02.s1 Soares fetal liver spleen	T78464		NP 00043
	0.020002	1NFLS IMAGE:113402 3')			
12197	0.019241	DKFZp586E2017_r1 586 (synonym: hute1)	AL 046885	Hs.413463	<del> </del>
12 137	0.013241	cDNA clone DKFZp586E2017 5', mRNA	ALO40003	113.413403	
	,	sequence /clone=DKFZp586E2017		-0	8.7
				*	
		/clone_end=5' /gb=AL046885 /gi=5936275		·	
		/ug=Hs.413463 /len=640			
	0.604505	HA OF 1000010	Doorse		
12198	0.024639	clone IMAGE:4606942, mRNA, partial cds	BC022881	Hs.369550	
		/cds=(1,188) /gb=BC022881 /gi=18605588	,	- "	1
		/ug=Hs.369550 /len=1749			
12200	0.022722	hypothetical protein FLJ10159 (FLJ10159),	NM_018013	Hs.22505	NP_06048
		mRNA /cds=(1,807) /gb=NM_018013		•	
		/gi=8922262 /ug=Hs.22505 /len=2070			
		*	•		
12213	0.026691	repetitive sequence (ALU SUBFAMILY J)	P39188		
12225		EST (83383 Platelet cDNA 3' end)	AA371536		
12227		cDNA, 3' end /clone=IMAGE:3038322	BE042649	Hs.275673	
	, , , , ,	/clone_end=3' /gb=BE042649 /gi=8359628			
	].	/ug=Hs.275673 /len=435	**		
12228	0.020932	TSLC1-like 2 (TSLL2), mRNA	NM 145296	Hs.164773	NP_66033
	3.020002	/cds=(50,1216) /gb=NM_145296	1-0250	1.19.107110	_000033
•		/gi=21686976 /ug=Hs.164773 /len=2176		9	
		1/91-2 1000310 /dy-115. 1041/3 /1011-21/0		J	

Genes	Correspon	nding To Differentially Expressed Genes i	n Figure 14 - D	iabetes	
	p-value	Description	Gene	Unigene	Prot in
			Accession	Accession	Accession
			No.	No.	No.
12236	0.039219	EST (RC2-BN0032-120200-011-h11	AW992887		1
*		BN0032)		ė.	•
12237	0.031491	EST (602496405F1 NIH_MGC_75 clone	BG433151	*	
		IMAGE:4610376 5')			
12240	0.013668	xq09e02.x1 NCI_CGAP_Ut1 cDNA clone	AW517395	Hs.445194	
		IMAGE:2750138 3' similar to contains Alu			
		repetitive element;, mRNA sequence			
		/clone=IMAGE:2750138 /clone_end=3'			
		/gb=AW517395 /gi=7155477			*
		/ug=Hs.445194 /len=519			
12246	0.042232	EST (yo20f05.r1 Soares adult brain	H46503	,	
		N2b5HB55Y cDNA clone IMAGE:178497		: : .	
		[5')			
12271	0.014917	EST(ne86c04.s1 NCI_CGAP_Kid1 clone	AA480776		1.1
100-0		IMAGE:911142 contains L1.t1 L1 repeat)			
12273	0.011297	EST (RC4-MT0235-061200-011-e04	BF900451		
* 4 5 6 6 '4'	2 2 2 2 2 4 4	MT0235)			
12294	0.012511	EST(7e58a12.x1	BE644843	1	NP_006845
		Soares_NSF_F8_9W_OT_PA_P_S1 cDNA	1.3		
10017	0.007000	clone IMAGE:3286654 3')	NIA 6 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		1.5
12311	0.007903	DKFZP566I1024 protein	NM_015411	Hs.279696	NP_056226
		(DKFZP566I1024), mRNA /cds=(48,953)			
		/gb=NM_015411 /gi=24308052	:	37.	
10000	0.040544	/ug=Hs.279696 /len=2005	2000000	11. 105001	
12328	0.012511	AGENCOURT_8877967	BQ932625	Hs.405864	4
	0 **	Lupski_sciatic_nerve cDNA clone			
		IMAGE:6198711 5', mRNA sequence		, j	*
		/clone=IMAGE:6198711 /clone_end=5'	*	,,	
		/gb=BQ932625 /gi=22348008			
10000	0.035422	/ug=Hs.405864 /len=1023	AOC02440		,
12333	0.045433	EST (HS_5378_B2_A05_T7A RPCI-11	AQ683118	*	4 2 9
		Human Male BAC Library genomic clone Plate=954 Col=10 Row=B)		*	
12344	0.042222		DIE07120	, - <del>- i</del>	
12344		EST(cDNA clone IMAGE:5303467 5') hypothetical protein FLJ30634 (FLJ30634),	BI597128	Ho 250065	ND COAFFO
12301	0.016163		NM_153014	Hs.350065	NP_694559
		mRNA /cds=(618,986) /gb=NM_153014 /gi=23308520 /ug=Hs.350065 /len=2796			
		/gi-25506520 /ug-Hs.550005 /ieii-2796		1	i
12376	0.042827	ESTs, cDNA, 5' end	BF032850	Hs.5367	
. 12370	0.042027	/clone=IMAGE:3859365 /clone_end=5'	DF032030	ns.5507	
. •		/gb=BF032850 /gi=10740562 /ug=Hs.5367			8
		(=ESTs, Weakly similar to T02670		1	
		probable thromboxane A2 receptor isoform			
· · · · · · · · · · · · · · · · · · ·		beta)		. 4	W -
12378	0 000373	cDNA FLJ31274 fis, clone KIDNE2006334.	AK055836	Hs:351722	-
12010	0.009373	/gb=AK055836 /gi=16550665	1,1100000	113.331722	
	0	/ug=Hs.351722 /len=1817			
12388	0.033724	EST(cDNA clone IMAGE:4398135 5')	BF984363		
	10.000/24	[LOT (CDIAN CIONE HANDEL 4090 100 0 )	101 204202		

Genes	Correspoi	nding To Differentially Expressed Genes i	n Figure 14 - D	iabetes	F. 1. 1
Spot	p-value	Description	G ne	Unigene	Protein
			Accession	Acc ssion	Accession
			No.	No.	No.
12389	0.026691	UI-HF-BN0-afr-f-07-0-UI.r1 NIH MGC 50	BU431616	Hs.202538	1
		cDNA clone IMAGE:3067908 5', mRNA			<b>.</b>
-		sequence /clone=IMAGE:3067908		<b>^</b>	
	٠	/clone_end=5' /gb=BU431616			*
		/gi=22770103 /ug=Hs.202538 /len=551			
12402	0.012511	clone 3938P1, complete sequence	AC004814		No. 1
12406		EST(CM0-HT1297-160201-781-b03	BG995501		
	· ·	HT1297 Homo sapiens cDNA, mRNA		7.0	
		sequence)			
12407	0.016185	cDNA FLJ10258 fis, clone	AK001120	Hs.258111	
		HEMBB1000908. /gb=AK001120	1.		96.
		/gi=7022181 /ug=Hs.258111 /len=1490		,	
12410	0.014917	BX094545 Soares_NFL_T_GBC_S1 cDNA	BX094545	Hs.445988	
		clone IMAGp998G143911, mRNA		* * * * * * * * * * * * * * * * * * * *	
		sequence			
		/clone=IMAGp998G143911_;_IMAGE:1544			
8		101 /gb=BX094545 /gi=27842004		11	*
		/ug=Hs.445988 /len=738			
12425	0.033724	FLJ32080 fis, clone OCBBF2000015	AK056642	Hs.336425	
		/cds=UNKNOWN /gb=AK056642	, , , , , , , , , , , , , , , , , , , ,	, ,	
•	1	/gi=16552101 /ug=Hs.336425 /len=3615			
12434	0.039219	EST(cDNA clone HTFABF07 5')	AV731260		·
12439		cDNA FLJ12048 fis, clone	AK022110	Hs.289044	
	1.	HEMBB1001990. /gb=AK022110			
	•	/gi=10433433 /ug=Hs.289044 /len=1805			
12452	0.031226	EST(cDNA clone IMAGE:784142 5')	AA446766		
12465		ESTs, cDNA, 5' end	BE894201	Hs.176376	1
		/clone=IMAGE:3922401 /clone end=5'			
٠.	0	/gb=BE894201 /gi=10356330		· .	*
		/ug=Hs.176376 /len=916			
12488	0.033724	ESTs, cDNA, 3' end	AI356348	Hs.369317	
		/clone=IMAGE:2028021 /clone end=3'			
· ::	:	/gb=Al356348 /gi=4107969 /ug=Hs.369317			
		/len=512	*		
12505	0.019262	EST(cDNA clone HTBBSD03 5')	AV722328		
12508		EST(Embryonic Heart cDNA Library Danio	AI617030	7.	1
	3"	rerio cDNA 5')			- A.
12514	0.039219	DCBCQH10 DCB cDNA, mRNA sequence	BU198777	Hs.50273	
		/gb=BU198777 /gi=22717083			
		/ug=Hs 50273 /len=867			
12574	0.039219	UI-H-ED0-awx-b-15-0-UI.s1	BQ020068	Hs.396278	
		NCI_CGAP_ED0 cDNA clone			
	]	IMAGE:5824814 3', mRNA sequence		* .	*
		/clone=IMAGE:5824814 /clone_end=3'	0		
		/gb=BQ020068 /gi=19755345			* '

sponding To Differentially Expressed Genes i	n Figure 14 - D	iabetes	
ue Description	Gene	Unigene	Protein
	Accession	Accession	Accession
	No.	No.	No.
232 zt59c06.s1 Soares_testis_NHT cDNA clone	AA398215	Hs.290951	
IMAGE:726634 3', mRNA sequence			***
/clone=IMAGE:726634 /clone_end=3'			
/gb=AA398215 /gi=2051324	. 0		
/ug=Hs.290951 /len=427			
1883 guanine nucleotide binding protein (G	NM_002070	Hs.77269	NP_002061
protein), alpha inhibiting activity polypeptide			_
2 (GNAI2), mRNA /cds=(124,1191)			
/gb=NM 002070 /gi=4504040	,		1
/ug=Hs.77269 /len=1702	* ,	×	
7903 UI-CF-FN0-aew-b-22-0-UI.s1 UI-CF-FN0	BU608314	Hs.432827	
cDNA clone UI-CF-FN0-aew-b-22-0-UI 3',			
mRNA sequence /clone=Ul-CF-FN0-aew-b-		-	1
22-0-UI /clone end=3' /gb=BU608314	7	-	-
/gi=23274529 /ug=Hs.432827 /len=1144	•		
5433 cDNA sequence FLJ14014 fis, clone	AK024076	7	NP_699204
HEMBA1000290			
1639 hypothetical protein FLJ10254	NP 060511		
1883 EST (CM3-HT0528-010200-086-f04	BE169870		
HT0528)			
9241 myxoid liposarcoma associated protein 4	NM 018192	Hs.42824	NP 060662
(MLAT4), mRNA /cds=(199,2325)	0.0.0		
/gb=NM_018192 /gi=27764881			
/ug=Hs.42824 /len=3396		ļ	<b>\</b>
2511 phosphoribosylaminoimidazole	NM_006452	Hs.117950	NP_006443
carboxylase			
phosphoribosylaminoimidazole			
succinocarboxamide synthetase (PAICS),	*		
mRNA /cds=(206,1483) /gb=NM_006452			
/gi=17388802 /ug=Hs.117950 /len=3322		* .	1
/g/ 1/000002/ug/1/000/ion/ 0022			
6261 EST UI-H-BI2-ahq-e-01-0-UI.s1	AW293540		NP 006816
NCI_CGAP_Sub4_cDNA clone	7.1.12000.10		
IMAGE:2727648 3'		-	
9219 qw21c02.x1 NCI_CGAP_Ut4 cDNA clone	AI290157	Hs.387096	
IMAGE:1991714 3' similar to contains Alu	17.11.200 107	110.007000	
repetitive element; contains element L1			
repetitive element ; mRNA sequence	0	Ì.	
/clone=IMAGE:1991714 /clone end=3'			- 3
/gb=Al290157 /gi=3931823 /ug=Hs.387096	3		
//len=571		1	
3668 xg60a08.x1 NCI_CGAP_Ut4 cDNA clone	AW168110	Hs.277648	<del>                                     </del>
IMAGE:2632694 3', mRNA sequence	1,144,100,110	13.277040	İ
/clone=IMAGE:2632694 /clone end=3'			
_ ·			1
			1
	Δ\Λ/004092	+	-
	AVV384U0Z		1
/( /( 9219 E	gb=AW168110 /gi=6399635 ug=Hs.277648 /len=475 EST (RC3-BN0036-090200-011-h11 BN0036 cDNA)	gb=AW168110 /gi=6399635 ug=Hs.277648 /len=475 ST (RC3-BN0036-090200-011-h11 AW994082	gb=AW168110 /gi=6399635 ug=Hs.277648 /len=475 EST (RC3-BN0036-090200-011-h11 AW994082

		nding To Differentially Expressed Genes i			<u></u>
Spot	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
12751	0.026691	NISC_gj03b10.x1 NCI_CGAP_Pr28 cDNA	CB048158	Hs.201018	
	, ,	clone IMAGE:3270498 3', mRNA sequence		*	
	- 12	/clone=IMAGE:3270498 /clone_end=3'			<b>.</b>
(3)		/gb=CB048158 /gi=27786445			
		/ug=Hs.201018 /len=384	·.		
12763	0.028884	UI-H-FG0-bct-g-21-0-UI.s1	BU627064	Hs.85999	
	.5.62666	NCI_CGAP_EN1_2 cDNA clone UI-H-FG0-	B0027007	119.9000	
,	a "	bct-g-21-0-UI 3', mRNA sequence			
		/clone=UI-H-FG0-bct-g-21-0-UI			
	)	/clone_end=3' /gb=BU627064	_		1
				·	
40707	0.000004	/gi=23293278 /ug=Hs.85999 /len=1075	414/070000		110 000004
12797	0.028884	EST(xu17f02.x1 NCI_CGAP_Co14 cDNA	AW272306		NP_002201
		clone IMAGE:2800443 3')			
12835	0.033724	AGENCOURT_8856629	BQ947179	Hs.356605	
	*.	Lupski_sciatic_nerve cDNA clone		141	.4 *
• ,		IMAGE:6200636 5', mRNA sequence		, .	
		/clone=IMAGE:6200636 /clone_end=5'	,		
	·	/gb=BQ947179 /gi=22362657	,		
		/ug=Hs.356605 /len=1277			
12846	0.031226	EST, cDNA, 5' end	AL137968	Hs.256115	
•		/clone=DKFZp761D0315 /clone_end=5'		7	· · · · ·
- ,	i	/gb=AL137968 /gi=6854648		1))	
		/ug=Hs.256115 /len=523			4.15
12862	0.001042	cDNA MR1-FN0210-301000-002-h09	BF854986		
12002	0.001042	FN0210	DI 034900		
12873	0.012511	EST53917 Fetal heart II cDNA 3' end	AA347584	Hs.332616	
120/3	0.012311		MA347304	[пѕ.ээго ю	-
		similar to EST containing Alu repeat,			
·		mRNA sequence /clone_end=3'			-
	İ	/gb=AA347584 /gi=1999822			
		/ug=Hs.332616 /len=408			ļ
12879	0.022722	hypothetical protein FLJ22415 (FLJ22415),	NM_024769	Hs.135121	NP_079045
	·	mRNA /cds=(342,1463) /gb=NM_024769			*
		/gi=13376114 /ug=Hs.135121 /len=2627			
-					
12886	0.028884	EST, 602309245F1 NIH_MGC_88 cDNA	BF981440		151
		clone IMAGE:4400362 5'		•	•
12918	0.042827	cDNA: FLJ21962 fis, clone HEP05564.	AK025615	Hs.7567	
		/gb=AK025615 /gi=10438186 /ug=Hs.7567	Ŷ.		
		/len=3323	,		1
12921	0.026691	BX106452 NCI_CGAP_Gas4 cDNA clone	BX106452	Hs.200841	
,,		IMAGp998N095583, mRNA sequence			
<b>1.</b>		/clone=IMAGp998N095583_;_IMAGE:2255		-	
	•	816 /gb=BX106452 /gi=27834105		1	1
			,	· ·	
12052	0.045400	/ug=Hs.200841 /len=458	A A G O O C O 4	Un 240460	<del></del>
12953	0.045433	cDNA, 3' end /clone=IMAGE:436024	AA699991	Hs.348162	
		/clone_end=3' /gb=AA699991 /gi=2702954	1	i	1
		/ug=Hs.348162 /len=614	l		

		nding To Differ ntially Expressed Genes in Description	Gene	Unigene	Protein
Shor	P-value	Poodiiktioi	Accession	Accession	Accession
			No.	No.	No.
12961	0.031491	yp92f09 r1 Soares fetal liver spleen 1NFLS	R91059	Hs.330761	INO.
12301	0.031491	cDNA clone IMAGE:194921 5', mRNA	11.91009	118.550701	
		sequence /clone=IMAGE:194921			*:
		/clone_end=5' /gb=R91059 /gi=958599			-30
٠.			*	0	•
12962	0.046434	/ug=Hs.330761 /len=430	CA420420	Lie 205500	
12902	Ų.040 į 3 I	UI-H-FH0-bco-e-02-0-UI.s1	CA420130	Hs.365560	
8-		NCI_CGAP_FH0 cDNA clone UI-H-FH0-			
		bco-e-02-0-UI 3', mRNA sequence			Ξ
		/clone=UI-H-FH0-bco-e-02-0-UI			
	*	/clone_end=3' /gb=CA420130	0.00	*	
40070	0.00700	/gi=24782785 /ug=Hs.365560 /len=716	414/000040	11 070400	
12973	0.022722	ESTs, cDNA, 3' end	AW009340	Hs.372482	
	}	/clone=IMAGE:2504343 /clone_end=3'	*	,	
		/gb=AW009340 /gi=5858118			-20- *
10000		/ug=Hs:372482 /len=490			
12996	0.00953	cDNA FLJ11366 fis, clone	AK021428	Hs.189002	
•		HEMBA1000282. /gb=AK021428	: -		
		/gi=10432610 /ug=Hs.189002 /len=2075		277	
12998	0.013668	UI-H-EU0-azv-i-13-0-UI.s1	BQ181732	Hs.442187	0.5
		NCI_CGAP_Car1 cDNA clone IMAGE:			-
	- 20	5854164 3', mRNA sequence	)"	(3)	
		/clone=IMAGE:_5854164 /clone_end=3'			***
		/gb=BQ181732 /gi=20357224		n 3	* .
		/ug=Hs.442187 /len=1042			
13000		EST(cDNA clone B853)	T19901		
13005	0.031226	zx55g04.r1	AA203502	Hs.192991	
٠.	ver	Soares_fetal_liver_spleen_1NFLS_S1			**
		cDNA clone IMAGE:446454 5', mRNA			
	- 20	sequence /clone=IMAGE:446454			
		/clone_end=5' /gb=AA203502 /gi=1799213			* =
,		/ug=Hs 192991 /len=952			
13011	0.04883	UI-E-DW1-ahd-k-04-0-UI.s1 UI-E-DW1	BM669289	Hs.352788	2
	-	cDNA clone UI-E-DW1-ahd-k-04-0-UI 3',		V 100	•
		mRNA sequence /clone=UI-E-DW1-ahd-k-		•	
		04-0-UI /clone_end=3' /gb=BM669289		}	
<u>.</u> :	,	/gi=18979186 /ug=Hs.352788 /len=1150	*		- J
13013	0.014917	EST(cDNA clone IMAGE:2542504 3'	AW057714		
	- "	similar to contains Alu repetitive element; )			
				1	
13021	0.004691	EST(cDNA clone GLCAOE01 3')	AV646538		
13024		cDNA FLJ12317 fis, clone	AK022379	Hs.288464	1
		MAMMA1002058. /gb=AK022379			λ <sub>1</sub>
	. *	/gi=10433764 /ug=Hs.288464 /len=2403			HI ,
13064	0.008683	No significant match (ORF:-1:37~186[150])	<del> </del>		· · · · · · · · · · · · · · · · · · ·
	1	]	SEQ.ID.No.63	I	l ·

		nding To Differentially Expressed Genes i			
Spot	p-value		Gene	Unigene	Protein
-			Accession	Accession	Accession
			No.	No.	No.
13072	0.039719	yr21g01.s1 Soares fetal liver spleen 1NFLS	H58501	Hs.347143	
		cDNA clone IMAGE:205968 3' similar to		*	
• .	ľ	contains Alu repetitive element;contains			•
•		MER35 repetitive element ;, mRNA			
		sequence /clone=IMAGE:205968			* *
		/clone_end=3' /gb=H58501 /gi=1011333			
	.0	/ug=Hs.347143 /len=461		0	
,,	+				
13098	0.00953	No significant match (ORF:-3:1~153[153])	SEQ.ID.No.61		
13101					:
13131		protocadherin 18 (PCDH18), mRNA	NM_019035	Hs.97266	NP_06190
		/cds=(388,3795) /gb=NM_019035	0.0000	1.10.01.200	
		/gi=14589928 /ug=Hs.97266 /len=5157			
13139	0.04883	chromosome 1 open reading frame 8	NM_004872	Hs.416495	NP_00486
.0100	0.07003	(C1orf8), mRNA /cds=(251,1222)	1.1111_004072	113.710733	_00400
		/gb=NM_004872 /gi=27545320			
		/ug=Hs.416495 /len=1709			
13144	0.042222	lethal giant larvae 1 (Drosophila) (LLGL1),	NM_004140	Hs.95659	NP 00413
13144	0.042232		NIVI_004 140	HS.90009	INP_00413
100		mRNA /cds=(7,3177) /gb=NM_004140			
10110	0.005040	/gi=22547226 /ug=Hs 95659 /len=3225	11.000100	005004	
13149	0.005916	mRNA; cDNA DKFZp686P1116 (from	AL832180	Hs.265891	· · · · ·
	* .	clone DKFZp686P1116) /gb=AL832180			
		/gi=21732725 /ug=Hs.265891 /len=2661	W112-7-1	1	
13164	0.020932	hypothetical protein FLJ12298 (FLJ12298),	NM_032164	Hs.284168	NP_11554
		mRNA /cds=(205,1890) /gb=NM_032164			
:		/gi=14149844 /ug=Hs.284168 /len=2180	**		
	Y			**	
13171	0.028884	hypothetical gene supported by	XM_064780		
		XM_064780 (LOC125750), mRNA			
13179	0.022722	similar to KH domain RNA binding protein	XM_037438		
		QKI-5A (H. sapiens) (LOC135473), mRNA			
13185	0.026691	mRNA; cDNA DKFZp667H216 (from clone	AL833204	Hs.356145	
		DKFZp667H216) /gb=AL833204			İ
		/gi=21733834 /ug=Hs.356145 /len=3782			
13189	0.003208	E74-like factor 2 (ets domain transcription	NM 006874	Hs.82143	NP 00686
.0.00	3.33223	factor) (ELF2), mRNA /cds=(122,1723)		1.0.021.0	55555
		/gb=NM 006874 /gi=6857815	-		*
		/ug=Hs.82143 /len=2993			·
13222	0.028884	yf95a11.s1 Soares infant brain 1NIB cDNA	R41424	Hs.387904	
13222	0.020004	clone IMAGE:30037 3", mRNA sequence	1424	113.307304	
	. :		£ 1	0	
		/clone=IMAGE:30037 /clone_end=3'	3	· ·	
		/gb=R41424 /gi=816727 /ug=Hs.387904			
10000	0.001000	/len=396	NI	111 400044	ND COL
13229	0.024639	runt-related transcription factor 1 (acute	NM_001754	Hs.129914	NP_00174
•		myeloid leukemia 1; aml1 oncogene)		* .	
	] :	(RUNX1), mRNA /cds=(445,1887)		**	6
	*	/gb=NM_001754 /gi=19923197			
		/ug=Hs.129914 /len=6212			2

		nding To Differentially Expressed Genes i			
Spot	p-value	Description	Gn	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
13236	0.024639	glutamate receptor, metabotropic 6	NM_000843	Hs.248131	NP_000834
		(GRM6), mRNA /cds=(179,2812)	Ť	1	
		/gb=NM_000843			·
		/gi=6006006/ug=Hs.248131 /len=6122			
13247	0.036386	phosphoserine phosphatase (PSPH),	NM 004577	Hs.56407	NP 004568
		mRNA /cds=(20,697) /gb=NM 004577			
		/gi=21614545 /ug=Hs.56407 /len=1432		-	
13281	0.033724	cDNA FLJ11379 fis, clone	AK021441	Hs.200113	700
		HEMBA1000469. /gb=AK021441			
5		/gi=10432627 /ug=Hs.200113 /len=1672	** ,		
13289	0.033724	cDNA: FLJ23538 fis, clone LNG08010,	AK027191	Hs.240443	
. 02.00	0.000, 2.	highly similar to BETA2 MEN1 region clone			
1		epsilon/beta mRNA. /gb=AK027191			
•		/gi=10440260 /ug=Hs.240443 /len=1746			* "
13315	0.012511	partial RANBP7 gene for RanBP7/importin7	A 1295844	11	
10010	0.012711	and partial ZNF143 gene	7.02.950-1-1		
	·	and partial 2141 145 gene			
13320	0.01/017	cDNA FLJ23879 fis, clone LNG13743.	AK074459	Hs.352648	<del> </del>
13320	0.014317	/gb=AK074459 /gi=18677071	AN074439	115.552040	*
		/ug=Hs.352648 /len=1514		*	
13384	0.026296	DKFZP586D2223 protein, mRNA full length	A 1420544	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	NP 061031
13304	0.036366	insert cDNA clone EUROIMAGE 1476271	AJ420544	×	NP_001031
		Illiseit CDNA Cione EUROIMAGE 1476271	***		
10405	0.040000	and and a ANOL COAR THA aRNA along	A1000457	11- 207000	
13405	0.013000	qw21c02.x1 NCI_CGAP_Ut4 cDNA clone	AI290157	Hs.387096	
	2	IMAGE:1991714 3' similar to contains Alu			. =
-	j. *	repetitive element;contains element L1	•		
	,	repetitive element ;, mRNA sequence			. "
		/clone=IMAGE:1991714 /clone_end=3'		,	
		/gb=Al290157 /gi=3931823 /ug=Hs.387096		18	
4444	2 2 1 2 2 2 2	/len=571			
13444		EST(ye47c11.r1 clone 120884 5')	T96079		NP_598014
13484	0.010447	hypothetical protein FLJ10956 (FLJ10956),	NM_018283	Hs.144407	NP_060753
	,	mRNA /cds=(181,675) /gb=NM_018283			
		/gi=8922791 /ug=Hs.144407 /len=2022			
-		·			
13513	0.020932	EST(PM3-SN0020-270300-001-h08	AW865025		NP_115668
		SN0020)	3.50		
13565	0.042232	EST ni39e06.s1 NCI_CGAP_Lu1 cDNA	AA522708		
		clone IMAGE:979234 3' similar to contains			
		Alu repetitive element; contains MER10.t2		· .	
		MER10 repetitive element ;	0.0		* .
13566	0.042232	EST (cDNA AV753014 NPDclone	AV753014		NP_055635
		NPDALH02 5')			<u></u> .
13592	0.007903	hypothetical gene supported by	XM_074528	200 100 100 1	
		XM_074528 (LOC123829), mRNA			
13594	0.028884	cDNA FLJ30806 fis, clone FEBRA2001334.	AK055368	Hs.150011	
		/gb=AK055368 /gi=16550081			
		/ug=Hs.150011 /len=2915	I /	1	I

		nding To Differentially Expr ssed Genes i			art i
Spot	p-valu	Description	Gene	Unigene	Protein
		÷ "	Accession	Accession	Accession
			No.	No.	No.
13606	0.012511	phosphoribosylaminoimidazole	NM_006452	Hs.117950	NP_006443
* • • •	,	carboxylase,	is t		*
		phosphoribosylaminoimidazole			0.0
		succinocarboxamide synthetase (PAICS),	· · · · · · · · · · · · · · · · · · ·	*	
	*	mRNA /cds=(206,1483) /gb=NM_006452		*	
		/gi=17388802 /ug=Hs.117950 /len=3322.			
13610	0.009373	karyopherin alpha 3 (importin alpha 4)	NM_002267	Hs.3886	NP_002258
:		(KPNA3), mRNA /cds=(92,1657)			
		/gb=NM_002267 /gi=4504898 /ug=Hs.3886			
	- 190	/len=2245			
13615	0.028884	mRNA full length insert cDNA clone	AJ420560	Hs.93231.	e per established
	,	EUROIMAGE 1476475 /gb=AJ420560			1
		/gi=17066424 /ug=Hs.93231 /len=1346			1.
13643	0.039219	glycyl-tRNA synthetase (GARS), mRNA	NM 002047	Hs.293885	NP 002038
	-	/cds=(519,2576) /gb=NM_002047			, -
\ .		/gi=6996009 /ug=Hs.293885 /len=2742			
13644	0.017708	AGENCOURT_6497573 NIH_MGC_125	BM544964	Hs.406354	7
	· · · ·	cDNA clone IMAGE:5588748 5', mRNA			
-		sequence /clone=IMAGE:5588748			1 1
		/clone_end=5' /gb=BM544964	. 1		
٠,		/gi=18776658 /ug=Hs.406354 /len=1184	-		*
13647	0.036799	signal transducer and activator of	NM_139276	Hs.321677	NP 644805
		transcription 3 (acute-phase response	-		
		factor) (STAT3), transcript variant 1, mRNA	-	0	
		/cds=(241,2553) /gb=NM_139276		,	
	· ·	/gi=21618339 /ug=Hs.321677 /len=3455			= ""
13660	0.004849	UI-CF-FN0-aew-b-22-0-UI.s1 UI-CF-FN0	BU608314	Hs.432827	1
		cDNA clone UI-CF-FN0-aew-b-22-0-UI 3',		7	
		mRNA sequence /clone=UI-CF-FN0-aew-b-			.00
	1	22-0-UI /clone_end=3' /gb=BU608314			Ξ .
-	. '	/gi=23274529 /ug=Hs.432827 /len=1144			
13672	0.045433	six transmembrane epithelial antigen of the	NM 012449	Hs.61635	NP_036581
		prostate (STEAP), mRNA /cds=(201,1220)			
		/gb=NM_012449 /gi=22027487		,	-1
	*	/ug=Hs.61635 /len=1330	90		
13675	0.020932	guanine nucleotide binding protein beta	NM_021629	Hs.172654	NP 067642
		subunit 4 (GNB4), mRNA /cds=(281,1303)			
	e .	/gb=NM_021629 /gi=20357531			
	* ;	/ug=Hs.172654 /len=3302			1
13676	0.008683	FLJ22485 fis, clone HRC10901, highly	AK026138	Hs.283473	<del></del>
. 45. 0		similar to AF116718 Homo sapiens	1.1020100		
		PRO2900 mRNA (AK026138.1)		·	
13732	0.04883	oxysterol binding protein-like 9 (OSBPL9),	NM 148909	Hs.21938	NP_683707
.07.02	0.07003	transcript variant 7, mRNA /cds=(20,2260)	140303	1 13.2 1330	-000707
		/gb=NM 148909 /gi=22547175			
		/ug=Hs.21938 /len=2949			1
- '-	1	/ug=118.21880 /1011=2848	F	<del></del>	

		nding To Differentially Expr ssed Genes i			
Spot	p-value	D scription	Gene	Unigene	Prot in
		Accession	Accession	Accession	
	· ,		No.	No.	No.
13734	0.039219	hypothetical protein IMAGE3455200	NM 024006	Hs.324844	NP_076869
		(IMAGE3455200), mRNA /cds=(48,539)			
		/gb=NM_024006 /gi=13124769		. "	
	· ·	/ug=Hs.324844 /len=871		i.	
13735	0.028884	lectin, galactoside-binding, soluble, 8	NM 006499	Hs.4082	NP_006490
13733	0.020004	(galectin 8) (LGALS8), mRNA	14141_000433	115.4002	INF_000490
		/cds=(384,1463) /gb=NM_006499			
10757	0.045400	/gi=21361353 /ug=Hs.4082 /len=2593	NN 040400		110 05-50
13757	0:045433	PABP-interacting protein 2 (PAIP2), mRNA	NM_016480	Hs.396644	NP_057564
		/cds=(150,533) /gb=NM_016480		=_	
		/gi=19923458 /ug=Hs.396644 /len=1514			
13762	0.007903	chloride intracellular channel 4 (CLIC4),	NM_013943	Hs.25035	NP_039234
•		mRNA /cds=(198,959) /gb=NM_013943			
- 5		/gi=7330334 /ug=Hs.25035 /len=4318			
13770	0.005916	Similar to hypothetical protein FLJ22789,	BC029120	Hs.48994	48.77
		clone MGC:34762 IMAGE:5189049,			
-	*	mRNA, complete cds /cds=(22,1833)	30		
	- 1	/gb=BC029120 /gi=20810106			1
	1	/ug=Hs.48994 /len=2085			
13778	0.024639	WD repeat domain 9, mRNA; cDNA	AL162036	Hs.225674	NP 387505
10770	0.024000	DKFZp434B249 (from clone	AL 102030	113.220074	_307303
		DKFZp434B249) (AL162036.1)			
13782	0.000000		NIN4 004077	11- 020700	ND 004066
13/62	0.002322	citrate synthase (CS), nuclear gene	NM_004077	Hs.239760	NP_004068
	]	encoding mitochondrial protein, mRNA	* .		
		/cds=(1,1401) /gb=NM_004077		-	
		/gi=4758075 /ug=Hs.239760 /len=1401	_		ļ
13783	0.001661	centrin, EF-hand protein, 2 (CETN2),	NM_004344	Hs.82794	NP_004335
		mRNA /cds=(48,566) /gb=NM_004344			1
		/gi=4757901 /ug=Hs.82794 /len=1087			
13792	0.009373	hypothetical protein MGC30052	NM_144721	Hs.143692	NP_653322
	, ,	(MGC30052), mRNA /cds=(35,703)	- 12		
		/gb=NM_144721 /gi=21389506		1	•
-		/ug=Hs.143692 /len=2260			
13793	0.034059	FLJ12671 Hypothetical protein, mRNA;	AL096734	Hs.301904	NP 112242
		cDNA DKFZp434M011 (from clone			
		DKFZp434M011) /cds=UNKNOWN	*		
	- 3-	/gb=AL096734 /gi=5419867		14.	
		/ug=Hs.301904 /len=3180	,		
13795	0.022722	<del></del>	NM 022901	Hs.128071	NP_075052
13795	0.02272,2	hypothetical protein FLJ21302 (FLJ21302),	NIVI_022901	IDS. 12007 1	NF_075052
	I	mRNA /cds=(91,1203) /gb=NM_022901		50.	
		/gi=12597640 /ug=Hs.128071 /len=3160	¥		
40700	0.044400	DET LESS AND A COSTORIO	NINA CASSES	01. 254545	ND OFFICE
13798	0.011439	SET binding protein 1 (SETBP1), mRNA	NM_015559	Hs.151717	NP_056374
		/cds=(6,4634) /gb=NM_015559			
		/gi=7662121 /ug=Hs.151717 /len=5744			
13812	0.045433	plasminogen activator, tissue (PLAT),	NM_000930	Hs.274404	NP_127509
	1.	transcript variant 1, mRNA /cds=(209,1897)		*	
		/gb=NM_000930 /gi=14702165	-\$c- ·		
		/ug=Hs.274404 /len=2653		1	1

		nding To Differentially Expressed Genes i			
Spot	p-value	Description	Gene	Unigene	Protein
	rie:		Accession	Accession	Accession
	· .		No	No.	No.
13816	0.006524	mRNA for FLJ00005 protein, partial cds.	AK000005	Hs.367690	
		/cds=(1,338) /gb=AK000005 /gi=7209310			·
30		/ug=Hs.367690 /len=4706			
13817	0.04883	MAD, mothers against decapentaplegic 7	NM 005904	Hs.100602	NP 005895
		(Drosophila) (MADH7), mRNA			
- '	-00	/cds=(296,1576) /gb=NM_005904	٠	*	
	•	/gi=5174516 /ug=Hs.100602 /len=3111	* *	.*	
13829	0.042232	FLJ11463 fis, clone HEMBA1001608	AK021525	Hs.288888	··· ,=
	0.0	/cds=UNKNOWN /gb=AK021525	, 1021	7.0.20000	:
	. /	/gi=10432722 /ug=Hs.288888 /len=1898			
13840	0.031226	FLJ11292 (FLJ11292) hypothetical protein,	NM_018382	Hs.272246	NP_060852
19040	0.031220	mRNA /cds=(150,614) /gb=NM_018382.	14141_010302	115.212240	_000032
		/gi=8922980 /ug=Hs.272246 /len=1948		1).	1
٠.		191-0922960 /ug-ns.2/2240 /leli=1946			. *
12047	0.020004	handhatiad matain MCC4544C	NINA 450200	11- 05005	ND 000044
13847	Ų.U20884	hypothetical protein MGC45416	NM_152398	Hs.95835	NP_689611
-		(MGC45416), mRNA /cds=(205,504)			
		/gb=NM_152398 /gi=22748848			
		/ug=Hs.95835 /len=660			
13849	0.022722	hypothetical protein FLJ31951 (FLJ31951),	NM_144726	Hs.349306	NP_653327
		mRNA /cds=(28,2103) /gb=NM_144726			
•,		/gi=21389514 /ug=Hs.349306 /len=3362			
			4		
13885	0.031226	EST DKFZp434H1418_r1 434	AL048856		NP_006531
	-	(synonym:htes3) cDNA clone			f .
		DKFZp434H1418			
13887	0.022722	EST (qh80g11.x1	AI249016		NP 115602
. •		Soares_fetal_liver_spleen_1NFLS_S1			_
'		IMAGE:1851044 3')			
13891	0.017708	cDNA FLJ38641 fis, clone	AK095960	Hs.24831	
	-	HHDPC2003983. /gb=AK095960			
	•	/gi=21755328 /ug=Hs.24831 /len=2685			·[
13914	0.024639	hypothetical protein FLJ11193 (FLJ11193),	NM_018356	Hs.151046	NP_060826
	0.02.000	mRNA /cds=(115,1443) /gb=NM_018356		17.0.101010	
		/gi=8922930 /ug=Hs.151046 /len=2719	ā	100	
.		/gi=0322330 /ug=[13:101040 /ieii=27 13	ļ	Į.	
13922	0.020033	cDNA FLJ36579 fis, clone	AK093898	Hs.48653	-
13322	0.020932	TRACH2012647. /gb=AK093898	AVOSSOSO	ITS.40003	
					· .
12022	0.044420	/gi=21752852 /ug=Hs.48653 /len=2318	A D 0 5 4 5 4 4	11- 00504	ND 000755
13923	0.011439	mRNA for KIAA1754 protein, partial cds.	AB051541	Hs.28501	NP_203755
	·	/cds=(32,1816) /gb=AB051541	-	•	
10000	0.040544	/gi=12698052 /ug=Hs.28501 /len=4088	1100==10	11.110=-12	<del> </del>
13926	0.012511	wo08b04.x1 NCI_CGAP_Pan1 cDNA clone	A1927713	Hs.137546	
		IMAGE:2454703 3', mRNA sequence			
		/clone=IMAGE:2454703 /clone_end=3'			
		/gb=Al927713 /gi=5663677 /ug=Hs.137546	1		
	.81	/len=509			
13952	0.007185	cDNA FLJ13342 fis, clone	AK023404	Hs.255890	
		OVARC1001950. /gb=AK023404			
	I	/gi=10435328 /ug=Hs.255890 /len=2490		I	1 '

Spot	p-value	nding To Differentially Expressed Genes i Description	Gene Accession	Unigene Accession	Protein Accession
			No.		
13956	0.011/30	zh79h09.s1	W92715	<b>No.</b> Hs.59358	No.
13930	0.011435	Soares_fetal_liver_spleen_1NFLS_S1	1	118.39330	
		cDNA clone IMAGE:418337 3', mRNA	*		
		sequence /clone=IMAGE:418337			•
	**	/clone_end=3' /gb=W92715 /gi=1421867			
÷		/ug=Hs.59358 /len=397	. *		
13958	0.020210	ws64f01.x1 NCI_CGAP_Brn23 cDNA clone	Ανμορέρρο	Hs.161332	
13930	0.0392 19   -	IMAGE:2501977 3', mRNA sequence	AVVU20029	Ins. 101332	* .
		/clone=IMAGE:2501977 /clone end=3'	30.		
1	·			Ì .	
		/gb=AW026829 /gi=5885633	_		
13962	0.04000	/ug=Hs.161332 /len=480	DC570444	Un 407445	
13962	0.04883	602591134F1 NIH_MGC_77 cDNA clone	BG570144	Hs.437115	
		IMAGE:4717761 5', mRNA sequence			
15		/clone=IMAGE:47,17761 /clone_end=5'	* (		
14		/gb=BG570144 /gi=13577797			
10000	0.000004	/ug=Hs.437115 /len=672	141,000,450	11 400700	7
13990	0.026691	mRNA, cDNA DKFZp686J19116 (from	AL833458	Hs.428760	
		clone DKFZp686J19116) /gb=AL833458			9.0
11001	75 75 75 75	/gi=21734100 /ug=Hs.428760 /len=3297	D14740704	070070	
14021	0.020932	UI-E-EJ0-ahg-j-09-0-UI.r1 UI-E-EJ0 cDNA	BM712784	Hs.278378	the second second
		clone UI-E-EJ0-ahg-j-09-0-UI 5', mRNA.			
		sequence /clone=UI-E-EJ0-ahg-j-09-0-UI	9.0		
		/clone_end=5' /gb=BM712784		*	
		/gi=19026042 /ug=Hs.278378 /len=1255			
14026	0.028884	EST (7b55g08.x1 NCI_CGAP_Lu24 cDNA	BE551192		NP_620278
		clone IMAGE:3232190 3')	1	<u> </u>	
14053	0.04883	EST (yg47c12.s1 Soares infant brain 1NIB	R45369		
		IMAGE:35771 3') (contains Alu repetitive	*:		
		element)			
14062	0.045433	P1-Cdc21 mRNA /cds=(1,2774)	X74794	Hs.154443	
		/gb=X74794 /gi=683749 /ug=Hs.154443			
		/len=3273			
14069	0.008683	EST np77c06.s1 NCI_CGAP_Pr2 cDNA	AA622809		
		clone IMAGE:1132330 similar to contains		•	-30
_		Alu repetitive element;			
14105	0.031226	Kruppel-like factor 12 (KLF12), transcript	NM_007249	Hs.23510	NP_057369
• •		variant 1, mRNA /cds=(199,1407)			
		/gb=NM_007249 /gi=21071073	•		·
		/ug=Hs.23510 /len=10891			<u> </u>
14108	0.020932	EST (381219 MAGE resequences MAGK)	AW969142		
14112	0.00953	BX094467 Soares fetal liver spleen 1NFLS	BX094467	Hs.122140	<del>                                     </del>
	0.00000	cDNA clone IMAGp998J03121, mRNA	7.00 1.101	]	
		sequence			1 .
		/clone=IMAGp998J03121_;_IMAGE:12451			1
	· v	4 /gb=BX094467 /gi=27827126			
	1	/ug=Hs 122140 /len=805	1	1	<u> </u>

		nding To Differentially Expressed Genes i			
Spot	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
	,		No.	No.	No.
14121	0.04883	spindlin-like protein 2 (SPIN2), mRNA	NM_019003	Hs.82577	NP_061876
:	,	/cds=(494,1192) /gb=NM_019003			
		/gi=9506850 /ug=Hs.82577 /len=2483			
14143	0.005359	xu31e02.x1 NCI_CGAP_Ov40 cDNA clone	AW419224	Hs.371445	7
• -		IMAGE:2801786 3' similar to contains Alu			
		repetitive element;, mRNA sequence	·		
		/clone=IMAGE:2801786 /clone_end=3'	1 46		*
		/gb=AW419224 /gi=6947156		*	
		/ug=Hs.371445 /len=471			,
14183	0.005916	EST(cDNA clone IMAGE:3212553 3')	BE467153		NP_059996
		EST(clone IMAGE:2509657 3')	AI955713		
14187		EST(RC5-HT0581-210300-021-B05	BE175638		
		HT0581)		*	*
14188	0.022722	mRNA; cDNA DKFZp547I1315 (from clone	AL 831836	Hs.356494	
		DKFZp547I1315) /cds=(1,299)	, 1200 1,000		X
-(-		/gb=AL831836 /gi=21732315		200	- V
		/ug=Hs.356494 /len=3552		, i	
14228	0.040798		AK122581	Hs.127830	
11220	9,040700	/gb=AK122581 /gi=28273117	/ ((12200)	113.127000	7 .
		/ug=Hs.127830 /len=4752			
14231	0.022722	wg85c11.x1	AI743032	Hs.310364	-
14231	0.022122	Soares_NSF_F8_9W_OT_PA_P_S1 cDNA		IU204	4
		clone IMAGE:2371892 3' similar to		\	
		contains Alu repetitive element;, mRNA			
**		sequence /clone=IMAGE:2371892			
		/clone_end=3' /gb=Al743032 /gi=5111320	e a		
4 40 40	0.000704	/ug=Hs.310364 /len=562	NO 004007		
14249		mitochondrion, complete genome	NC_001807		<u> </u>
14279	0.033724	AL535026 LTI_FL013_FBrn1 cDNA clone	AL535026	Hs.268474	
		CS0DF007YJ21 3 prime, mRNA sequence			-00
•	1	/clone=CS0DF007YJ21 /clone_end=3'			9
	* *	/gb=AL535026 /gi=12798519			
		/ug=Hs.268474 /len=921			
		EST(clone ADBAOB04 5')	AV705982		NP_006633
14343	0.036386	UI-H-FH1-bfp-m-06-0-UI.s1	BU619573	Hs.312629	0.
		NCI_CGAP_FH1 cDNA clone UI-H-FH1-		. *	
		bfp-m-06-0-UI 3', mRNA sequence			
0		/clone=UI-H-FH1-bfp-m-06-0-UI			
40		/clone_end=3' /gb=BU619573			
	-	/gi=23285788 /ug=Hs.312629 /len=1168		400	
14346	0.042232	cDNA clone CBLAPH08 5'	AV739829		
14374	0.024639	RC4-HT0277-160200-013-d07 HT0277	BE151126	Hs.158600	7.
		cDNA, mRNA sequence /gb=BE151126			
		/gi=8613847 /ug=Hs.158600 /len=571	*		
14379	0.022722	Similar to hypothetical protein FLJ20489,	BC039535	Hs.440840	NP_77616
		clone MGC:50559 IMAGE:5744381,	,		
		mRNA, complete cds /cds=(290,1078)			
		/gb=BC039535 /gi=24659157	*	3	
	1	/ug=Hs.440840 /len=2078			

		nding To Differ ntially Expr ssed Gen s			
Spot	p-value	Description	Gene	Unigene	Prot in
		380	Accession	Accession	Acc ssion
•	41		No.	No.	No.
14386	0.033724	UI-E-EJ0-aik-i-20-0-UI r1 UI-E-EJ0 cDNA	BM727413	Hs.112619	
	<u>'</u>	clone UI-E-EJ0-aik-i-20-0-UI 5', mRNA			, A.
	*	sequence /clone=UI-E-EJ0-aik-i-20-0-UI			,
		/clone_end=5' /gb=BM727413			
		/gi=19048746 /ug=Hs.112619 /len=1667			
14428	0.033724	EST(cDNA clone IMAGE:1760118 3')	Al209166		NP 07922
14451		No significant match	SEQ.ID.No.13		141 07322
14472			OEQ.10.140.10		
14478		EST(Erythroid Cells (LCB ax library) cDNA	BG943485	. ITE	NP 71491
1.4470	0.020091		DG945400		1149 IV
4.405	0.005750	clone ax38c12 random )	050 ID N - 74		-
		No significant match	SEQ.ID.No.74		1,000
14504		No significant match (ORF:none)	SEQ.ID.No.22		
14517	0.024639	xq09e02.x1 NCI_CGAP_Ut1 cDNA clone	AW517395	Hs.445194	* .
		IMAGE:2750138 3' similar to contains Alu			
		repetitive element;, mRNA sequence			**
	ļ	/clone=IMAGE:2750138 /clone_end=3'			
•		/gb=AW517395 /gi=7155477			· .
		/ug=Hs.445194 /len=519			
14519	0.019241	ATP-binding cassette, sub-family A	NM 018672	Hs.180513	NP_75842
		(ABC1), member 5 (ABCA5), transcript			
	2.5	variant 1, mRNA /cds=(1219,6147)		*	*
		/gb=NM_018672 /gi=27262623	,		
	ĺ	/ug=Hs.180513 /len=7044	1 . 1	*	
14521	0.040642	HSC15D092 normalized infant brain cDNA	Z39248	Hs.27328	
14321	0.049042	cDNA clone c-15d09 3', mRNA sequence	239240	IDS.27320	
			· ,		
		/clone=c-15d09 /clone_end=3' /gb=Z39248			
		/gi=562440 /ug=Hs.27328 /len=352	*- /	. ~	
11222			10.5		
14526		EST (UI-HF-BL0-adc-e-05-0-UI.s1	AW575379		
14535	0.034059	EST (oh07d11.s1 NCI_CGAP_Kid3 cDNA	AA862627		•
*		clone IMAGE:1457109 3')			
14536	0.026691	hypothetical protein FLJ14117 (FLJ14117),	NM_022777	Hs.61809	NP_07361
	- N	mRNA /cds=(41,598) /gb=NM_022777			
		/gi=12232462 /ug=Hs.61809 /len=2359			
	1		• • /		
14551	0.049642	EST (ng23f02.s1 NCI_CGAP_Ov2 cDNA	AA502813		1
		clone IMAGE:930267 similar to contains		-	
	•	Alu repetitive element)	**	• .	
14553	0.036799	hypothetical protein H41 (H41), mRNA	NM 017548	Hs.283690	NP_06001
	3,555,55	/cds=(324,1100) /gb=NM_017548	1.1111_0 17070	1.13.20000	_99001
		/gi=24475997 /ug=Hs.283690 /len=3346			
14565	0.020210		A10742C0	LI 200207	
14303	0.039219	oq98a10.x1 NCI_CGAP_Co12 cDNA clone	Al074369	Hs.386367	
	, r	IMAGE:1594362 3' similar to contains Alu	*		-
	1	repetitive element;, mRNA sequence		1.	
		/clone=IMAGE:1594362 /clone_end=3'	-00		
		/gb=Al074369 /gi=3401013 /ug=Hs.386367			
	1	/len=478			

		nding To Differentially Expressed Genes i			<b>D</b>
Spot	p-valu	Description	Gene	Unigene	Protein
	200		Accession	Accession	Accession
			No.	No.	No.
4567	0.017708	UI-H-FH1-bfp-m-06-0-UI.s1	BU619573	Hs.312629	
		NCI_CGAP_FH1 cDNA clone UI-H-FH1-			=
		bfp-m-06-0-UI 3', mRNA sequence			-
		/clone=UI-H-FH1-bfp-m-06-0-UI			8
		/clone_end=3' /gb=BU619573			1
		/gi=23285788 /ug=Hs.312629 /len=1168			. *
14572	0.034059	hi79g03.x1 Soares_NFL_T_GBC_S1 cDNA	AW661990	Hs.409964	
· · · · · ·		clone IMAGE:2978548.3' similar to	```		
,		gb:M97016 BONE MORPHOGENETIC			
	4.11	PROTEIN 8 PRECURSOR mRNA		1	
		sequence /clone=IMAGE:2978548			
		/clone_end=3' /gb=AW661990 /gi=7454526			9
14610	0.022724	/ug=Hs.409964 /len=528 EST (AL536815 LTI FL013_FBrn1 clone	AL536815		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
14612	0.033724		AE000010		- (
14600	0.012511	CS0DF020YK05 5') UI-H-ED1-axs-i-05-0-UI.s1	PO014144	Ho 105045	
14629	0.012511		BQ014114	Hs.195045	0.0
		NCI_CGAP_ED1 cDNA clone			
		IMAGE:5833036 3', mRNA sequence	, e t		7-
		/clone=IMAGE:5833036 /clone_end=3'		6	
		/gb=BQ014114 /gi=19739015	*	*	
		/ug=Hs.195045 /len=1024			
14638	0.03318	602623674F1 NCI_CGAP_Skn4 cDNA	BG677029	Hs.123445	
		clone IMAGE:4748515 5', mRNA sequence			
	- 1	/clone=IMAGE:4748515 /clone_end=5'	,		
		/gb=BG677029 /gi=13908426	•	9	
		/ug=Hs.123445 /len=882			
14648	0.012381	mRNA; cDNA DKFZp667J1615 (from clone	AL713792	Hs.120388	
		DKFZp667J1615) /gb=AL713792			: .
		/gi=19584550 /ug=Hs.120388 /len=4127			
14653	0.011439	EST (MR0-BT0798-280400-001-d04	BE095198	- 19	
		BT0798 cDNA)	28		
14663	0.039219	EST(zs14a10.r1 NCI_CGAP_GCB1 cDNA	AA243380		NP_05731
		clone IMAGE:685146 5')			
14668	0.039219	UI-H-BI3-akn-c-08-0-UI.s1	AW450357	Hs.438438	, -==
		NCI_CGAP_Sub5 cDNA clone			
	- 22	IMAGE:2734839 3', mRNA sequence			
,		/clone=IMAGE:2734839 /clone_end=3'			
	. \	/gb=AW450357 /gi=6991133	, ,		
	. ,	/ug=Hs.438438 /len=794			,
14682	U UNBBS	clone IMAGE:5277612, mRNA	BC043650	Hs.378059	<del> </del>
17002	0.04003	/gb=BC043650 /gi=27693174	1200-3030	13.070003	*
		/ug=Hs.378059 /len=3723	0		
14694	0:020740		VK003330	Hs.348902	
14094	0.0397 19	cDNA FLJ35910 fis, clone TESTI2009987	AK093229	175.540902	-
		/gb=AK093229 /gi=21752038			*
14005	0.04000	/ug=Hs.348902 /len=2035	A A O O O O A E		ļ
14695	0.04883	EST(cDNA clone IMAGE:1240639 3'	AA808945		
		similar to contains Alu repetitive element)			L

Genes	Correspoi	nding To Differentially Expressed Genes i	n Figure 14 - D	iabetes	
		Description	Gene	Unigene	Protein
•			Accession	Accession	Accession
			No.	No.	No.
14697	0.033724	EST00015 NCI_CGAP_Lu5 cDNA clone	BF707422	Hs.298289	110.
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	IMAGE:1568018 3', mRNA sequence			~ '
		/clone=IMAGE:1568018 /clone_end=3'			
		/gb=BF707422 /gi=11999083	Ċ	161	
		/ug=Hs.298289 /len=858			
14709	2.56E-04	Similar to hypothetical protein FLJ20378,	BC035643	Hs.202613	
		clone IMAGE:5547904, mRNA, partial cds			
		/cds=(1,802) /gb=BC035643 /gi=23274249			
	*	/ug=Hs.202613 /len=1653	,		-;
14719	0.036386	EST(cDNA clone IMAGE:2387836 3'	AI760555	18 5 :	NP_658913
	***************************************	similar to contains Alu repetitive			-3333
	*	element contains element MER22 repetitive			••
		element;)			
14720	0.039219	cDNA FLJ32224 fis, clone PLACE6004336.	AK056786	Hs.406907	<del></del>
	-;;	/gb=AK056786 /gi=16552290			
- ,		/ug=Hs.406907 /len=3076			,
14735	0.031226	cDNA, 5' end /clone=IMAGE:3536351	BE264613	Hs.335864	NP_663302
-		/clone end=5' /gb=BE264613 /gi=9138170			
		/ug=Hs.335864 /len=759			
14736	0.00208	FLJ33160 fis, clone UTERU2000485	AK057722	Hs.124733	
		/cds=UNKNOWN /gb=AK057722			1
		/gi=16553641 /ug=Hs.124733 /len=2328	*		
14746	0.039219	tw36f05.x1 NCI_CGAP_Ut1 cDNA clone	AI889108	Hs.311004	
		IMAGE:2261793 3' similar to contains Alu	et		
-		repetitive element;, mRNA sequence			
		/clone=IMAGE:2261793 /clone_end=3!			1
		/gb=Al889108 /gi=5594272 /ug=Hs.311004			· .
		/len=489	-		·
14747	0.003954	ESTs, cDNA, 3' end /clone=IMAGE:432611	AA699443	Hs.193213	
, .		/clone_end=3' /gb=AA699443 /gi=2702637			1
ļ		/ug=Hs.193213 /len=391 zi33f06.s1	ļ		
	·				-
14754	0.04883		AL832702	Hs.125019	
		clone DKFZp313P0434) /gb=AL832702			
		/gi=21733281 /ug=Hs.125019 /len=2995			
	0.024734				
14770	0.014917	EST48277 Fetal spleen cDNA 3' end	AA342474	Hs.291585	
		similar to EST containing Alu repeat,	=		
*		mRNA sequence /clone_end=3'			
		/gb=AA342474 /gi=1994946			
1.55	2.2.2	/ug=Hs.291585 /len=430	5.1055-5		1
14797	0.045433	EST (3' end clone=IMAGE:2540192)	BI495875	Hs.347887	NP_003109
		/clone_end=3' /gb=BI495875 /gi=15335219	-50	,	1
		/ug=Hs.347887 /len=354	410.470	· · · · · · · · · · · · · · · · · · ·	
14801		EST(cDNA clone IMAGE:2236988 3'.)	AI917081		
14806	0.013668	cDNA FLJ14279 fis, clone PLACE1005574.	AK024341	Hs.250383	
	·	/gb=AK024341 /gi=10436703			
<u></u>	<u> </u>	/ug=Hs.250383 /len=2005	L		

Spot	p-value	Description	Gene Acc ssion	Unigene Accession	Protein Accession
			No.	No.	No.
14814	0.033724	EST387118 MAGE resequences, MAGN	AW975013	Hs.292437	
		cDNA, mRNA sequence /gb=AW975013			
		/gi=8166216 /ug=Hs.292437 /len=685			100
14819	0.034059	FLJ14036 fis, clone	AK024098	Hs.306663	'
		HEMBA1004709/cds=UNKNOWN	•	-	
		/gb=AK024098 /gi=10436394	7		÷ .=
		/ug=Hs.306663/len=2067		1-8	L
14851	0.024639	UI-H-BW1-amm-h-09-0-UI.s1	BF512783	Hs.443691	, , , , , , , , , , , ,
	•	NCI_CGAP_Sub7 cDNA clone	) ·		Į.
	. ,	IMAGE:3070696 3', mRNA sequence	* 1		1
•		/clone=IMAGE:3070696 /clone_end=3'		`	
	*	/gb=BF512783 /gi=11597962		•	
	,	/ug=Hs.443691 /len=568		4	
14874	0.045433	yp52f01.s1 Soares retina N2b4HR cDNA	H40700	Hs.33792	- 11111
	1	clone IMAGE:191065 3'; mRNA sequence			-
	] . , ,	/clone=IMAGE:191065 /clone end=3'		0) -	
	]	/gb=H40700 /gi=916752 /ug=Hs 33792			9
		/len=504			
14933	0.002753	No significant match, ORF-2(2~412)	SEQ.ID.No.96		-
14937					
14962	0.017657	No significant match,			
		ORF+3(30~140),+2(131~232)	SEQ.ID.No.72		l

		TABLE 3H	01		
		nding To Differentially Express d Genes			
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
75	0.020001	GC20 protein (=AF077052 protein	AF064607	No.	No. NP_005866
75		translation factor sui1 homologue)	AF004007		NF_005666
103		supervillin (SVIL), transcript variant 2,	NM_021738	Hs.154567	NP 068506
103	0.024024	mRNA /cds=(754,7398) /gb=NM_021738	14141_021730	ПS. 154567	NP_00000
		/gi=11496981 /ug=Hs.154567 /len=8300			*
		7gi=114909017ug=11s.1343017lett=6300			
120	0.007323	Sjogren's syndrome/scleroderma	NM_006396	Hs.25723	NP_006387
120	1.007020	autoantigen 1 (SSSCA1), mRNA	000000	110.20720	
1		/cds=(21,620) /gb=NM_006396	*	32.00	
		/gi=5453837 /ug=Hs.25723 /len=661			
131	0.030461	AD-012 protein (LOC55833) (=AB040924	NM 018449	i i i i	NP_060919.
-		KIAA1491)			
152	0.004433	mRNA; cDNA DKFZp761P18121 (from	AL834147.	Hs.44198	
-		clone DKFZp761P18121)	7		40
	. 11	/cds=(127,2289) /gb=AL834147			
		/gi=21739620 /ug=Hs.44198 /len=4286			
153	0.037129	cDNA, 5' end /clone=IMAGE:5405127	BI868971	Hs.25523	NP_036231
	- (	/clone_end=5' /gb=BI868971	1		
		/gi=16042644 /ug=Hs 25523 /len=730			
154	0.028474	hypothetical protein DJ328E19.C1.1	NM_015383	Hs.218329	NP_056198
		(DJ328E19.C1.1), mRNA /cds=(18,2783)		,	1
		/gb=NM_015383 /gi=7657016		(10)	
4 4		/ug=Hs.218329 /len=3689			
175	0.023151	KIAA1415 protein (PRex1), mRNA	NM_020820	Hs.109315	NP_065871
		/cds=(24,5003) /gb=NM_020820			
	* 6	/gi=19882228 /ug=Hs.109315 /len=5861	4		•
					ND 000700
278	0.014988	coatomer protein complex, subunit	NM_016128	Hs.266914	NP_663768
		gamma (COPG), mRNA /cds=(76,2700)			
	*	/gb=NM_016128 /gi=21359909		*	•
004	0.000000	/ug=Hs.266914 /len=3075	NIM OOFOOO	U- 00047	ND 005000
284	0.039603	translin-associated factor X (TSNAX),	NM_005999	Hs.96247	NP_005990
		mRNA /cds=(159,1031) /gb=NM_005999		-	, ·
	\$*	/gi=20302159 /ug=Hs.96247 /len=2667			
345	0.004433	cofactor required for Sp1 transcriptional	NM 004270	Hs.279902	NP_004261
545	0.004433	activation, subunit 9, 33kDa (CRSP9),	14141_004270	113.275502	
		mRNA /cds=(63,764) /gb=NM_004270	, 0		
		/gi=22001418 /ug=Hs.279902 /len=1235	÷		
354	0.018694	stromal cell-derived factor 2 (SDF2),	NM_006923	Hs.118684	NP_008854
3.	1.5.5004	mRNA /cds=(40,675) /gb=NM_006923	-333320		
		/gi=14141194 /ug=Hs.118684 /len=1075		-	
		/ / / / / / / / / / / / / / / / / / /			
418	0.013901	tumor protein D52-like 1 (TPD52L1),	NM 003287	Hs.16611	NP_003278
		mRNA /cds=(181,795) /gb=NM_003287			
		/gi=4507640 /ug=Hs.16611 /len=1325	,		1 '

G nes	Correspon	nding To Differentially Expressed Gene	s in Figure 15 - F	lyperlipidemi	a
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
429	0.01738	NPD009 protein (NPD009), mRNA	NM_020686	Hs.283675	NP_065737
		/cds=(1327,1677) /gb=NM_020686		*	. +
		/gi=24476005 /ug=Hs.283675 /len=2514		,	
	-				
451	0.047854	golgi phosphoprotein 2 (GOLPH2),	NM_016548	Hs.182793	NP_808800
		mRNA /cds=(151,1353) /gb=NM_016548	<u> </u>		-
		/gi=7706084 /ug=Hs.182793 /len=3042	-		
	, , , , , , , , , , , , , , , , , , ,		*	*	
469	0.041375	Similar to adducin 1 (alpha), clone	BC042998	Hs.183706	NP_789771
		MGC:44427 IMAGE:5297337, mRNA,			_ ;
* • , 3		complete cds /cds=(869,2857)			
		/gb=BC042998 /gi=28175763			
	-	/ug=Hs.183706 /len=4761			
512	0.030461	myosin IXB (MYO9B), mRNA	NM_004145	Hs.159629	NP_004136
. :		/cds=(1,6069) /gb=NM_004145			<del>-</del>
		/gi=4758749 /ug=Hs.159629 /len=6069			-0
572	0.047755	APG5 autophagy 5-like (S. cerevisiae)	NM 004849	Hs.11171	NP 004840
		(APG5L), mRNA /cds=(327,1154)			
		/gb=NM_004849 /gi=4757797	. , ,		
		/ug=Hs.11171 /len=3247			
573	0.005942	ancient ubiquitous protein 1 (AUP1),	NM 012103	Hs.173736	NP 036235
91.5		mRNA /cds=(69,1499) /gb=NM_012103			
	*	/gi=6912259 /ug=Hs.173736 /len=1664	,		
608	0.009862	OTF3 gene	Z11900	2 - 2 - 4	1
611	0.036892	podocalyxin-like (PODXL), mRNA	NM 005397	Hs.16426	NP_005388
		/cds=(251,1837) /gb=NM 005397	,		
•		/gi=4885556 /ug=Hs.16426 /len=5869			,
687	0.039603	mutS 3 (E. coli) (MSH3), mRNA	NM_002439	Hs.42674	NP_002430
		/cds=(17,3403) /gb=NM_002439			
		/gi=4505248 /ug=Hs.42674 /len=4374	,		
711	0.047854	NADH dehydrogenase (ubiquinone) 1	NM_005002	Hs.75227	NP 004993
		alpha subcomplex, 9, 39kDa (NDUFA9),			
		mRNA /cds=(20,1153) /gb=NM_005002			
		/gi=20127470 /ug=Hs.75227 /len=1343			
:		<b></b>	*	,	
825	0.024824	thioredoxin-like 2 (TXNL2), mRNA	NM_006541	Hs.42644	NP_006532
		/cds=(5,1012) /gb=NM 006541			
	•	/gi=5730103 /ug=Hs.42644 /len=1942		. *	
839	0.037129	KIAA0781	AB018324		
840		MAX interacting protein 1 (MXI1),	NM 005962	Hs.118630	NP_569157
- :•		transcript variant 1, mRNA	1		
		/cds=(308,994) /gb=NM_005962	.v.		
:	-	/gi=18641369 /ug=Hs.118630 /len=2643			1
		1. 3. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	,		
865	0.034784	mitochondrion, complete genome	NC 001807		
941		polybromo 1 (PB1), mRNA /cds=(15,935)		Hs.44143	NP 060783
	3.332.000	/gb=NM_018165 /gi=8922564	7.00	1,0.7,10	
		/ug=Hs.44143 /len=3131	-		
	1	/ 4g   110.77 170 /101170 10 1	I	1	

		nding To Differentially Expressed Genes				
Spot	p-valu	- 1 1 1 • 1 • 1 • 1 · 1 · 1 · 1 · 1 · 1 ·	Gene	Unigene	Protein	
			Acc ssion No.	Accession	Accession	
				No.	No.	
985	0.011929	PABP-interacting protein 2 (PAIP2),	NM_016480	Hs.396644	NP_057564	
200	0.911525	mRNA /cds=(150,533) /gb=NM_016480	11111_0 10400	1113.000044	_007001	
	-		(7)			
		/gi=19923458 /ug=Hs.396644 /len=1514				
*						
993	0.039603	CREB binding protein (Rubinstein-Taybi	NM_004380	Hs.23598	NP_004371	
		syndrome) (CREBBP), mRNA				
		/cds=(199,7527) /gb=NM_004380	•		,	
		/gi=4758055 /ug=Hs.23598 /len=8694	D. &			
4000	0.044000	v-fos FBJ murine osteosarcoma viral	NIM ODEDED	LIS OF CAT	ND OCEDAS	
1023	0.011929		NM_005252	Hs.25647	NP_005243	
	4. 1	oncogene (FOS), mRNA /cds=(156,1298)	7 71			
		/gb=NM_005252 /gi=6552332		. ,		
200	-0.7	/ug=Hs.25647 /len=2084				
1051	0.006254	HSPC133 protein (HSPC133), mRNA	NM_014168	Hs.273063	NP_054887	
	*, * * * * * * * * * * * * * * * * * *	/cds=(83,481) /gb=NM_014168	=			
144	• • •	/gi=7661791 /ug=Hs.273063 /len=963	*			
4070	0.04466		NINA 044040	11- 40050	ND 054700	
1073	0.04496	HSPC009 protein (HSPC009), mRNA	NM_014019	Hs.16059	NP_054738	
	'	/cds=(20,340) /gb=NM_014019	1 * 1 2		+,	
		/gi=7661731 /ug=Hs.16059 /len=793		·		
1091	0.028474	retinoblastoma binding protein 2	NM 005056	Hs.76272	NP 005047	
	0.020	(RBBP2), mRNA /cds=(153,5321)	-			
				.y		
		/gb=NM_005056 /gi=4826967				
		/ug=Hs.76272 /len=6455		n 90		
1115	0.032563	H3 histone, family 3A (H3F3A), mRNA	NM_002107	Hs.181307	NP_002098	
7		/cds=(116,526) /gb=NM_002107			4 4	
		/gi=22027640 /ug=Hs.181307 /len=1047			* ,	
		<b>3</b>				
1134	0.030603	cDNA FLJ30093 fis, clone	AK054655	Hs.349261		
1,134	0.039003		AK034033	1115.545201	. * *	
		BNGH41000033. /gb=AK054655	* #	· .		
-		/gi=16549241 /ug=Hs.349261 /len=2926	in the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the		. •	
				Or .	*	
1143	0.020091	mRNA, chromosome 1 specific transcript	AB007962	Hs.406706		
		KIAA0493. /gb=AB007962 /gi=3413936			• • • •	
		l	- 1			
4400	0.040004	/ug=Hs.406706 /len=5734	A1400 4400	11- 070004	<del> </del>	
1169	0.013901	cDNA FLJ14044 fis, clone	AK024106	Hs.278004		
		HEMBA1006124. /gb=AK024106	İ			
		/gi=10436404 /ug=Hs.278004 /len=1398	-		1.	
	*		i	*		
1171	0.021575	integrin, beta 1 (fibronectin receptor, beta	NM 002211	Hs.287797	NP 596867	
1171	0.021373	,	002211	110.207707		
	*	polypeptide, antigen CD29 includes				
		MDF2, MSK12) (ITGB1), transcript	1, ,			
	. (	variant 1A, mRNA /cds=(127,2523)			= 100	
٠.	4	/gb=NM_002211 /gi=19743812		1		
•		/ug=Hs 287797 /len=3700				
• •					-	
1100	0.005075	E hay only protein 25 (EDVO25) mDNA	NM 012172	Hs.81001	NP_036305	
1183	0.005275	F-box only protein 25 (FBXO25), mRNA	NM_012173	1 10.0 1001	_030303	
		/cds=(177,1052) /gb=NM_012173				
		/gi=16306503 /ug=Hs 81001 /len=1320			<u></u>	
1230	0.030461	DKFZp434B102 (from clone	AL080192			

		nding To Differ ntially Expressed Gener			
Spot	p-value		Gene	Unigen	Protein
-	. *		Accession No.	Accession	Accession
				No.	No.
1236	0.030461	matrix metalloproteinase 9 (gelatinase B,	NM_004994	Hs.151738	NP 004985
		92kDa gelatinase, 92kDa type IV			-
		collagenase) (MMP9), mRNA			
•		/cds=(20,2143) /gb=NM_004994		· //	
		/gi=4826835 /ug=Hs.151738 /len=2334			
1257	0.020001	isovaleryl-CoA dehydrogenase (IVD)	AF038318	1 1	
12,01			AI 030310		
4200		gene, exon 12 and partial cds	NIM ODIOZ	115 00000	ND 440507
1280	0.035142	hypothetical protein FKSG32 (FKSG32),	NM_031307	Hs.98682	NP_112597
	·. (	mRNA /cds=(31,1476) /gb=NM_031307			
		/gi=13775233 /ug=Hs.98682 /len=1776			*
	<sub>20</sub> 1		1		
1283	0.029795	interleukin 1 receptor accessory protein	NM_002182	Hs.173880	NP_608273
		(IL1RAP), transcript variant 1, mRNA			
		/cds=(207,1919) /gb=NM 002182			
		/gi=24430220 /ug=Hs.173880 /len=4726	*		
	*	· · · · · · · · · · · · · · · · · · ·			
1286	0.004838	FLJ22781 fis, clone KAIA1958	AK026434	Hs.213236	
1200	0.00	/cds=UNKNOWN /gb=AK026434	711020404	113.2 10200	
•		/gi=10439298 /ug=Hs.213236 /len=2599			
		/gi=10439296 /ug=HS.213236 /ieii=2399		*	*
4000	0.000.474	II	1114 004000	11 00000	ND 470500
1308	0.028474	collagen, type VI, alpha 3 (COL6A3),	NM_004369	Hs.80988	NP_476508
		transcript variant 1, mRNA			
		/cds=(256,9786) /gb=NM_004369		0 2 0	
· · ·		/gi=4758027 /ug=Hs.80988 /len=10558			
1316	0.004822	ubiquitin-like 5 (UBL5), mRNA	NM_024292	Hs.13836	NP_077268
		/cds=(66,287) /gb=NM_024292	:		
		/gi=13236509 /ug=Hs.13836 /len=413			*
1323	0.020091	KIAA1630 protein (KIAA1630), mRNA	NM 018706	Hs.271586	NP_061176
· 4.		/cds=(72,2831) /gb=NM 018706	<del></del>		
		/gi=18375677 /ug=Hs.271586 /len=3180			101
	. *				
1336	0.024824	Novel mRNA from chromosome 1, which	AL006857	Hs.69559	NP 055987
1330	0.024024		AL090031	118.09339	WF_055907
	``·	has similarities to BAT2 genes			
	1	/cds=(58,8163) /gb=AL096857			
1000		/gi=5541862 /ug=Hs.69559 /len=10174			ND 000045
1362	0.016146	ADP-ribosylation factor related protein 1	NM_003224	Hs.389277	NP_003215
1.		(ARFRP1), mRNA /cds=(12,617)		00	
		/gb=NM_003224 /gi=4507448			
		/ug=Hs.389277 /len=1559			
1387	0.024313	hypothetical protein FLJ10335	NM_018062	Hs.279841	NP_060532
		(FLJ10335), mRNA /cds=(34,1161)		- *	· ·
		/gb=NM_018062 /gi=8922359		* *.	*
		/ug=Hs.279841 /len=1678		10	
1407	0.037120	zinc finger protein 9 (a cellular retroviral	NM_003418	Hs.2110	NP_003409
1407	0.03/129		14W_003410	113.2110	_000409
		nucleic acid binding protein) (ZNF9),			
, N	'	mRNA /cds=(103,636) /gb=NM_003418	B	]	
	1 .	/gi=4827070 /ug=Hs.2110 /len=1500	l:	1	<u></u>

		nding To Differentially Expressed General			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No	No.
1449	0.0068	apoptosis related protein APR-3 (APR-3),	NM_016085	Hs.9527	NP_542159
		transcript variant 1, mRNA			
		/cds=(336,851) /gb=NM_016085			
		/gi=18105011 /ug=Hs.9527 /len=1086			*
1464	0.013901	Escherichia coli K-12 MG1655 section	AE000461		
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	351 of 400 of the complete genome		. *	
1481.	0.047854	polymerase (RNA) II (DNA directed)	NM_005034	Hs.351475	NP_005025
		polypeptide K, 7.0kDa (POLR2K), mRNA		×	_
		/cds=(67,243) /gb=NM_005034			
1 04		/gi=14589955 /ug=Hs.351475 /len=540		*	
1530	0.011037	fibroblast growth factor receptor 3	NM 000142	Hs 1420	NP_075254
1000	0.011037	(achondroplasia, thanatophoric dwarfism)	14141_000142	113.1720	141, _019294
•	0	(FGFR3), transcript variant 1, mRNA		· .	-10
	1	/cds=(40,2460) /gb=NM_000142	* *		
		· · · · · · · · · · · · · · · · ·			*
4.FOF	0.045700	/gi=13112046 /ug=Hs.1420 /len=4093	A D 040205	Un 406770	ND. 775024
1535	0.015/33	mRNA for KIAA0752 protein, partial cds.	AB018295	Hs.126779	NP_775934
	*	/cds=(1,1006) /gb=AB018295			
4 = 4 =		/gi=3882224 /ug=Hs.126779 /len=4332	70000		_
1549	0.005746	BRCA1, Rho7 and vatl genes, complete	L78833	*	1 1 1
		cds, and ipf35 gene, partial cds		<u> </u>	
1553	0.047854	lymphocyte cytosolic protein 1 (L-plastin)	NM_002298	Hs.381099	NP_002289
		(LCP1), mRNA /cds=(174,2057)		. V.	
		/gb=NM_002298 /gi=7382490	* *		, it
		/ug=Hs.381099 /len=3723		*	
1581	0.032563	SH3 domain binding glutamic acid-rich	NM_031286	Hs.109051	NP_112576
	1 .	protein like 3 (SH3BGRL3), mRNA			1
•		/cds=(72,353) /gb=NM_031286		1	. 0
		/gi=13775197 /ug=Hs.109051 /len=764	· .		*
1583	0.01738	BTB (POZ) domain containing 1	NM_025238	Hs.21332	NP_079514
		(BTBD1), mRNA /cds=(84,1532)		*	
		/gb=NM_025238 /gi=13376847	*		
		/ug=Hs.21332 /len=3177			* 10
1692	0.026596	DKFZp564L0678 (from clone	AL137514		NP_057375
		DKFZp564L0678)			_
1,724	0.026596	zinc finger RNA binding protein (ZFR),	NM 016107	Hs.173518	NP_057191
- K. E.	0.05,000	mRNA /cds=(44,1300) /gb=NM_016107	_		_
	~	/gi=7706372 /ug=Hs.173518 /len=2734			-0
1756	0.030461	uronyl-2-sulfotransferase (UST), mRNA	NM_005715	Hs.134015	NP_005706
1700	0.000401	/cds=(104,1324) /gb=NM_005715	0007 10		
•		/gi=5032218 /ug=Hs.134015 /len=4196			*
1758	0.030461	cyclin-dependent kinase inhibitor 1C	NM_000076	Hs.106070	NP 000067
1730	0.030401	(p57, Kip2) (CDKN1C), mRNA	11111_000070	113.100070	
	, * .		4.		' :
		/cds=(261,1211) /gb=NM_000076			
4704	000500	/gi=4557440 /ug=Hs.106070 /len=1511	NIM 005704	Un 100000	ND OOF745
1784	0.026596	tetraspan 3 (TSPAN-3), mRNA	NM_005724	Hs.100090	NP_005715
		/cds=(218,979) /gb=NM_005724			
		/gi=21264581 /ug=Hs.100090 /len=1842	· .		
	1	<u> </u>	<u> </u>	<u></u>	1

Spof	p-value	nding To Diff r ntially Expressed Genes Description	Gene	Unigene	Protein	
Shot	p-value					
		a a c	Accession No.	Accession	Accession	
1793	0.002342	nuclear receptor subfamily 4, group A,	NM 002135	<b>No.</b> Hs.1119	<b>No.</b> NP 775181	
1733	0.002042	member 1 (NR4A1), transcript variant 1,	14141_002133	113.1113	NIC ( 19 10 1	
	- "->			ν.		
		mRNA /cds=(315,2111) /gb=NM_002135		٠. ،	•	
		/gi=27894342 /ug=Hs 1119 /len=2699	,	•		
1803	0.022757	endogenous retroviral element clone	U12969	17.0	x 12	
	7	pCRTK6 nucleocapsid protein (gag) and			.* *	
	÷	protease/reverse transcriptase (pol)	*		a .	
		pseudogenes, partial cds				
1844	0.042212	cDNA FLJ32247 fis, clone	AK056809	Hs.293663		
1044	0.042212	PROST1000120. /gb=AK056809	7,110000000	113.233003	· ·	
5.		/gi=16552317 /ug=Hs.293663 /len=3019				
		/gi=10002017 /dg=115.290000 /ieii=0019				
1850	0.034784	DKFZP564K1964 protein	NM_015544	Hs.3447	NP_056359	
		(DKFZP564K1964), mRNA	0			
		/cds=(207,887) /gb=NM 015544			· · · · · · ·	
·		/gi=7661615 /ug=Hs.3447 /len=1560	. 8		-X-	
1852	0.015143	CGI-41 protein (CGI-41), mRNA	NM 015997	Hs.5056	NP_057081	
	1 2	/cds=(620,2047) /gb=NM_015997				
	. 49	/gi=21361524 /ug=Hs.5056 /len=2258	*	·		
1873	0.001756	Finkel-Biskis-Reilly murine sarcoma virus	NM 001997	Hs.177415	NP 001988	
1070	0.001700	(FBR-MuSV) ubiquitously expressed (fox	11111_001007	113.177410	111 _00 1000	
•	100	derived); ribosomal protein S30 (FAU),				
		mRNA /cds=(106,507) /gb=NM_001997		i.c.		
		/gi=17981709 /ug=Hs.177415 /len=574		*		
		/gi=1/901/09/dg=115.1//413/lef1=3/4	***			
1877	0.01738	signal recognition particle receptor	NM 003139	Hs.75730	NP 003130	
1077	0.01750	('docking protein') (SRPR), mRNA	14141_003139	115.75750	NF_003130	
7			*			
	1	/cds=(52,1968) /gb=NM_003139	-8-			
4040	0.000570	/gi=23308696 /ug=Hs.75730 /len=2958	NIM 005770	i.i. 200740	ND 005704	
1913	0.002573	small EDRK-rich factor 2 (SERF2),	NM_005770	Hs.380718	NP_005761	
		mRNA /cds=(1023,1319)			*	
	90 (V)	/gb=NM_005770 /gi=21361286				
		/ug=Hs.380718 /len=1408	Ŷ.			
1970	0.002824	Yeast centromere vector pRS315 with	U03441	]		
		LEU2 marker, complete sequence		1		
1976	0.026596	likely ortholog of mouse exocyst	NM_015219	Hs.325530	NP_056034	
		component protein 70 kDa (S. cerevisiae)				
		Exo70: exocyst component protein 70		.00		
ž.	a 9	kDa (S. cerevisiae) (EXO70), mRNA				
	. *	/cds=(4,1965) /gb=NM_015219			l	
		/gi=24308034 /ug=Hs.325530 /len=4596	*			
		· · · · · · · · · · · · · · · · · · ·				
2005	0.042212	class I histone deacetylase (HDAC8)	AF230097		NP_060956	
2011		RING1 and YY1 binding protein (RYBP),	NM_012234	Hs.7910	NP_036366	
		mRNA /cds=(189,875) /gb=NM_012234			_	
	1	/gi=24432049 /ug=Hs.7910 /len=2344	, i	7)	· ·	

		nding To Differentially Expressed General			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
2048	0.011037	mRNA for KIAA0701 protein, partial cds.	AB014601	Hs.153293	
		/cds=(1,4065) /gb=AB014601			
٠.		/gi=20521136 /ug=Hs.153293 /len=4625			
(1)		/gi=20021100/dg=113.100230/lejt=4020		-0.0	
2057	0.008339	chromosome 1 open reading frame 21	NM 030806	Hs.12532	NP 110433
2001	0.00000	(C1orf21), mRNA /cds=(400,765)	<b>                                   </b>	113.12002	1110400
		/gb=NM 030806 /gi=13540595	0		
		/ug=Hs.12532 /len=10215			
2000	0.047054		NIM ODADOG	110 05455	NP 004917
2069	0.047654	zinc finger protein 36, C3H type-like 1	NM_004926	Hs.85155	INP_004917
		(ZFP36L1), mRNA /cds=(131,1147)	• , •	·	
-		/gb=NM_004926 /gi=15812179	·	8	
		/ug=Hs.85155 /len=3022			
2077		musculus exoribonuclease 1 (Xrn1)	NM_011916	- 000	NP_036046
2115	0.023151	eukaryotic translation initiation factor 1A,	NM_004681	Hs 155103	NP_004672
		Y chromosome (EIF1AY), mRNA			."
		/cds=(133,567) /gb=NM_004681	* .		
9		/gi=4758253 /ug=Hs.155103 /len=1384		St.	: :
2124	0.037129	splicing factor 1 (SF1), mRNA	NM 004630	Hs.180677	NP_004621
F (7)		/cds=(383,2254) /gb=NM_004630			
	l	/gi=4759339 /ug=Hs.180677 /len=3131			
2137	0.011020	NAD(P)H dehydrogenase, quinone 1	NM_000903	Hs.406515	NP_000894
2137	0.011323	(NQO1), mRNA /cds=(51,875)	14141_000303	113.400010	111 _000034
					**
		/gb=NM_000903 /gi=4505414			
0440	0.004704	/ug=Hs.406515 /len=2447	NIA 007000	11. 474045	ND 004000
2149	0.034784	phospholipase A2 receptor 1, 180kDa	NM_007366	Hs.171945	NP_031392
		(PLA2R1), mRNA /cds=(207,4604)			
	·	/gb=NM_007366 /gi=19923388	0	*	
		/ug=Hs.171945 /len=5633			1
2154	0.023151	PDZ domain containing 1 (PDZK1),	NM_002614	Hs.15456	NP_002605
		mRNA /cds=(107,1666) /gb=NM_002614			
		/gi=21361141 /ug=Hs.15456 /len=2140			
			γ	,	• -8-
2184	0.008019	highly charged protein (D13S106E),	NM_005800	Hs.151236	NP_005791
		mRNA /cds=(178,3456) /gb=NM_005800	-		_
1		/gi=5031648 /ug=Hs.151236 /len=3650			
- 30				* '	
2194	0.013901	monocytic leukemia zinc finger protein-	NM_012330	Hs.27590	NP_036462
2107	0.010301	related factor (MORF), mRNA	5 12050	1, 10.27 000	000702
·		/cds=(316,6537) /gb=NM_012330			
			·		1.
2200	0.020404	/gi=6912511 /ug=Hs.27590 /len=6537	AL832314	He 100700	
2209	0.030461	mRNA; cDNA DKFZp667O2119 (from	AL032314	Hs.180789	
	· ·	clone DKFZp667O2119) /gb=AL832314			
		/gi=21732861 /ug=Hs.180789 /len=6868			
				1	
2211	0.037129	L-isoaspartyl/D-aspartyl O-	U49740		1
		methyltransferase (PCMT1) gene, exon	-		1
	**	1,	1 .		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2214	0.042212	ts79a05.x1 NCI_CGAP_GC6 cDNA clone	Δ1917390	Hs.99415	NO.
-2 17	0.042212	IMAGE:2237456 3', mRNA sequence	7.13 17 000	113.55415	-5-
	-	/clone=IMAGE:2237456 /clone_end=3'	a g	ĺ.	
	•	/gb=Al917390 /gi=5637245			* =
		/ug=Hs.99415 /len=462		17.00	= "
228	0.032563	clone MGC:15451 IMAGE:2960796,	BC014640	Hs.403836	
,2,20	0.002000	mRNA, complete cds /cds=(381,2660)	DC014040	113.403030	
		/gb=BC014640 /gi=15779149			
		/ug=Hs.403836 /len=3479	(To.)	9	
232	0.034794	ubiquilin 2 (UBQLN2), mRNA	NM_013444	Un 4550	ND 020470
.232	0.034764		NIVI_U13444	Hs.4552	NP_038472
		/cds=(236,2110) /gb=NM_013444			
200	0.004.535	/gi=16753206 /ug=Hs.4552 /len=3324	NINA" CO 4077	11- 5040	ND 00 toos
236	0.0215/5	glia maturation factor, gamma (GMFG),	NM_004877	Hs.5210	NP_004868
		mRNA /cds=(5,433) /gb=NM_004877		*-	
000	0.04	/gi=4758439 /ug=Hs.5210 /len=561			
238	0.011929	RAD50 (S. cerevisiae) (RAD50),	NM_005732	Hs.41587	NP_597816
	(3)	transcript variant 1, mRNA			
-1		/cds=(388,4326) /gb=NM_005732	·	*	
		/gi=19924128 /ug=Hs.41587 /len=5891	*		
253	0.034784	small EDRK-rich factor 2 (SERF2),	NM_005770	Hs.380718	NP_005761
٠.	. '	mRNA /cds=(1023,1319)			
		/gb=NM_005770 /gi=21361286		·	
		/ug=Hs.380718 /len=1408		, ,	·
2267	0.007388	frizzled 10 (Drosophila) (FZD10), mRNA	NM_007197	Hs.31664	NP_009128
	÷ .	/cds=(457,2202) /gb=NM_007197			
		/gi=22035684 /ug=Hs.31664 /len=3260		*	
276	0.001756	F-box only protein 32 (FBXO32),	NM_058229	Hs.61661	NP_680482
		transcript variant 1, mRNA			
	<i>'</i>	/cds=(193,1260) /gb=NM_058229		7	
	-	/gi=22547142 /ug=Hs.61661 /len=1530	. 0_0		
2296	0.021575	serine/threonine kinase 38 like (STK38L),	NM_015000	Hs.184523	NP_055815
	¥.	mRNA /cds=(174,1568) /gb=NM_015000			_
		/gi=24307970 /ug=Hs.184523 /len=4725		-	
	i.				=
2297	0.009424	zinc finger protein 2 (A1-5) (ZNF2),	NM_021088	Hs.192285	NP_066574
		mRNA /cds=(855,1733) /gb=NM_021088	_		
	,	/gi=20304090 /ug=Hs.192285 /len=2630			] .
•	*		<u> </u>	~	,
2305	0.004059	KIAA0970 protein (KIAA0970), mRNA	NM_014923	Hs.103329	· · · · · · · · · · · · · · · · · · ·
-000	0.004000	/cds=(335,2668) /gb=NM_014923	0 , .020		
		/gi=7662419 /ug=Hs.103329 /len=4863			
2306.	0.011020	S100 calcium binding protein A4 (calcium	NM 002961	Hs.81256	NP_062427
<u> </u>	0.011929		14141_002301	113.01230	1141 -002421
		protein, calvasculin, metastasin, murine			1
		placental (S100A4), transcript variant 1,			1
		mRNA /cds=(70,375) /gb=NM_002961	1.		1
		/gi=9845514 /ug=Hs.81256 /len=512	2	I	1

Spot	p-value	Description	Gene	Unigene	Protein
opo.	p value	2000 pas.	Accession No.	Accession	Accession
	8		Accession No.		
2207	0.000004	matrilin 3 (MATN3) precursor, mRNA	NIM CODDO	No.	No.
2307	0.020091		NM_002381	Hs.278461	NP_002372
		/cds=(64,1524) /gb=NM_002381	*		·
		/gi=13518040 /ug=Hs.278461 /len=2599	200		
				* · ·	
2309		GTPase-activating protein GAPIII	U20238		NP_033051
2317	0.001935	mRNA for KIAA0570 protein, partial cds.	AB011142	Hs.180948	
	,	/cds=(480,10718) /gb=AB011142			*
. 0		/gi=20521084 /ug=Hs.180948 /len=11269			
				i	
2324	0.04496	hypothetical protein KIAA0883	AB020690		NP 009188
2348		neuropilin-2 (a5)	AF022861		
2365		ring finger protein 38 (RNF38), mRNA	NM 022781	Hs.77823	NP 073618
	3.555551	/cds=(563,1861) /gb=NM_022781		1.5520	
		/gi=21918874 /ug=Hs.77823 /len=4694		. ×	
2370	0.024924	exosome component Rrp41 (FLJ20591),	NM 019037	Hs.343589	NP 061910
23/0	0.024024		14141_019037	ns.545569	NF_001910
	. 2	mRNA /cds=(104,841) /gb=NM_019037			
•		/gi=9506688 /ug=Hs.343589 /len=896			
*					
2385	0.012883	Nedd4 binding protein 1 (N4BP1), mRNA	NM_014664	Hs.323712	NP_055479
•		/cds=(238,2928) /gb=NM_014664	1.8	1.	
1.5		/gi=7662203 /ug=Hs.323712 /len=3319	,		
			·	*	
2440	0.014988	ubiquitin conjugating enzyme type UBC9	X96427		NP_003336
	-				
2448	0.047854	KIAA1077	AB029000		NP_055985
2451		collagen, type IX, alpha 1 (COL9A1),	NM_001851	Hs.154850	NP 511040
2011		transcript variant 1, mRNA	· · · · · · · · · · · · · · · · · · ·		, <del>-</del>
	* 5	/cds=(147,2912) /gb=NM_001851			1)1
	- 4	/gi=17978501 /ug=Hs.154850 /len=3287		* 8	
		17970001749=113:10400071611=0207	*		
2452	0.044957	jun B proto-oncogene (JUNB), mRNA	NM 002229	Hs.400124	NP_002220
2452	0.044657		14141_002229	HS.400124	14002220
• .	· .	/cds=(254,1297) /gb=NM_002229		<i>*.</i> '	* * *
0.400	0.000500	/gi=4504808 /ug=Hs.400124 /len=1797	1114 040040	11- 070040	ND: 007074
2466	0.026596	likely ortholog of mouse gene trap locus 3	NM_013242	Hs.279818	NP_037374
•		(GTL3), mRNA /cds=(257,838)			*
		/gb=NM_013242 /gi=8392874		*	
. 1		/ug=Hs.279818 /len=1278	<u> </u>	ļ .	7
2490	0.04496	gonadotropin-releasing hormone receptor	NM_000406	Hs.73064	NP_000397
		(GNRHR), mRNA /cds=(1749,2735)			
		/gb=NM_000406 /gi=4504058	04	l' ÿ	* .
-X-		/ug=Hs.73064 /len=2735			
2491	0.021575	clone IMAGE:5265791, mRNA	BC035170	Hs.385807	
		/gb=BC035170 /gi=23958673			
		/ug=Hs.385807 /len=3000	, ,	-	
2536	0.021575	H3 histone, family 3B (H3.3B) (H3F3B),	NM 005324	Hs.180877	NP_005315
7000	1.0.02 1979	• · · · · · · · · · · · · · · · · · · ·	14141-000254	113.100077	141 -0000
	,				
		mRNA /cds=(118,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662			0.0

		nding To Differentially Expressed Gene			
Spot	p-value	Description	Gene	Unigene	Protein
	-10	; <sub>*</sub>	Accession No.	Accession	Accession
		*		No.	No
2573	0.04496	general transcription factor IIF,	NM_002096	Hs.68257	NP_002087
		polypeptide 1 (74kD subunit) (GTF2F1),	7 × 2		-
		mRNA /cds=(179,1732) /gb=NM_002096		·	
	1 4	/gi=4504196 /ug=Hs.68257 /len=2440			
	-	9	0.00	* *	, ,
2583	0.030461	receptor (calcitonin) activity modifying	NM_005856	Hs.25691	NP 005847
	, 3.000	protein 3 (RAMP3), mRNA /cds=(30,476)			110000 ;;
		/gb=NM 005856 /gi=5032022	8		
		/ug=Hs.25691 /len=1312			
2592	0.023151	GC box bindig protein	D31716	-	NP 001197
2611		mRNA for KIAA1604 protein, partial cds.	AB046824	Hs.209464	147_001137
2011	0.030401	/cds=(33,2846) /gb=AB046824	AD040024	115.209404	
		/gi=10047282 /ug=Hs.209464 /len=3098	0.0		
		/gi=1004/262/ug=ns.209464/leti=3096			
2024	0.000464	DADO7A	NIM COAFOO	LI- 50477	ND 004574
2624	0.030461	RAB27A, member RAS oncogene family	NM_004580	Hs.50477	NP_004571
		(RAB27A), mRNA /cds=(246,911)	*		-
		/gb=NM_004580 /gi=19923263		٠.	
		/ug=Hs.50477 /len=2496	NICE AND LOCAL		
2628	0.028474	methyltransferase reductase (MTRR),	NM_024010	Hs.153792	NP_076915
		transcript variant 2, mRNA		• -1	
		/cds=(31,2208) /gb=NM_024010		* /	
	-	/gi=13325067 /ug=Ḥs.153792 /len=3291			1.0
2637	0.005746	ribosomal protein L41 (RPL41), mRNA	NM_021104	Hs.356795	NP_066927
		/cds=(84,161) /gb=NM_021104			
		/gi=10863874 /ug=Hs.356795 /len=478	3-	n .	-010
2641	0.003392	phospholipase A2, group IIA (platelets,	NM_000300	Hs.76422	NP_000291
		synovial fluid) (PLA2G2A), nuclear gene			
		encoding mitochondrial protein, mRNA	*		. 7
	,	/cds=(273,707) /gb=NM_000300			
		/gi=20149501 /ug=Hs.76422 /len=997		*, •,	ž .
2650	0.023151	fatty-acid-Coenzyme A ligase, long-chain	NM_021122	Hs.154890	NP_066945
		2 (FACL2), mRNA /cds=(14,2110)			-
	-	/gb=NM_021122 /gi=12669906		10	
		/ug=Hs.154890 /len=3635		N: .	•
		[ ]	. ,		
2652	0.034784	membrane metallo-endopeptidase	NM 007289	Hs.1298	NP_009220
ĻUUL	0.00.1101	(neutral endopeptidase, enkephalinase,			
		CALLA, CD10) (MME), transcript variant			
•		2b, mRNA /cds=(229,2481)	*	. 7	
		/gb=NM_007289 /gi=6042203			
		1		. (*)	
2677	0.000040	/ug=Hs.1298 /len=5725	NIM 000110	Hs.1602	NP_000101
2677	0.0080 19	dihydropyrimidine dehydrogenase	NM_000110	115.1002	NF_000 10 1
		(DPYD), mRNA /cds=(102,3179)			-
		/gb=NM_000110 /gi=4557874		10	*
	1 :	/ug=Hs.1602 /len=4407		l	J

Spot	p-value	Description	Gene	Unigene	Prot in
			Accession No.	Accession No.	Accession No.
2687	0.003712	v-fos FBJ murine osteosarcoma viral	NM_005252	Hs.25647	NP 005243
	0.0007	oncogene (FOS), mRNA /cds=(156,1298)		1, 10,200	1,5552.15
٠, ٠		/gb=NM 005252//gi=6552332	*		
		/ug=Hs.25647 /len=2084			1
2688	0.013001	mRNA for KIAA0573 protein, partial cds.	AB011145	Hs.154023	
2000	0.013301	/cds=(1,1357) /gb=AB011145	AB011143	113,104020	
		/gi=3043669 /ug=Hs.154023 /len=4796	9.		
2699	0.010203	t-complex-associated-testis-expressed 1-	NM 006510	Hs.266940	NP 006510
2033	0.010203	like 1 (TCTEL1), mRNA /cds=(1,342)		115.200940	NF_000310
	+ 0	/gb=NM_006519 /gi=5730084		**	
0705	0.00000	/ug=Hs.266940 /len=713	NIA 005004	11- 400077	ND 005045
2705	0.039603	H3 histone, family 3B (H3.3B) (H3F3B),	NM_005324	Hs.180877	NP_005315
		mRNA /cds=(118,528) /gb=NM_005324			
		/gi=21264598 /ug=Hs.180877 /len=1662		,	
1	3 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7				
2735	0.001592	mRNA for KIAA1694 protein, partial cds.	AB051481	Hs.19597	NP_085132
•	1	/cds=(1,2275) /gb=AB051481			
		/gi=12697932 /ug=Hs:19597 /len=4235			
2762	0.020091	golgi autoantigen, golgin subfamily b,	NM_004487	Hs 7844	NP_004478
		macrogolgin (with transmembrane			
		signal), 1 (GOLGB1), mRNA		)(-	*
	* ×	/cds=(127,9906) /gb=NM_004487		.0	
		/gi=4758453 /ug=Hs.7844 /len=10300			
2774	0.026596	myristoylated alanine-rich protein kinase	NM_002356	Hs.75607	NP_002347
-		C substrate (MARCKS), mRNA		*	
		/cds=(370,1368) /gb=NM_002356			
	- 4.	/gi=11125771 /ug=Hs.75607 /len=2589			
2775	0.04496	ribosomal protein L12 (RPL12), mRNA	NM_000976	Hs.405042	NP_000967
		/cds=(89,586) /gb=NM_000976			
		/gi=15431291 /ug=Hs.405042 /len=632	• 1		
2782	0.016146	high mobility group 2 protein (HMG-2)	M83665	. 1	
2787		meningioma expressed antigen 6 (coiled-		Hs.117242	NP_005921
		coil proline-rich) (MGEA6), mRNA	×		
	-55	/cds=(315,2729) /gb=NM_005930	4.5		
		/gi=5174560 /ug=Hs.117242 /len=3676			
٠.				*	. *
2792	0.009424	xf50g03 x1 NCI_CGAP_Gas4 cDNA	AW130421	Hs.329722	
_, 0	3.000727	clone IMAGE:2621524 3' similar to			7.1.
		contains element MER4 repetitive			
		element ,, mRNA sequence			1.
	*	/clone=IMAGE:2621524 /clone_end=3'	a .		Í
	0 0	/gb=AW130421 /gi=6132026			
	1	1 9	· ·		* *
0707	0.047054	/ug=Hs.329722 /len=719	NIM 044705	Uo 24974	ND 055640
2797	0.04/854	zinc finger homeobox 1b (ZFHX1B),	NM_014795	Hs.34871	NP_055610
	:	mRNA /cds=(445,4089) /gb=NM_014795		N 1	· ·
	-	/gi=7662183 /ug=Hs.34871 /len=5523			1
	1			1.	

Spot	p-value	Description	Gen	Unigene	Prot in
	F 13.123			Accession	Accession
	. * = *	·	,,0000001011110.	No.	No.
2798	0.024824	CCAAT/enhancer binding protein	NM_005195	Hs.76722	NP_005186
-, 00	0.92.192.1	(C/EBP), delta (CEBPD), mRNA		110.70722	000.00
•		/cds=(41,850) /gb=NM_005195	- 2-		
		/gi=4885130 /ug=Hs.76722 /len=1248			
2810	0.028474	ATP synthase, H transporting,	NM 001689	Hs.429	NP_001680
2010	0.020-7-	mitochondrial F0 complex, subunit c	14141_00 1003	113.423	
		(subunit 9) isoform 3 (ATP5G3), mRNA		* )	
		/cds=(255,683) /gb=NM_001689	- *		*2
•					
2015	0.004004	/gi=4502300 /ug=Hs.429 /len=826	NIM 000704	H= 440070	ND 000700
2815	0.024824	proteasome (prosome, macropain)	NM_002791	Hs.410276	NP_002782
	$e^{-\epsilon} = f^{\epsilon}$	subunit, alpha type, 6 (PSMA6), mRNA	*		
٠.		/cds=(110,850) /gb=NM_002791			
		/gi=23110943 /ug=Hs.410276 /len=1035	***		
0000	2 2 2 2 2 2 2		N. 00 ( 10 )	0.000	Nin on the least
2823	0.006254	eukaryotic translation elongation factor 1	NM_001404	Hs 256184	NP_001395
		gamma (EEF1G), mRNA /cds=(38,1351)		*	
	-	/gb=NM_001404 /gi=25453475			
		/ug=Hs.256184 /len=1429			
					1
2846	0.008697	N-ethylmaleimide-sensitive factor (NSF),	NM_006178	Hs.108802	NP_006169
. · · ·		mRNA /cds=(61,2295) /gb=NM_006178			
		/gi=11079227 /ug=Hs.108802 /len=3960			
•				*	
2848	0.007388	BJ-HCC-24 tumor antigen mRNA,	AY121805	Hs.433489	
		complete cds /cds=(2,1240)			* *
		/gb=AY121805 /gi=22002585	a **		1
	0	/ug=Hs.433489 /len=1488			
2858	0.010203	hypothetical protein HSPC228	NM 016485.	Hs.267288	NP_057569
		(HSPC228), mRNA /cds=(16,939)	_		-
	-	/gb=NM_016485 /gi=21361740			
	•	/ug=Hs.267288 /len=3273	- 1		
2869	0.009424	dual specificity phosphatase 1 (DUSP1),	NM 004417	Hs.171695	NP 004408
	* .	mRNA /cds=(249,1352) /gb=NM_004417			-
	v.	/gi=7108342 /ug=Hs.171695 /len=2015	Č=		0
2872	0.042212	oxysterol binding protein-like 8	NM 020841	Hs.109694	NP_065892
_0, _	0.0-722 12	(OSBPL8), mRNA /cds=(481,3150)	020071	1.10.100004	
	-0	/gb=NM 020841/gi=22035617			. •
. •		,			
2875	0.012002	/ug=Hs.109694 /len=7239 deubiquitinating enzyme (UNPH4)=	AF106069		NP_006304
2875	0.012003		VE 100009		111-000304
		AF153604 ubiquitin-specific protease	1.00	- 14	
2004	0.000555	homolog (UPH)	NIN 447400	11- 50400	ND CZ4Z4
2901 ,	0.032563	A kinase (PRKA) anchor protein (yotiao)	NM_147166	Hs.58103	NP_671714
		9 (AKAP9), transcript variant 4, mRNA			
		/cds=(223,5190) /gb=NM_147166			
	1	/gi=22538388 /ug=Hs.58103 /len=6058	1 .	1	I .

Snot	p-value	Description	G ne	Unigene	Protein
Spot	p-value	Describtion		_	1
			Acc ssion No.	Accession	Accession
2912	0.032563	KIAA0690 protein (KIAA0690), mRNA	NM_015179	No. Hs.60103	No. NP_055994
2312	0.032303	/cds=(87,3980) /gb=NM_015179	14141_015179		111-000994
J	-	/gi=15987120 /ug=Hs.60103 /len=4396	*		
2918	0.029474	ribosomal protein S8 (RPS8), mRNA	NM 001012	Hs.399720	NP 001003
2910	0.020474	/cds=(24,650) /gb=NM_001012		ПS.399/20.	INP_00 1003
		/gi=4506742 /ug=Hs.399720 /len=705			i
2937	0.021575	high-mobility group box 1 (HMGB1),	NM_002128	Hs.6727	NP 002119
2931	0.02 15/5	mRNA /cds=(77,724) /gb=NM 002128	NIVI_002 120	IDS.0727	NP_002119
1		/gi=20149538 /ug=Hs.6727 /len=1207	•		
2938	0.007389	ribosomal protein L7a (RPL7A), mRNA	NM 000972	Hs.99858	NP_000963
2930	0.007300	/cds=(31,831) /gb=NM_000972	NiNi_000972	IUS.88000	INP_000963
				- 3	*
2050	0.047954	/gi=18390348 /ug=Hs.99858 /len=890 cytochrome c oxidase subunit IV isoform	NIM COACCA	LID 422440	ND 004060
2950	0.047654		NM_001861	Hs.433419	NP_001852
		1 (COX4I1), nuclear gene encoding	3		
		mitochondrial protein, mRNA			
	11	/cds=(165,674) /gb=NM_001861			
0054	0.040004	/gi=17017985 /ug=Hs.433419 /len=802	N. 4 . 0 4 0 0 0 0	11 407444	ND 057447
2951	0.018694	serine/arginine repetitive matrix 2	NM_016333	Hs.197114	NP_057417
		(SRRM2), mRNA /cds=(226,8484)		. :	
	' -	/gb=NM_016333 /gi=19923465	8		
0070	0047057	/ug=Hs.197114 /len=9027	N. 1. 000005		115004
2973	0.047854	hypothetical protein MGC3200	NM_032305	Hs.9088	NP_115681
		(MGC3200), mRNA /cds=(108,764)			00
		/gb=NM_032305 /gi=14150063			,
		/ug=Hs.9088 /len=1191			
2975	0.032563	actin related protein 2/3 complex, subunit	NM_005719	Hs.293750	NP_005710
		3, 21kDa (ARPC3), mRNA /cds=(94,630)		'	
•		/gb=NM_005719 /gi=23397667	1 1		
·	ļ	/ug=Hs.293750 /len=912			
2976	0.042212		NM_079425	Hs.77385	NP_524149
		muscle and non-muscle (MYL6),			
ź		transcript variant 3, mRNA /cds=(41,514)	· ·		
		/gb=NM_079425 /gi=17986263	×	·	- %
		/ug=Hs.77385 /len=717			77
2987	0.047854	nucleolar autoantigen (55kD) similar to	NM_006455	Hs.446459	NP_006446
		rat synaptonemal complex protein			
	] .	(SC65), mRNA /cds=(12,1325)	· ·	a a	
	ļ	/gb=NM_006455 /gi=5454037			
		/ug=Hs.446459 /len=2347			
3008	0.013901		NM_021005	Hs.347991	NP_066285
		member 2 (NR2F2), mRNA			
	}	/cds=(343,1587) /gb=NM_021005	Ý		*
	_	/gi=14149745 /ug=Hs.347991 /len=1740		· .	
			·	•	
3012	0.009424	hypothetical protein PRO1843	NM_018507	Hs.283330	NP_060977
٠,	'	(PRO1843), mRNA /cds=(965,1255)		·	
		/gb=NM_018507 /gi=8924082			~
	1, '	/ug=Hs.283330 /len=1268	L	İ	

C	a malina	nding To Diff r ntially Express d Gen s			
Spot	p-value	Description	Gene	Unigen	Protein
	· , · · ·		Accession No.	Accession	Accession
:			1114 605000	No.	No.
3030	0.034784	neuroblastoma, suppression of	NM_005380	Hs.76307	NP_005371
		tumorigenicity 1 (NBL1), mRNA	÷ .		
•		/cds=(62,604) /gb=NM_005380	-8-		
		/gi=4885508 /ug=Hs.76307 /len=1929			
3034	0:012883	serine (or cysteine) proteinase inhibitor,	NM_004568	Hs.41072	NP_004559
•		clade B (ovalbumin), member 6			
		(SERPINB6), mRNA /cds=(75,1205)	**		
- 3		/gb=NM_004568 /gi=28077084			
		/ug=Hs.41072 /len=1361			1
3044		hypothetical protein LOC51321	NM_016627	Hs.268122	NP 057711
		(LOC51321), mRNA /cds=(635,1195)	_		
	· .	/gb=NM_016627 /gi=7706167			
		/ug=Hs.268122 /len=1304		8	
3062	0.016146	myosin, light polypeptide, regulatory, non-	NM 006471	Hs.180224	NP_006462
	0.0 (0.1-0	sarcomeric (20kD) (MLCB), mRNA	55547 1	1.35.10022	
		/cds=(115,630) /gb=NM 006471			ľ · ·
. 1					
2440	0.004422	/gi=5453739 /ug=Hs.180224 /len=944	AV002464		NP 057295
3116	0.004433	Hypothetical protein(cDNA FLJ11299 fis,	AK002161		NP_05/295
		clone PLACE1009845, highly similar to			
201212		KIAA0905 protein)		1	
3135	0.039603	mRNA, cDNA DKFZp586C1019 (from	AL049397	Hs.12314	
		clone DKFZp586C1019) /gb=AL049397		*	
	*	/gi=4500188 /ug=Hs.12314 /len=1737			
3136	0.023151	splicing factor, arginine/serine-rich 5	NM_006925	Hs.166975	NP_008856
		(SFRS5), mRNA /cds=(219,542)			
	4	/gb=NM_006925 /gi=5902077			
		/ug=Hs.166975 /len=1865		· ·	
3172	0.042212	myocyte-specific enhancer factor 2A	U49020		
	-	(MEF2A) gene, last coding exon, and			
		complete cds			1
3174	0.04496	lectin, galactoside-binding, soluble, 1	NM_002305	Hs.382367	NP_002296
		(galectin 1) (LGALS1), mRNA			<del>-</del>
	-	/cds=(69,476) /gb=NM_002305			000
		/gi=6006015 /ug=Hs.382367 /len=526		, ,	
3192	0.011929	mitochondrial ribosomal protein S24	NM 032014	Hs.284286	NP 114403
J 10,2	1 0.01 1020	(MRPS24), nuclear gene encoding			- 1   100
		Imitochondrial protein, mRNA			1
		/cds=(4,507) /gb=NM_032014			
		/gi=15721936 /ug=Hs.284286 /len=667			
3197	0.002007	NDRG family member 2 (NDRG2),	NM 016250	Hs.243960	NP 057334
319/	0.003097		NIVI_0 10230	113.243800	114F_007334
		mRNA /cds=(97,1170) /gb=NM_016250			
•	**	/gi=10280619 /ug=Hs.243960 /len=2024			· ·
000		11. 11. 05 500501	000077.40	11. 40040	<b> </b>
3204	0.034784	clone IMAGE:5263531, mRNA	BC037740	Hs.18016	
	, ,	/gb=BC037740 /gi=22902216			
	1.	/ug=Hs.18016 /len=5036	l		

		nding To Diff r ntially Expressed Gene			
Spot	p-value	Description	Gene	Unigene	Protein
•		Talan San San San San San San San San San S	Accession No.	Accession	Accession
				No.	No.
3254	0.028124	splicing factor, arginine/serine-rich 2	NM_003016	Hs.73965	NP_003007
1.		(SFRS2), mRNA /cds=(156,821)		*	
		/gb=NM 003016 /gi=4506898	*		*
	* :	/ug=Hs.73965 /len=1879	4.5		
3280	0.030461	RETROVIRUS-RELATED POL	P11369	70.000	
0200	0.000.101	POLYPROTEIN			
3287	0.010303	FtsJ 1 (E. coli) (FTSJ1), mRNA	NM_012280	Hs.23170	NP 803188
0201	0.010203	/cds=(301,1290) /gb=NM_012280	14101_012200	113.23170	141 _003 100
0	·		W 12.		
0000	0.001500	/gi=7110660 /ug=Hs.23170 /len=1867	10044000	-1. 2	
3293		AF-6, complete cds	AB011399		
3294	0.013901	NCK adaptor protein 1 (NCK1), mRNA	NM_006153	Hs.54589	NP_006144
		/cds=(117,1250) /gb=NM_006153	00		[:
1		/gi=20070226 /ug=Hs.54589 /len=1947	- 1		<u>.                                    </u>
3316	0.012883	glutathione S-transferase M3 (brain)	NM_000849	Hs.2006	NP_000840
		(GSTM3), mRNA /cds=(311,988)		17.	
		/gb=NM_000849 /gi=23065551			
		/ug=Hs.2006 /len=1572	* 0		
3324	0.016146	transformer-2 alpha (htra-2 alpha)	NM_013293	Hs.130829	NP_037425
		(HSU53209), mRNA /cds=(158,1006)			
		/gb=NM_013293 /gi=9558732	3		* *
		/ug=Hs.130829 /len=1563			
3326	0.002242	of yeast long chain polyunsaturated fatty	NIM 004044	110 050475	ND OCOFOC
3320	0.002342		NM_021814	Hs.250175	NP_068586
		acid elongation enzyme 2 (HELO1),			
		mRNA /cds=(345,1244) /gb=NM_021814			
		/gi=21361903 /ug=Hs.250175 /len=3011	,		
					, ,
3328	0.034784	retinoblastoma-like 2 (p130) (RBL2),	NM_005611	Hs.79362	NP_005602
	,	mRNA /cds=(70,3489) /gb=NM_005611		100	
		/gi=21361291 /ug=Hs.79362 /len=4853			
3367	0.028474	nuclear receptor subfamily 3, group C,	NM 000176	Hs.75772	NP 000167
		member 1 (glucocorticoid receptor)	_		
		(NR3C1), mRNA /cds=(133,2466)			
		/gb=NM_000176 /gi=4504132			
		/ug=Hs.75772 /len=4788			
3384	0.012003	GDP dissociation inhibitor 1 (GDI1),	NM_001493	Hs.74576	NP_001484
3304	0.012003		1493	ITIS. 74376	INP_001404
٠		mRNA /cds=(81,1424) /gb=NM_001493		•	
2204	0.007000	/gi=4503970 /ug=Hs 74576 /len=2225	1114 000704	11 75000	ND 000705
3394	0.007388	immunodeficiency virus type I enhancer	NM_006734	Hs.75063	NP_006725
		binding protein 2 (HIVEP2), mRNA			
• • •		/cds=(16,7518) /gb=NM_006734			}
:	,,	/gi=19923373 /ug=Hs.75063 /len=9175		1	
3397	0.042212	chromosome 20 open reading frame 6	NM_016649	Hs.88820	NP_057733
	."	(C20orf6), mRNA /cds=(109,2664)			A.
	1	/gb=NM_016649 /gi=22507381			1
	*	/ug=Hs.88820 /len=3216			
			1.01.00	11.054074	110 004000
3406	0.030461	ICTP synthase (CTPS) mRNA	INM 001405 *	THS 251871	INP (IIITX96
3406	0.030461	CTP synthase (CTPS), mRNA /cds=(76,1851) /gb=NM 001905	NM_001905	Hs.251871	NP_001896

C4	n value	nding To Differentially Expressed Gene				
Spot	p-value		G ne	Unig n	Protein	
			Accession No.	Accession	Accession	
		* * * * * * * * * * * * * * * * * * * *		No.	No.	
3412	0.021575	hypothetical protein FLJ22301	NM 024836	Hs.181406	NP 079112	
		(FLJ22301), mRNA /cds=(696,2054)		,	, -, -, -, -, -, -, -, -, -, -, -, -, -	
		/gb=NM_024836 /gi=13376246				
	-				· · ·	
· • • • • • • • • • • • • • • • • • • •		/ug=Hs.181406 /len=2952				
3432	0.01738	polypyrimidine tract binding protein 1	NM_002819	Hs.172550	NP_787041	
-		(PTBP1), transcript variant 1, mRNA		*		
		/cds=(89,1762) /gb=NM_002819		<b>.</b>		
		/gi=14165462 /ug=Hs.172550 /len=3322	9.77	-		
		, g,				
3440	0.004838	TERF1 (TRF1)-interacting nuclear factor	NIM 012461	Hs.7797	NP_036593	
3440	0.004636		14141_012401	I	INF_030393	
		2 (TINF2), mRNA /cds=(263,1327)				
		/gb=NM_012461 /gi=6912715				
		/ug=Hs.7797 /len=2095		*		
3445	0.037129	mRNA; cDNA DKFZp434A1520 (from	AL137544	Hs.406722		
		clone DKFZp434A1520); partial cds			10	
	1	/cds=(1,551) /gb=AL137544 /gi=6808224			-	
		/ug=Hs.406722 /len=2775		* * * * *		
2470	0.004050		NIM O14500	Ha 270042	ND OFFICE	
3473	0.004059	LIM and cysteine-rich domains 1	NM_014583	Hs.279943	NP_055398	
		(LMCD1), mRNA /cds=(115,1212)		- 35		
-	r	/gb=NM_014583 /gi=14277673				
		/ug=Hs.279943 /len=1754				
3476	0.018694	arginine-glutamic acid dipeptide (RE)	NM 012102	Hs.194369	NP 036234	
	0.0 ,000	repeats (RERE), mRNA /cds=(637,5337)	1,1,1,1			
:	-	/gb=NM_012102 /gi=19923392				
•			71:			
		/ug=Hs.194369 /len=8035				
3482	0.003392	proteasome (prosome, macropain) 26S	NM_002805	Hs:79387	NP_002796	
		subunit, ATPase, 5 (PSMC5), mRNA				
		/cds=(42,1262) /gb=NM_002805			:	
		/gi=24497434 /ug=Hs.79387 /len=1332				
2400	0.04720		AF111168	<del>*************************************</del>		
3498	0.01/38	serine palmitoyl transferase, subunit II			l * · · .	
		gene, complete cds, and unknown genes				
1 .	**		1 1 1 1	* -		
3513	0.039603	chromosome 1 open reading frame 29	NM_006820	Hs.75470	NP_006811	
		(C1orf29), mRNA /cds=(242,1483)			*	
		/gb=NM 006820 /gi=5803026	1		1	
••		/ug=Hs.75470 /len=2058	1		1	
3527	0.036506	UI-H-FL1-bge-c-14-0-UI.s1	CA430953	Hs.397680	- 10E m	
3321	0.020390	1	CV420323	1113.337.000		
	-X	NCI_CGAP_FL1 cDNA clone UI-H-FL1-			·	
	1	bge-c-14-0-UI 3', mRNA sequence			4	
		/clone=UI-H-FL1-bge-c-14-0-UI	,	1	. :	
	1	/clone_end=3' /gb=CA430953				
		/gi=24793679 /ug=Hs.397680 /len=1105				
2507	0.000570	hobby say (Dresembile) (DDV) DNA	NIM 020225	He 25200	ND 064620	
3537	0.002573	bobby sox (Drosophila) (BBX), mRNA	NM_020235	Hs.35380	NP_064620	
		/cds=(321,3056) /gb=NM_020235			. * .	
		/gi=18378730 /ug=Hs.35380 /len=3462		1 .		

	p-value	nding To Differentially Express d Genes Description	Gene	Unig ne	Protein
Spor	havaine	Description		_	
			Accession No.	Accession	Accession
0.00	6 0 1 0 0 0 1		200	No.	No.
3582	0.013901	fibroblast activation protein, alpha (FAP),	NM_004460	Hs.418	NP_004451
		mRNA /cds=(209,2491) /gb=NM_004460	(4)	o .*	
		/gi=16933539 /ug=Hs.418 /len=2788	•		÷
			* .		
3584	0.034784	mRNA; cDNA DKFZp586L081 (from	AL080234	Hs.432862	
		clone DKFZp586L081) /gb=AL080234			
	٠.	/gi=5262727 /ug=Hs.432862 /len=2159		1	* - +
3587	0.008019	cAMP responsive element binding protein	NM 134442	Hs.79194	NP 604391
	0.0000	1 (CREB1), transcript variant B, mRNA	101442	1113.70134	141 _00400,1
	υχο	/cds=(182,1207) /gb=NM_134442			
					· .
	. • 1	/gi=22219460 /ug=Hs.79194 /len=3006			
0.500	0 010110		4.0000010	,	
3596	J 0.016146	mRNA for KIAA0447 protein, partial cds.	AB007916	Hs.214646	
		/cds=(234,1634) /gb=AB007916		*	
		/gi=6683704 /ug=Hs.214646 /len=5932			× .
3605	0.021575	KIAA0062 mRNA, partial cds	D31887	Hs:89868	
-		/cds=(1,1598) /gb=D31887 /gi=505101		•	
		/ug=Hs.89868 /len=4573		7.1	
3606	0.003392	nucleolar protein family A, member 3	NM_018648	Hs.14317	NP 061118
		(H/ACA small nucleolar RNPs) (NOLA3),			
	45.00	mRNA /cds=(98,292) /gb=NM_018648			<u> </u>
•		/gi=15011920 /ug=Hs.14317 /len=556			
		/gi=13011920/ug=118.1431/ /lef1=330			*
3611	0.042242	hungthatiaal arataia EL 1204E2	NIM 040000	11- 02272	ND 004070
3011	0.042212	hypothetical protein FLJ20152	NM_019000	Hs.82273	NP_061873
		(FLJ20152), mRNA /cds=(217,1287)	0.		, ,
• ` .	0.	/gb=NM_019000 /gi=21361616	- "		
		/ug=Hs.82273 /len=2989			<u> </u>
3619	0.032563	cytochrome c oxidase subunit IV isoform	NM_001861	Hs.433419	NP_001852
- 2		1 (COX4I1), nuclear gene encoding		*	
		mitochondrial protein, mRNA			* ;
		/cds=(165,674) /gb=NM_001861 \	<u>.</u>	ļ.	
× .	·	/gi=17017985 /ug=Hs.433419 /len=802			.00
3622	0.006254	mitogen-activated protein kinase 1	NM 002745	Hs.324473	NP 620407
		(MAPK1), transcript variant 1, mRNA			
	è	/cds=(241,1323) /gb=NM_002745		,	,
		/gi=20986528 /ug=Hs.324473 /len=2934		8	
		/gi=20900020 /ug=ns.324473 /ien=2934   		*	* *
2644	0.004050	hundhatiaal asstate OLOGOO (OLOGOO)	NIM : 045704	Up 7400	ND OCCESO
3641	J 0.004059	hypothetical protein CL25084 (CL25084),	NM_015701	Hs.7100	NP_056516
		mRNA /cds=(132,1583) /gb=NM_015701	*.,		8
		/gi=20070263 /ug=Hs.7100 /len=2412			
					~ .
3642	0.003392	chromosome 1 open reading frame 22	NM_025191	Hs.279951	NP_079467
		(C1orf22), mRNA /cds=(54,2723)	• .	0	
		/gb=NM_025191 /gi=19923618		-	-
•		/ug=Hs.279951 /len=6298			
3653	0.047854	cDNA FLJ39355 fis, clone	AK096674	Hs.416902	
		PEBLM2003426. /gb=AK096674			
		/gi=21756218 /ug=Hs.416902 /len=2809	+	ľ	
		rgi-217502107ug-H\$.4109027leij-2009 I			v-
	<u> </u>			L	<u> </u>

Spot:	p-valu	nding To Differentially Expressed General Description	Gene	Unigene	Protein
- 10-0-0	p , a.a.				Accession
			Acc ssion No.	No.	No.
3690	0.012883	IK cytokine, down-regulator of HLA II (IK),	NM 006083	Hs.8024	NP_006074
		mRNA /cds=(112,1785) /gb=NM_006083			
		/gi=11038650 /ug=Hs.8024 /len=1785		*.	
3716	0.013901	FLJ21563 fis, clone COL06445	AK025216	Hs.24341	NP_056287
		(AK025216.1)	***	• *	
3717	0.028474	dimethylarginine dimethylaminohydrolase	NM_013974	Hs.247362	NP_039268
		2 (DDAH2), mRNA /cds=(277,1134)			_
	*	/gb=NM_013974 /gi=7524353		V	
	,	/ug=Hs.247362 /len=1351	8	.68	
			*		
3742	0.011037	conserved gene amplified in	NM_005730	Hs.355816	NP_005721
	, **	osteosarcoma (OS4), mRNA	_		
	,	/cds=(306,1157) /gb=NM_005730	*		
		/gi=19923329 /ug=Hs.355816 /len=4833			1
	00				
3751	0.003392	S100 calcium binding protein A11	NM 005620	Hs.417004	NP 005611
		(calgizzarin) (S100A11), mRNA	_		
		/cds=(121,438) /gb=NM 005620		Ĭ .	
		/gi=5032056 /ug=Hs.417004 /len=595			
3756	0.002342	Ste20-related serine/threonine kinase	NM 014720	Hs.105751	NP_055535
	, ×	(SLK), mRNA /cds=(512,3970)		40	
		/gb=NM_014720 /gi=7661993			,
*		/ug=Hs.105751 /len=5988		. *	
3757	0.039603	tubulin, gamma complex associated	NM_006659	Hs.13386	NP_006650
		protein 2 (TUBGCP2), mRNA			
		/cds=(64,2772) /gb=NM_006659			
		/gi=5729839 /ug=Hs.13386 /len=2846	1		· ,
3762	0.008697	heat shock 70kDa protein 8 (HSPA8),	NM_006597	Hs.180414	NP_694881
0,02	0.000007	transcript variant 1, mRNA	111111_0000007	113.100414	111 _054001
		/cds=(79,2019) /gb=NM_006597			ā: ,
		/gi=24234684 /ug=Hs.180414 /len=2276	(0)		, .
		/gi=24234004 /dg=11s. 1004 14 /lei1=2270			·
3765	0.037129	cold inducible RNA binding protein	NM_001280	Hs.119475	NP 001271
3,00	3.557 129	(CIRBP), mRNA /cds=(81,599)	1.1.1001200	1.75.115475	
		/gb=NM 001280 /gi=4502846			
		/ug=Hs.119475 /len=1322			
3783	0.039603		U76992		NP_055315
3786		bone gamma-carboxyglutamate (gla)	NM_000711	Hs.2558	NP 000702
5,00	3.01730	protein (osteocalcin) (BGLAP), mRNA	11111_0007   1	13.2000	-000/02
		/cds=(19,321)./gb=NM 000711		0.	
		/gi=4502400 /ug=Hs.2558 /len=451			1
3793	0.026506	myosin, light polypeptide 5, regulatory	NM 002477	Hs.170482	NP 002468
J133	0.020090		TAIVI_002477	113.170402	_002400
	*	(MYL5), mRNA /cds=(106,627)	l	· .	
	,	/gb=NM_002477 /gi=4505304	- X-	*	141
2707	0.0000	/ug=Hs.170482 /len=661	D40000	11. 70074	
3797	0.0068	KIAA0081 mRNA, partial cds	D42039	Hs.78871	
		/cds=(1,708) /gb=D42039 /gi=20521875	,		-
		/ug=Hs.78871 /len=4174			l

Genes	Correspon	nding To Differentially Expressed Genes	s in Figure 15 - H	lyperlipidemi	a
	p-value	Description	Gene	Unigene	Protein
•			Accession No.	Accession	Accession
				No.	No.
3801	0.016146	ribosomal protein S7 (RPS7), mRNA	NM_001011	Hs.301547	NP_001002
		/cds=(91,675) /gb=NM_001011	<del>-</del>		
		/gi=15431308 /ug=Hs.301547 /len=729			
3803	0.026596	forkhead box P1 (FOXP1), mRNA	NM 032682	Hs.274344	NP 116071
		/cds=(432,2465) /gb=NM_032682	· <del>-</del>		
		/gi=19923670 /ug=Hs.274344 /len=4954			
- 1					
3806	0.021575	period 1 (Drosophila) (PER1), mRNA	NM 002616	Hs.68398	NP_002607
		/cds=(188,4060) /gb=NM_002616			
	-	/gi=4505712 /ug=Hs.68398 /len=4656	*		
3824	0.018694		D67015		NP 032405
3827		helicase C-terminal domain- and SNF2 N-	NM 032221	Hs.45207	NP 115597
		terminal domain-containing protein		0	
-		(CHD6-pending), mRNA /cds=(185,8326)			
		/gb=NM_032221 /gi=21362041			
1		/ug=Hs.45207 /len=8326			
3848	0.042212	PRP4 pre-mRNA processing factor 4	NM 004697	Hs.374973	NP 004688
		(yeast) (PRPF4), mRNA /cds=(60,1628)	- m		
	- 1	/gb=NM_004697 /gi=24431949			
l:		/ug=Hs.374973 /len=2765			
3871	0.026596	ATP-binding cassette, sub-family B	NM 004299	Hs.125856	NP 004290
		(MDR/TAP), member 7 (ABCB7), nuclear			x
] :		gene encoding mitochondrial protein,		·	1
	·	mRNA /cds=(69,2327) /gb=NM_004299			
1.0		/gi=9665249 /ug=Hs.125856 /len=2444	,		
3872	3.60E-04	6-phosphogluconolactonase (PGLS),	NM_012088	Hs.100071	NP_036220
		mRNA /cds=(18,794) /gb=NM_012088			
1		/gi=6912585 /ug=Hs.100071 /len=1010			
3901	0.010203	estrogen receptor 1 (ESR1), mRNA	NM_000125	Hs.1657	NP_000116
		/cds=(361,2148) /gb=NM_000125			
<u> </u>		/gi=4503602 /ug=Hs.1657 /len=6450			
3902	0.037129	RAB, member of RAS oncogene family-	NM_006860	Hs.50267	NP_006851
1		like 4 (RABL4), mRNA /cds=(364,921)		, Y	
		/gb=NM_006860 /gi=9257237	0	•Y•	1
	<u> </u>	/ug=Hs.50267 /len=1021			
3908	0.013901	KIAA1287 protein (KIAA1287), mRNA	NM_020748	Hs.50187	NP_065799
		/cds=(77,3691) /gb=NM_020748			
		/gi=24308210 /ug=Hs.50187 /len=5894		ļ	0
3924	0.023151	ubiquitin specific protease 10 (USP10),	NM_005153	Hs.78829	NP_005144
{		mRNA /cds=(114,2510) /gb=NM_005153			
		/gi=24307888 /ug=Hs.78829 /len=3009			
3925	0.01738	similar to RIKEN cDNA 1110059E24,	BC028019	Hs.112993	
]		clone IMAGE:5218126, mRNA			
ļ	1	/gb=BC028019 /gi=20380167		}	
٠,	=6	/ug=Hs.112993 /len=3343	L	<u> </u>	

Spot :	p-value	ue Description	Gene	Unigene	Protein
•			Accession No.	Accession	Accession
		× *		No.	No
3932	0.023151	cDNA FLJ10952 fis, clone	AK001814	Hs.381077	-
		PLACE1000374. /gb=AK001814		-	
,		/gi=7023319 /ug=Hs.381077 /len=1871			
3940	0.012883	calpain 2, (m/II) large subunit (CAPN2),	NM 001748	Hs.76288	NP 001739
		mRNA /cds=(143,2245) /gb=NM 001748		,	
	1	/gi=12408645 /ug=Hs.76288 /len=3419			, ,
	* a :		*	$\sim$	
3942	0.020091	spectrin, alpha, non-erythrocytic 1 (alpha-	NM 003127	Hs.77196	NP 003118
		fodrin) (SPTAN1), mRNA			
		/cds=(103,7521) /gb=NM 003127	F		1.8
		/gi=4507190 /ug=Hs.77196 /len=7787		1	
3948	0.037129	Repetitive sequence(ALU SUBFAMILY	P39194	. 1	, ,
- J . J .	3.007 120	SQ)	. 55 15 1		
3954	0.004433	esophageal cancer related gene 4 protein	NM 032411	Hs.43125	NP 115787
, ,	0.00 1 100 	(ECRG4), mRNA /cds=(109,555)	002-7,11	113.40123	110707
	. '	/gb=NM_032411 /gi=14165275		*/	2.2
		/ug=Hs.43125 /len=772			. *
3971	0.004433	sirtuin (silent mating type information	NM_012238	Hs.31176	NP_036370
3311	Ų.004433	regulation 2 1 (S. cerevisiae) (SIRT1),	NIVI_012230	118.31170	JINF_030370
	1 in				
	~	mRNA /cds=(54,2297) /gb=NM_012238			
2000	0.047054	/gi=13775598 /ug=Hs.31176 /len=4107	NNA 040400	11- 477507	ND 057400
3990	0.047854	hypothetical protein HSPC155	NM_016406	Hs.177507	NP_057490
	ich i	(HSPC155), mRNA /cds=(241,744)	. 0		
	·	/gb=NM_016406 /gi=7705480			. *
0004	·	/ug=Hs.177507 /len=1137	4.1007070		
3991	0.011929		AJ007973		
3994	0.002342	mitochondrial ribosomal protein L42	NM_172178	Hs.112110	NP_751918
	E	(MRPL42), transcript variant 3, nuclear	*		
*		gene encoding mitochondrial protein,			1
		mRNA /cds=(179,607) /gb=NM_172178			
		/gi=26667173 /ug=Hs.112110 /len=2093	}		-
					<u> </u>
3997	0.004838	NADH dehydrogenase (ubiquinone)	NM_021074	Hs.51299	NP_066552
		flavoprotein 2, 24kDa (NDUFV2), mRNA			
	-	/cds=(19,768) /gb=NM_021074	1	Ì	
		/gi=10835024 /ug=Hs.51299 /len=827			
4028	0.011037	ATP synthase, H transporting,	NM_005175	Hs.80986	NP_005166
		mitochondrial F0 complex, subunit c		.1	
	-00	(subunit 9), isoform 1 (ATP5G1), mRNA			,
		/cds=(120,530) /gb=NM_005175			* -
		/gi=4885080 /ug=Hs.80986 /len=631		*	
4047	0.021575	mitogen-activated protein kinase kinase	NM 005923	Hs.151988	NP_005914
		kinase 5 (MAP3K5), mRNA	100 <del>7</del>	ļ	
	Į.	/cds=(362,4486) /gb=NM_005923	7		
		/gi=21536459 /ug=Hs.151988 /len=5215			
		3		i '	1

		nding To Differentially Expressed G nes			
Spot	p-valu	Description	Gene	Unigen	Protein
,	•	* **	Accession No.	Accession	Accession
	w .			No.	No.
4054	0.004838	histamine N-methyltransferase (HNMT),	NM 006895	Hs.81182	NP 008826
Ţ,	:	mRNA /cds=(253,1131) /gb=NM_006895		,	_
		/gi=5901969 /ug=Hs.81182 /len=1667	* 1		
	-	, g. 1000 1000 10g 110.0 110.0 110.0		•	
4062	0.028474	B-cell CLL/lymphoma 6 (zinc finger	NM 138931	Hs.155024	NP 620309
-100Z	0.020474	protein 51) (BCL6), transcript variant 2,	14141_100001	113.100024	02000
		mRNA /cds=(421,2541) /gb=NM_138931			. '
· .r ·					
		/gi=21040335 /ug=Hs.155024 /len=3630	8		
1.100	000405		NIN COSCO	11 70000	NE ACTOR
4100	0.039405	splicing factor 30, survival of motor	NM_005871	Hs.79968	NP_005862
	. *	neuron-related (SPF30), mRNA	451		
٠.	(	/cds=(193,909) /gb=NM_005871		<b>.</b>	
		/gi=21361283 /ug=Hs.79968 /len=2033			
4105		PRO0245 protein (PRO0245)	NM_014122		ı
4106	0.020091	pre-B-cell colony-enhancing factor	NM_005746	Hs 239138	NP_005737
		(PBEF), mRNA /cds=(28,1503)	**		
•		/gb=NM_005746 /gi=5031976			
	*	/ug=Hs.239138 /len=2376	. '		
4109	0.0068	autonomously replicating sequence	L08437		NP 006594
		(ARS)		*	_
4131	0.004433	thymosin, beta 4, X chromosome	NM_021109	Hs.75968	NP 066932
		(TMSB4X), mRNA /cds=(78,212)		21	
0		/gb=NM_021109 /gi=11056060	. 8	,	. ,
		/ug=Hs.75968 /len=556		()	
4136	0.023151	602361518F1 NIH_MGC_89 cDNA clone	BG249265	Hs.280777	
1100.	0.020.01	IMAGE:4469716 5', mRNA sequence	02.10200	110.2007.7	-
		/clone=IMAGE:4469716 /clone_end=5			
.,		/gb=BG249265 /gi=12759081	*		
		/ug=Hs.280777 /len=947	1		
11E0	0.002824	immunoglobulin superfamily, member 6	NIM ODERAD	Hs.135194	NP 005840
4158	0.002824		NM_005849	IUS. 199 194	NP_005640
		(IGSF6), mRNA /cds=(45,770)			9 0
		/gb=NM_005849 /gi=5031672			
		/ug=Hs.135194 /len=1019		· ·	115
4169		ribosomal protein S16	M60854		NP_001011
4172	0.024824	cDNA FLJ14762 fis, clone	AK027668	Hs.7886	NP_065702
		NT2RP3003491, weakly similar to			
		Drosophila melanogaster Pelle			
	,	associated protein Pellino (Pli) mRNA.			
		/cds=(66,1028) /gb=AK027668			. *
		/gi=14042516 /ug=Hs.7886 /len=2866	*	·	·
4176	0.018694	mitotic control protein dis3 (DIS3), mRNA	NM_014953	Hs.323346	NP_055768
		/cds=(37,2913) /gb=NM_014953		}	,
		/gi=19923415 /ug=Hs.323346 /len=7320			
	· .				
4178	0.047854	hypothetical protein (KIAA0536)	AB011108		NP_789770
		leucine aminopeptidase 3 (LAP3), mRNA		Hs.182579	NP_056991
4180	T U.UZ-04 / 4				
4180	0.020474	1.			/
4180	0.020474	/cds=(187,1746) /gb=NM_015907 /gi=7705687 /ug=Hs.182579 /len=2147	_		/

		nding To Differentially Expressed G n				
Spot	p-value		Gene	Unigene	Protein	
			Accession No.	Accession	Accession	
				No.	No.	
4181	0.018694	KIAA0663 gene product (KIAA0663),	NM 014827	Hs.17969	NP_055642	
		mRNA /cds=(214,2646) /gb=NM_014827			=	
•		/gi=7662231 /ug=Hs.17969 /len=4365	•			
		791-100223174g 113.11003 Nett 4000			· ·	
4496	0.000454	this reducing interacting protein (TVNID)	NM 006472	Hs.179526	ND 006462	
4186	0.023131	<b>.</b>	14141_000472	IDS.179526	NP_006463	
		mRNA /cds=(222,1397) /gb=NM_006472				
	· i	/gi=5454161 /ug=Hs.179526 /len=2704	,	1		
			,			
4189	0.014988	fatty-acid-Coenzyme A ligase, long-chain	NM_022977	Hs.81452	NP_075266	
•		4 (FACL4), transcript variant 2, mRNA				
		/cds=(507,2642) /gb=NM_022977	8		,	
<b>'</b> *		/gi=12669908 /ug=Hs.81452 /len=5356				
		.g	30	1		
4190	0.042212	protein x 0001 (LOC51185), mRNA	NM 016302	Hs:18925	NP 057386	
7130	0.042212	/cds=(34,1044) /gb=NM_016302	11111_010302	113.10020	1111 _007 500	
-			**	8	,	
	2 22 122	/gi=10047097 /ug=Hs.18925 /len=1668	1111 000070	11 00 1700	115 115751	
4217	0.024824	eukaryotic translation elongation factor 1	NM_032378	Hs.334798	NP_115754	
		delta (guanine nucleotide exchange		ŗ		
		protein) (EEF1D), transcript variant 1,				
		mRNA /cds=(198,2141) /gb=NM_032378			8	
		/gi=25453473 /ug=Hs.334798 /len=2216		l .		
			- 70		0	
4218	0.028474	activin beta-C chain	X82540	· · · · · · ·	700	
4223		solute carrier family 25	NM_000387	Hs.13845	NP 000378	
	0.0	(carnitine/acylcarnitine translocase),				
		member 20 (SLC25A20), mitochondrial				
				0 (4)		
		protein encoded by nuclear gene, mRNA				
		/cds=(37,942) /gb=NM_000387				
		/gi=6006040 /ug=Hs.13845 /len=1219				
4224	0.008019	fibroblast growth factor receptor 1 (fms-	NM_023109	Hs.748	NP_075599	
		related tyrosine kinase 2, Pfeiffer				
		syndrome) (FGFR1), transcript variant 7,		4		
	1	mRNA /cds=(727,2715) /gb=NM_023109				
٠.		/gi=13186244 /ug=Hs.748 /len=4066				
		79. 1010024474g 110.74071611 4000		0		
4226	0.020464	KIAA0436 mRNA, partial cds.	AB007896	Hs.110		
4220	0.030461		V DOO LOSO	JE15. 1 10	,	
	1.	/cds=(1,2070) /gb=AB007896			* .	
		/gi=2662152 /ug=Hs.110 /len=4661		,		
4234	0.028474	ribosomal protein S4, Y-linked (RPS4Y),	NM_001008	Hs.180911	NP_000999	
	a ·	mRNA /cds=(13,804) /gb=NM_001008		<b>.</b>		
	1.	/gi=17981706 /ug=Hs.180911 /len=931			7	
					*	
4239	0.010203	mercaptopyruvate sulfurtransferase	NM_021126	Hs.248267	NP 066949	
.,_00	1 4.5.9230	(MPST), mRNA /cds=(148,1041)		1	-555546	
•	1				,	
	T .	/gb=NM_021126 /gi=23510449 /ug=Hs.248267 /len=1349		ľ		
1						

Spot	p-valu	nding To Differentially Expressed General Description	Gene	Unigen	Protein
			Accession No.	Accession	Accession
	٠			No.	No.
4300	0.039603	hypothetical protein MBC3205	NM_033408	Hs.43621	
		(MBC3205), mRNA /cds=(215,784)	_		
		/gb=NM 033408 /gi=15529965	*		
•		/ug=Hs.43621 /len=961	-0		
4308	2.01E-04	Kruppel-like factor (LOC51713), mRNA	NM_016270	Hs.107740	NP_057354
		/cds=(85,1152) /gb=NM_016270	<del></del>		_
	·	/gi=7706468 /ug=Hs.107740 /len=1647		* * * * * * * * * * * * * * * * * * * *	, ` .
4309	0.007388	aminopeptidase puromycin sensitive	NM_006310	Hs.293007	NP 006301
		(NPEPPS), mRNA /cds=(196,2823)			
		/gb=NM_006310 /gi=15451906			
:	*	/ug=Hs.293007 /len=4177			
4320	0.034784	lysosomal associated protein	NM_018407	Hs.296398	NP_060877
	)	transmembrane 4 beta (LAPTM4B),	0.0.0.		
		mRNA /cds=(234,914) /gb=NM_018407			
		/gi=27597070 /ug=Hs.296398 /len=2045			
4339	0.001606	lamin B receptor (LBR), mRNA	NM_002296	Hs.152931	NP 002287
4009	0.001000	/cds=(76,1923) /gb=NM_002296	14141_002230	113.102931	NF_002201
		/gi=4504960 /ug=Hs.152931 /len=3714			
4350	0.024924	hypothetical protein FLJ10081	NM 017991	Hs.7871	ND 060461
4330	0.024024		14141-017991		NP_060461
	*	(FLJ10081), mRNA /cds=(437,2812)		* .	
	0.	/gb=NM_017991 /gi=21361733			
4205	0.04720	/ug=Hs.7871 /len=5249	NINA Ododod	115 44450	ND 057570
4395	0.01738	hypothetical protein LOC51255	NM_016494	Hs.11156	NP_057578
		(LOC51255), mRNA /cds=(31,492)	*		
		/gb=NM_016494 /gi=24475978	- 1		÷ 0 .
	2 2 2 2 4 2	/ug=Hs.11156 /len=601	100-1-10	11. 2700	ND 00005
4404	0.00213	KIAA1723 protein, partial cds	AB051510	Hs.8700	NP_006085
	1	/cds=UNKNOWN /gb=AB051510			
-	ļ. <u> </u>	/gi=12697990 /ug=Hs.8700 /len=7365	7		
4408	0.004433	mRNA for KIAA1165 protein, partial cds.	AB032991	Hs.30340	,
		/cds=(1,855) /gb=AB032991 /gi=6330170			* *
		/ug=Hs.30340 /len=4415			<u> </u>
4436	0.021575	interleukin 16 (lymphocyte	NM_172217	Hs.82127	NP_757366
	· ·	chemoattractant factor) (IL16), transcript			
		variant 2, mRNA /cds=(267,4001)			
,	1	/gb=NM_172217 /gi=27262656			9
		/ug=Hs.82127 /len=8615			
4440	0.042212	alcohol dehydrogenase 5 (class III), chi	NM_000671	Hs.78989	NP_000662
		polypeptide (ADH5), mRNA			
	0.	/cds=(163,1287) /gb=NM_000671		100	,
		/gi=11496890 /ug=Hs.78989 /len=2496	,		1
4464	0.04496	suCRase-isomaltase (SI)	M84646		
4466	+	cDNA: FLJ21659 fis, clone COL08743.	AK025312	Hs.248862	1
		/gb=AK025312 /gi=10437802			-/
	1	/ug=Hs.248862 /len=2423			1
4467	0.016146	ureidopropionase, beta (UPB1), mRNA	NM_016327	Hs.126926	NP_057411
	0.010140	/cds=(61,1215) /gb=NM_016327	10.0027	1.10.120020	,00,411
		/gi=7706508 /ug=Hs.126926 /len=2006	χ.	1	1 1

	p-value	nding To Differentially Expressed General Description	Gene	Unigene	Protein
Shor	p-value	Description	Accession No.	Accession No.	Accession No.
4468	0.047854	cDNA FLJ13771 fis, clone	AK023833	Hs.288934	NO
	0.047.004	PLACE4000270. /gb=AK023833	711020000	113.200004	- P
		/gi=10435888 /ug=Hs.288934 /len=6133		, ,	
4473	0.016146	matrilin 2 (MATN2), transcript variant 1,	NM_002380	Hs.19368	NP_085072
		mRNA /cds=(126,2996) /gb=NM_002380	-		_
* .		/gi=13518036 /ug=Hs.19368 /len=3496			,
4511	0.001592	syndecan binding protein (syntenin)	NM_005625	Hs.8180	NP_005616
		(SDCBP), mRNA /cds=(149,1045)	*		
		/gb=NM_005625 /gi=5032082			-
		/ug=Hs.8180 /len=2193	77. 77 2.2. 7.2.	le c	
4513	0.011929	hepatitis B virus x interacting protein	NM_006402	Hs.433355	NP_006393
		(HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169	*		
		/ug=Hs.433355 /len=605	4		
4515	0.028474	cell recognition molecule CASPR3	NM 033655	Hs.212839	NP 387504
	4	(CASPR3), transcript variant 1, mRNA			
		/cds=(408,3872) /gb=NM_033655			
		/gi=16306508 /ug=Hs.212839 /len=5017			
4525	0.018604	U5 snRNP-specific protein, 116 kD (U5-	NM 004247	Hs.151787	NP 004238
4020	0.010034	116KD), mRNA /cds=(61,2979)	14141_004247	113.131707	141-004230
		/gb=NM_004247 /gi=4759279	4		
		/ug=Hs.151787 /len=3784			*
4532	0.018281	endonuclease/reverse transCRiptase	AAC53542	7	
		[Mus musculus]	, , , , , , , , , , , , , , , , , , , ,		
4535	0.034512	PC326 protein (PC326), mRNA	NM_018442	Hs.279882	NP_060912
•		/cds=(695,2296) /gb=NM_018442		· · · · · · · · · · · · · · · · · · ·	
×		/gi=8923955 /ug=Hs.279882 /len=2727			
4537	0.013901	cleavage and polyadenylation specific	NM_007006	Hs.9605	NP_008937
	4,	factor 5, 25 kDa (CPSF5), mRNA		*	*
•		/cds=(1,684) /gb=NM_007006	o ÷	,	
		/gi=5901925 /ug=Hs.9605 /len=764		<del> </del>	
4540	0.016146	decay accelerating factor for complement	NM_000574	Hs.1369	NP_000565
		(CD55, Cromer blood group system)			
	0	(DAF), mRNA /cds=(66,1211)	*	*****	
		/gb=NM_000574 /gi=10835142		-	197
4554	0.003303	/ug=Hs.1369 /len=2102 integral membrane protein 2B (ITM2B),	NM_021999	Hs.239625	NP_068839
4004	0.003382	mRNA /cds=(171,971) /gb=NM_021999	1999 	175.235025	1,4-7000038
		/gi=11527401 /ug=Hs.239625 /len=1843			
4556	0.011037	phosphorylase, glycogen, liver (Hers	NM 002863	Hs.771	NP 002854
		disease, glycogen storage disease type			
. *	3-4	VI) (PYGL), mRNA /cds=(52,2595)	9		
		/gb=NM_002863 /gi=4506352			
		/ug=Hs.771 /len=2643			

	p-value	nding To Differentially Expressed Genes Description	Gene Accession No.	Unigene	Protein Accession No.
4583		restin (Reed-Steinberg cell-expressed intermediate filament-associated protein) (RSN), mRNA /cds=(133,4416) /gb=NM_002956 /gi=4506750 /ug=Hs.31638 /len=5857	NM_002956	Hs.31638	NP_002947
4616	0.028474	603054284F1 NIH_MGC_122 cDNA clone IMAGE:5203652 5', mRNA sequence /clone=IMAGE:5203652 /clone_end=5' /gb=BI767055 /gi=15758633 /ug=Hs.356004 /len=1067	BI767055	Hs.356004	
4647	0.04496	S-phase kinase-associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930	Hs. 171626	NP_733779
4650	0.04496	WW domain binding protein 11 (WBP11), mRNA /cds=(162,2087) /gb=NM_016312 /gi=18375679 /ug=Hs.334811 /len=2690	NM_016312	Hs.334811	NP_057396
4653	0.003392	degenerative spermatocyte lipid desaturase (Drosophila) (DEGS), transcript variant 1, mRNA /cds=(112,1083) /gb=NM_003676 /gi=21614503 /ug=Hs 185973 /len=2058	NM_003676	Hs.185973	NP_659004
4659	0.026596	retinoic acid induced 2 (RAI2), mRNA /cds=(379,1971) /gb=NM_021785 /gi=12056469 /ug=Hs.49597 /len=2338	NM_021785	Hs.49597	NP_068557
4689		t-complex-associated-testis-expressed 1- like (TCTE1L), mRNA /cds=(69,419) /gb=NM_006520 /gi=5730086 /ug=Hs.446392 /len=2156	NM_006520	Hs.446392	NP_006511
4693	0.001442	H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(1'18,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662	NM_005324	Hs.180877	NP_005315
4695°	0.032563	oxytocin receptor (OXTR), mRNA /cds=(622,1791) /gb=NM_000916 /gi=12707575 /ug=Hs.2820 /len=4357	NM_000916	Hs 2820	NP_000907
4698	0.030409	retinoic acid receptor, beta (RARB), transcript variant 1, mRNA /cds=(469,1815) /gb=NM_000965 /gi=14916493 /ug=Hs.171495 /len=3119	NM_000965	Hs.171495	NP_057236
4701	0.024824	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs 13836 /len=413	NM_024292	Hs.13836	NP_077268

Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
	•			No.	No.
4720	0.013901	heterogeneous nuclear ribonucleoprotein	NM 005826	Hs.15265	NP_005817
		R (HNRPR), mRNA /cds=(91,1992)			
		/gb=NM 005826 /gi=14141188			
	*	/ug=Hs.15265 /len=2663			
4722	0.011929	S-phase kinase-associated protein 1A	NM_006930	Hs.171626	NP 733779
		(p19A) (SKP1A), transcript variant 1,			
		mRNA /cds=(140,622) /gb=NM_006930			
		/gi=25777710 /ug=Hs.171626 /len=2172			· .
		,	ļ	ļ	
4723	8.65E-04	Escherichia coli K-12 MG1655 section	AE000453	· · · · ·	1. 7
		343 of 400 of the complete genome			
4728	0.042212	pp21 (LOC51186), mRNA	NM 016303	Hs.15984	NP_057387
		/cds=(263,577) /gb=NM_016303			
	V	/gi=10047099 /ug=Hs.15984 /len=1038	,		
4736	0.008019	E74-like factor 1 (ets domain	NM 172373	Hs.154365	NP 758961
		transcription factor) (ELF1), mRNA			_
		/cds=(256,2115) /gb=NM_172373			
		/gi=27363483 /ug=Hs.154365 /len=3526	•		*
				,	
4737	0.032563	deoxyribonuclease II, lysosomal	NM 001375	Hs.118243	NP_001366
		(DNASE2), mRNA /cds=(94,1176)	_		
		/gb=NM_001375 /gi=4503348	* ,.		* -
		/ug=Hs.118243 /len=1975			
4741	0.018694	hypothetical protein MGC21981	NM_153267	Hs.131987	NP_694999
,	1	(MGC21981), mRNA /cds=(66,764)	_	·	_
	,	/gb=NM_153267 /gi=23397567			
	, , )	/ug=Hs.131987 /len=1727			
4757	0.0068	sarcoma amplified sequence (SAS),	NM_005981	Hs.50984	NP_005972
	**	mRNA /cds=(155,787) /gb=NM_005981			
		/gi=21264346 /ug=Hs.50984 /len=1809			·
4761	0.015733	calpastatin (CAST), transcript variant 2,	NM_173060	Hs.359682	NP_775085
		mRNA /cds=(155,2215) /gb=NM_173060			
		/gi=27765084 /ug=Hs.359682 /len=4296			
			,		
47,65	0.013901	N-myc (and STAT) interactor (NMI),	NM_004688	Hs.54483	NP_004679
		mRNA /cds=(281,1204) /gb=NM_004688	}		
		/gi=4758813 /ug=Hs.54483 /len=1426	10		
4700	-   0 00 10 5 5		111111111111111111111111111111111111111	1000	NE CERE
4769	0.004059	mitochondrial ribosomal protein L37	NM_016491	Hs.4209	NP_057575
		(MRPL37), nuclear gene encoding			
	• •	mitochondrial protein, mRNA			
		/cds=(78,1349) /gb=NM_016491	<b>(</b>	*	
, 4 <del>55</del> 2	0.00475	/gi=22547133 /ug=Hs 4209 /len=1511	1114 704 202	11. 00000	ND CO (O (C
4774	0.034784	ribosomal protein S19 (RPS19), mRNA	NM_001022	Hs.298262	NP_001013
		/cds=(70,507) /gb=NM_001022		· · · · · y · · · ·	
4===		/gi=14591914 /ug=Hs.298262 /len=569	 		100 0000
4782	0.01738	CDC-like kinase1 (CLK1), mRNA	NM_004071	Hs.2083	NP_004062
		/cds=(156,1610) /gb=NM_004071	1		
		/gi=4758007 /ug=Hs.2083 /len=1834		L	

Spot	p-value	nding To Differentially Expressed General Description	Gene	Unigene	Protein
Opot	p yalac	Description	Accession No.	Accession	Accession
			Accession No.	No.	No.
4798	0.008697	Rho-associated, coiled-coil containing	NM_004850	Hs.58617	NP_004841
		protein kinase 2 (ROCK2), mRNA		1.0.000	
		/cds=(455,4621) /gb=NM 004850		· ()	
		/gi=6633807 /ug=Hs.58617 /len=6409			
4807	0.01738	glypican 6 (GPC6), mRNA	NM_005708	Hs.118407	NP 005699
		/cds=(616,2283) /gb=NM_005708			
		/gi=8051601 /ug=Hś.118407 /len=2760			*.
4814	0.024441	ribosomal protein L10a (RPL10A), mRNA	NM 007104	Hs.425293	NP_009035
		/cds=(16,669) /gb=NM_007104		,	
	× .1	/gi=15431287 /ug=Hs.425293 /len=700	-		4 11 1
4830	0.034784	golgin-67 (KIAA0855), mRNA	NM 015003	Hs 182982	NP_851422
,		/cds=(343,2238) /gb=NM_015003			
		/gi=19923417 /ug=Hs.182982 /len=4578			
4831	7.78E-04	protein kinase C, theta (PRKCQ), mRNA	NM 006257	Hs.211593	NP 006248
		/cds=(22,2142) /gb=NM 006257	_	, , , , , , , , , , , , , , , , , , , ,	
		/gi=5453975 /ug=Hs.211593 /len=2705			, 19
4835	4.04E-04	tj81f06.x1	Al472273	Hs.228361	1 7 7 7
		Soares_NSF_F8_9W_OT_PA_P_S1		**	
•	100	cDNA clone IMAGE:2147939 3' similar to		k .	* ** .
		gb:M11050 GLUCOCORTICOID	-		
	1	RECEPTOR, BETA mRNA sequence	0		
		/clone=IMAGE:2147939 /clone end=3'		*	
		/gb=Al472273 /gi=4334363			
		/ug=Hs.228361 /len=555			
4837	0.018694	UI-H-BW1-amj-g-07-0-UI.s1	BF513214	Hs.445888	r
		NCI_CGAP_Sub7 cDNA clone			
		IMAGE:3070261 3', mRNA sequence	Se 1		
F .		/clone=IMAGE:3070261 /clone_end=3'			
	<i>4</i>	/gb=BF513214 /gi=11598393		)*	
• •		/ug=Hs.445888 /len=620			
4855		KIAA0795 protein(KIAA0795), mRNA	XM_016166		
4856	0.042212	similar to unknown protein (low aa match)	XP_066236		
			-		
4874	0.011929	ankyrin repeat domain 10 (ANKRD10),	NM_017664	Hs.172572	NP_060134
	,	mRNA /cds=(136,1398) /gb=NM_017664			- <del>-</del>
		/gi=8923103 /ug=Hs.172572 /len=2509	· :		
4881	0.004433	glyoxylate reductase/hydroxypyruvate	NM_012203	Hs.155742	NP_036335
		reductase (GRHPR), mRNA		* .	
	, V	/cds=(42,1028) /gb=NM_012203	*1		
		/gi=6912395 /ug=Hs.155742 /len=1235	t		
4884	0.003808	geranylgeranyl diphosphate synthase 1	NM_004837	Hs.55498	NP_004828
		(GGPS1), mRNA /cds=(233,1135)			
		/gb=NM_004837 /gi=21359876			
	- 1	/ug=Hs.55498 /len=1489		]-	

Spot	Correspoi p-value	Description	G ne	Unigen	Protein
•		* · · · · · · · · · · · · · · · · · · ·	Accession No.	Accession	Accession
, i	٠.			No.	No.
4909	0.009424	hypothetical protein FLJ20542	NM_032179	Hs.6449	NP_115555
		(FLJ20542), mRNA /cds=(63,899)			
1.		/gb=NM_032179 /gi=14149862	4.8		
		/ug=Hs.6449 /len=1984			· ·
4915	0.0068	hypothetical protein FLJ13149	NM 021826	Hs.112188	NP 068598
		(FLJ13149), mRNA /cds=(291,2585)			
		/gb=NM_021826 /gi=11141902			
		/ug=Hs.112188 /len=2836	- '		
4919	0.034784	KIAA0436 mRNA, partial cds.	AB007896	Hs.110	He control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con
		/cds=(1,2070) /gb=AB007896			
*	· .	/gi=2662152 /ug=Hs.110 /len=4661	*		
4943	0.018694	DKFZp434N1717 (from clone	AL133655		NP_473357
		DKFZp434N1717)	1		
4946	0.001935	myosin, light polypeptide 6, alkali, smooth	NM 079425	Hs.77385	NP_524149
	1 1	muscle and non-muscle (MYL6),			
		transcript variant 3, mRNA /cds=(41,514)		•	
		/gb=NM_079425 /gi=17986263			
		/ug=Hs.77385 /len=717			
4956	0.032563	hypothetical protein FLJ20671	NM_017924	Hs.180201	NP_060394
		(FLJ20671), mRNA /cds=(43,465)			
		/gb=NM_017924 /gi=19923511			
-		/ug=Hs.180201 /len=2855		*	
4969	0.042212	mRNA; cDNA DKFZp434A163 (from	AL110218	Hs.127401	
	*	clone DKFZp434A163); partial cds			
		/cds=(1,4964) /gb=AL110218		* =	
	- X-1	/gi=5817150 /ug=Hs.127401 /len=5084		1.	
4979	0.047854	ribosomal protein L6 (RPL6), mRNA	NM 000970	Hs.409045	NP_000961
		/cds=(32,898) /gb=NM 000970			
	0	/gi=16753226 /ug=Hs 409045 /len=950		*	in a
4980	0.034784	Gene 33/Mig-6 (MIG-6), mRNA	NM 018948	Hs.11169	NP 061821
		/cds=(213,1601) /gb=NM_018948			
		/gi=21314673 /ug=Hs.11169 /len=3099	*		
4981	0.004838	hypothetical protein FLJ13386	NM_025180	Hs.300876	NP 079456
ě	,	(FLJ13386), mRNA /cds=(428,2539)	<del>-</del>		
	Ì	/gb=NM 025180 /gi=22095366			-
	ļ.:.	/ug=Hs.300876 /len=2770			
4988	0.012883	translocase of outer mitochondrial	NM_014820	Hs.21198	NP_055635
. 0		membrane 70 A (yeast) (TOMM70A),			
4	l '	mRNA /cds=(92,1918) /gb=NM 014820			
		/gi=7662672 /ug=Hs.21198 /len=4017			·
4992	6.28E-04	tissue factor pathway inhibitor (lipoprotein-	NM 006287	Hs.170279	NP 006278
• .		associated coagulation inhibitor) (TFPI),			
	, ,	mRNA /cds=(1,915) /gb=NM_006287	. %		· *
		/gi=6715569 /ug=Hs.170279 /len=915		,	
	1	J		1	,

Spot	Correspoi	Description	Gene	Unigene	Protein
ypy.				Accession	Accession
	*		Accession No.	No.	No.
4993	0.037129	likely ortholog of mouse hepatoma-	NM 016073	Hs.127842	NP 057157
.,,,,,	9.991 .20	derived growth factor, related protein 3		110.127012	1007 101
		(HDGFRP3), mRNA /cds=(156,767)			i ·
		/gb=NM_016073 /gi=21359902			
		/ug=Hs.127842 /len=1973			
5010	0.011037	DKFZp586E0524 (from clone	AL110153	<del> </del>	NP 000974
50.0	0.011007	DKFZp586E0524)	/\E110100		141 _000974
5017	0.010203	HMG-box containing protein 1 (HBP1),	NM_012257	Hs.10882	NP_036389
3017	0.010200	mRNA /cds=(187,1731) /gb=NM_012257	14101_012201	113.10002	147_030303
		/gi=21361410 /ug=Hs.10882 /len=2857			
		/gi=21301410/ug=115.10002/iei1=2837			
5024	0.012883	xylosylprotein beta 1,4-	NM 007255	Hs.54702	NP 009186
JU27	2.012003	galactosyltransferase, polypeptide 7	14.41_007233	113.04702	144 -009100
• *	<b> </b> :	(galactosyltransferase I) (B4GALT7);	- A		*
•		mRNA /cds=(41,1024) /gb=NM_007255			
•		/gi=6005951 /ug=Hs.54702 /len=1669	8		*
5029	0.005275	mortality factor 4 like 1 (MORF4L1),	NM_006791	Hs.6353	NP_006782
J029	0.003273	mRNA /cds=(132,1103) /gb=NM 006791	14141_000791	115.0000	NF_000702
		/gi=5803101 /ug=Hs.6353 /len=1766	0		
	- 10	/gi=3003101/ag=118:0333/iei1=1700	· · ·	-	
5037	0.0068	MAP kinase-interacting serine/threonine	NM 017572	Hs.261828	NP_060042
000.	0.0000	kinase 2 (MKNK2), mRNA	11111_017072	110.201020	141 _000042
	7	/cds=(23,1267) /gb=NM_017572			
	·	/gi=9994196 /ug=Hs.261828 /len=1549		· .	
5044	0.039603	S100 calcium binding protein A4 (calcium	NM 002961	Hs.81256	NP 062427
	0.00000	protein, calvasculin, metastasin, murine		1,10.0,1200	
	-	placental (S100A4), transcript variant 1,	1 1/2		1
		mRNA /cds=(70,375) /gb=NM_002961	<u> </u>		
		/gi=9845514 /ug=Hs.81256 /len=512			- ''
	8	, g., g. g. g. g. g. g. g. g. g. g. g. g. g.			
5047	0.005746	hypothetical protein DJ328E19.C1.1	NM_015383	Hs.218329	NP_056198
		(DJ328E19.C1.1), mRNA /cds=(18,2783)			
		/gb=NM_015383 /gi=7657016	,		
	·	/ug=Hs.218329 /len=3689			
5049	0.011037	mRNA for KIAA0592 protein, partial cds.	AB011164	Hs.439367	
7 7		/cds=(1,4062) /gb=AB011164			
	0.0	/gi=3043707 /ug=Hs.439367 /len=4623			
5050	0.006254	protein phosphatase 3 (formerly 2B),	NM 000944	Hs.272458	NP_000935
		catalytic subunit, alpha isoform			
		(calcineurin A alpha) (PPP3CA), mRNA			
		/cds=(407,1972) /gb=NM_000944			
	l	/gi=19923130 /ug=Hs.272458 /len=4425	Ļ		
-	* .				
5053	0.008019	tubulin-specific chaperone d (TBCD),	NM 005993	Hs.12570	NP 005984
2,000	5.555575	mRNA /cds=(110,3688) /gb=NM_005993			
		/gi=8400735 /ug=Hs.12570 /len=3927			
		1.g. 0 100100 14g 110, 12010 11011 10021		1	

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
5062	0.007388	KIAA1208 protein, partial cds	AB033034	Hs.7041	NP_077288
i.		/cds=UNKNOWN /gb=AB033034			
		/gi=6382021 /ug=Hs.7041 /len=6447	, , , , , , , , , , , , , , , , , , , ,		
5069	0.023151	hsp70-interacting protein (HSPBP1),	NM_012267	Hs.53066	NP 036399
		mRNA /cds=(312,1400) /gb=NM 012267			
		/gi=21361406 /ug=Hs.53066 /len=1795		2 (3	
	•	79. 2.40 (100 rdg 110.00000 71011 1100			
5102	5 63F-04	cofilin 1 (non-muscle) (CFL1), mRNA	NM 005507	Hs.180370	NP 005498
:	0.002 0.1	/cds=(52,552) /gb=NM_005507	11111_000007	113.100070	1111 _000400
	, *	/gi=5031634 /ug=Hs.180370 /len=1059			
5111	0.016146	chromosome 14 open reading frame 94	NM_017815	Hs.8886	NP_060285
2111	0.010140	(C14orf94), mRNA /cds=(211,1302)	NIVI_017613	IUS.0000	NF_000205
		/gb=NM_017815 /gi=8923395	*		7
E4.47	0.000007	/ug=Hs.8886 /len=1618	1.00005	11 400440	
5147	0.000097	blue cone opsin gene, complete cds	L32835	Hs.102119	A-
E407	0.04.4000	(L32835.1)			NID ADDAY
5187	0.014988		NM_012482	Hs.59757	NP_036614
		/cds=(24,2711) /gb=NM_012482		*	
		/gi=6912751 /ug=Hs.59757 /len=3029	,		
5188	0.026596	p53R2 mRNA for ribonucleotide	AB036063	Hs.94262	
		reductase, complete cds.			
•-		/cds=(245,1300) /gb=AB036063	2		
-	, +	/gi=7229085 /ug=Hs.94262 /len=4955			
5193	0.014988	RAB23, member RAS oncogene family	NM_016277	Hs.94769	NP_057361
-		(RAB23), mRNA /cds=(151,864)		0	
		/gb=NM_016277 /gi=19923480	•		
		/ug=Hs.94769 /len=2588	<u> </u>		
5204	0.04496	stathmin-like 3 (STMN3), mRNA	NM_015894	Hs.285753	NP_056978
		/cds=(83,625) /gb=NM_015894	* *	,	-
• •	*	/gi=14670374 /ug=Hs.285753 /len=2255			10
				0	
5206	0.047854	CAAX box 1 (CXX1), mRNA	NM_003928	Hs.250708	NP_003919
	* • (*)	/cds=(335,964) /gb=NM_003928	<del>-</del> ,		_
		/gi=4503180 /ug=Hs.250708 /len=1209	9		
5220	0.04496	calcium-independent alpha-latrotoxin	AF063102		
	. *	receptor homolog 2 (CIRL-2) mRNA,			
	,	complete cds	,		
5224	0.028474	ubiquitously-expressed transcript (UXT),	NM 153477	Hs.172791	NP_705582
		transcript variant 1, mRNA			- 33,02
		/cds=(155,664) /gb=NM 153477	* - 8		
		/gi=24041017 /ug=Hs.172791 /len=734			
5235	0.003097	major histocompatibility complex, class II,	NM 002124	Hs.375570	NP 002115
5255	9.000007	DR beta 1 (HLA-DRB1), mRNA		11-13,57 557 0	_002113
		/cds=(63,863) /gb=NM 002124	. "		'
	1	/Qua-(00,000) /gb-14141_002 124	l .	1	

Spot	p-value	nding To Diff rentially Express d Genes Description	Gene	Unig ne	Protein
			Accession No.	Accession	Accession
t	7.3-0			No.	No.
5241	0.012883	RNA binding motif, single stranded	NM_016839	Hs.241567	NP_058523
		interacting protein 1 (RBMS1), transcript			-8-
		variant MSSP-2, mRNA /cds=(266,1435)			·
•		/gb=NM_016839 /gi=8400723		· · · · · · · · · · · · · · · · · · ·	
		/ug=Hs.241567 /len=1679			
5243	0.010203	chromosome 14 open reading frame 2	NM_004894	Hs.109052	NP_004885
		(C14orf2), mRNA /cds=(61,237)			1
		/gb=NM_004894 /gi=4758939	• •	× × ×	
50.40	<u> </u>	/ug=Hs.109052 /len=627	. =		,
5249	0.047854	Escherichia coli K-12 MG1655 section	AE000453		
<u> </u>	0.000404	343 of 400 of the complete genome	V11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		9.70 HI
5274		lysosomal apyrase-like 1 (LYSAL1)	XM_040572		NE SESSE
5275	0.032563	DKFZP434F091 protein	NM_015453	Hs.30488	NP_056268
	1,353	(DKFZP434F091), mRNA			
1		/cds=(335,1858) /gb=NM_015453 /gi=14149689 /ug=Hs.30488 /len=2897			
5277	0.00001	reversion-inducing-cysteine-rich protein	NM 021111	Hs.29640	NP 066934
3211	0.020091	with kazal motifs (RECK), mRNA	14101_021111	ms.29040	INP_000934
		/cds=(93,3008) /gb=NM_021111	*	* <u>. **</u>	
		/gi=11863155 /ug=Hs.29640 /len=4414			
5283	0.037129	transforming, acidic coiled-coil containing	NM_006997	Hs 272023	NP_008928
0200	0.007 120	protein 2 (TACC2), mRNA	1444_000007	113.272020	111 _000320
		/cds=(87,3167) /gb=NM_006997			
		/gi=11119413 /ug=Hs.272023 /len=3686			, ,
		<b>3</b>			
5302	0.002824	poly(rC) binding protein 1 (PCBP1),	NM_006196	Hs.2853	NP_006187
		mRNA /cds=(178,1248) /gb=NM_006196			
		/gi=14141164 /ug=Hs.2853 /len=1634			*
5317	0.042059	ribosomal protein S2 (RPS2), mRNA	NM_002952	Hs.356360	NP_002943
		/cds=(12,893) /gb=NM_002952			,
		/gi=15055538 /ug=Hs.356360 /len=978			//-
5323	0.012883	epithelial membrane protein 3 (EMP3),	NM_001425	Hs.9999	NP_001416
		mRNA /cds=(242,733) /gb=NM_001425			
5005	0.040004	/gi=4503562 /ug=Hs.9999 /len=817	NIN 004004	11. 75000	ND 004050
5325	0.013901	eukaryotic translation elongation factor 2	NM_001961	Hs.75309	NP_001952
3		(EEF2), mRNA /cds=(69,2645) /gb=NM_001961 /gi=25453476			
		/ug=Hs.75309 /len=3148			
5330	0.01738	discs, large 7 (Drosophila) (DLG7),	NM_014750	Hs.77695	NP 055565
٥٥٥٥	0.01750	mRNA /cds=(218,2758) /gb=NM_014750	14/0	113.77090	_000000
•		/gi=21361644 /ug=Hs.77695 /len=2979	.*	.*	
	*	= 1301044749 113.77000 /1011-2070			:
5344	0.034784	Similar to hypothetical protein	BC041843	Hs.259412	
		dJ465N24.2.1, clone IMAGE:5269181,			
	1	mRNA /gb=BC041843 /gi=27693120		,	**
•		/ug=Hs.259412 /len=3079			-
5364	0.047854	hypothetical protein DKFZp547l224	NP_064606	-	
		(RefSeq aa 9e-31)		i i	

Spot	p-value	value Description	Gene	Unigene	Protein
	•		Accession No.	Accession	Accession
5393	0.020001	ubiquitination factor E4B (UFD2 yeast)	NM 006048	<b>No.</b> Hs.24594	No. NP 006039
	0,020091	(UBE4B), mRNA /cds=(86,3994)	NIVI_000046	ns.24594	MB_00003a
		/gb=NM_006048 /gi=5174482	· .	2	
		/ug=Hs.24594 /len=5314		-	=
5400	0.04496	dUTP pyrophosphatase (DUT), mRNA	NM 001948	Hs.367676	NP_001939
	1	/cds=(20,514) /gb=NM_001948		1.0.90,0,0	
		/gi=21361335 /ug=Hs.367676 /len=1816			0.
	*				
5401	0.023151	clone MGC:46380 IMAGE:4524661,	BC038805	Hs.32425	NP_076870
		mRNA, complete cds /cds=(296,2071)	*		
		/gb=BC038805 /gi=24416461			
,		/ug=Hs.32425 /len=2554			
5402		brain cDNA, clone:QnpA-21421	AB050422		
5408	0.018694	mitogen-activated protein kinase kinase	NM_145342	Hs.109727	NP_663317
		kinase 7 interacting protein 2	1.1	,	
		(MAP3K7IP2), transcript variant 2, mRNA	•		
		/cds=(176,1786) /gb=NM_145342	×.		
		/gi=21735558 /ug=Hs.109727 /len=4359			
5413	0.016146	mRNA for hypothetical protein (ORF1)	AJ297792	Hs.11114	
		/cds=(327,989) /gb=AJ297792	7.02017.02		·
		/gi=27526568 /ug=Hs.11114 /len=4110			
5433	0.030461	actin related protein 2/3 complex, subunit	NM 005717	Hs.82425	NP 005708
•		5, 16kDa (ARPC5), mRNA		, , ,	
		/cds=(192,647) /gb=NM_005717			
		/gi=23238212 /ug=Hs.82425 /len=2000			
5471	0.002342		AF055376		NP_005351
		maf)		9	
5477	0.005275	lectin, galactoside-binding, soluble, 3	NM_002306	Hs.621	NP_002297
		(galectin 3) (LGALS3), mRNA			1
-	,	/cds=(19,771) /gb=NM_002306			
		/gi=4504982 /ug=Hs.621 /len=914			
5489	0.0068	DKFZP566H073 protein	NM_015528	Hs.7158	NP_056343
		(DKFZP566H073), mRNA			
		/cds=(450,1502) /gb=NM_015528			
5500	0.004704	/gi=14149701 /ug=Hs.7158 /len=1723	411440000	11.000700	
5506	0.034784	xf26f10.x1 NCI_CGAP_Ut1 cDNA clone	AW130007	Hs.389726	•
		IMAGE:2619211 3', mRNA sequence	•		
	· .	/clone=IMAGE:2619211 /clone_end=3'			
	. *	/gb=AW130007 /gi=6131612			
5508	0.034834	/ug=Hs.389726 /len=423 KIAA0185 mRNA, complete cds.	D80007	Hs.239499	<del>                                     </del>
2200	0.024024	/cds=(1,5656) /gb=D80007 /gi=1136429	00000/	115.238488	
		/cas=(1,5656)/gb=D8000//gi=1136429 /ug=Hs.239499 /len=5823	*	1	
5510	0.004050	eukaryotic translation initiation factor 3,	NM_003753	Hs.55682	NP_003744
0010	1 0.004039	subunit 7 zeta, 66/67kDa (EIF3S7),		13.00002	JINE _003/44
• .		mRNA /cds=(372,2018) /gb=NM_003753			
		/gi=23238220 /ug=Hs.55682 /len=2169			
	· ,	791, 20200220 149-113.00002 11611-2 103		I	1

Snot	p-valu	Description	s in Figure 15 - I Gene	Unigene	Protein
Opot	Valu	Besonption		Accession	Accession
			Accession No.	No.	No.
5514	0.024824	ribosomal protein L4 (RPL4), mRNA	NM_000968	Hs.286	NP 000959
		/cds=(57,1340) /gb=NM_000968	7		7
		/gi=16579884 /ug=Hs.286 /len=1449			
5516	0.012883	dihydrofolate reductase (DHFR), mRNA	NM_000791	Hs.83765	NP_000782
<u>-</u> ,		/cds=(480,1043) /gb=NM_000791			
	. •	/gi=7262376 /ug=Hs.83765 /len=3900			÷
5520	0.01738	transforming growth factor-beta type I	AF035669		7.7
		receptor			
5521	0.032563	papillomavirus L2 interacting nuclear	NM_052850	Hs.83135	NP 443082
<del>.</del> .		protein 1 (PLINP-1), mRNA /cds=(1,669)		,	
		/gb=NM_052850 /gi=18959277		, ,	
· · ·		/ug=Hs.83135 /len=669			•
5549	0.042212	N-methylpurine-DNA glycosylase (MPG),	NM 002434	Hs.79396	NP_002425
		mRNA /cds=(147,1043) /gb=NM_002434			
	· ·	/gi=4505232 /ug=Hs.79396 /len=1108	14		
					* *
5574	0.04496	hypothetical protein FLJ20452	NM 017828	Hs.351327	NP_060298
		(FLJ20452), mRNA /cds=(15,614)		,	
,		/gb=NM_017828 /gi=21361660	:-		*
		/ug=Hs.351327 /len=1948			
5576	0.037129	mRNA; cDNA DKFZp451A0419 (from	AL833070	Hs.146233	
		clone DKFZp451A0419) /gb=AL833070			1
		/gi=21733661 /ug=Hs.146233 /len=4831	100	f	
					· · ·
5581	0.011037	cDNA FLJ35019 fis, clone	AK092338	Hs.348799	
		OCBBF2014541. /gb=AK092338		1 11 11 -	Ì
	at .	/gi=21750910 /ug=Hs.348799 /len=2778		_	
5584	0.037129	regulator of nonsense transcripts 1	NM_002911	Hs.12719	NP_002902
٠,	6	(RENT1), mRNA /cds=(232,3588)	_		<del>-</del>
		/gb=NM_002911 /gi=18375672			
		/ug=Hs.12719 /len=5300		0	
5591	0.037129	SEC22 vesicle trafficking protein-like 3	NM_004206	Hs.12942	NP_116752
		(S. cerevisiae) (SEC22L3), transcript			
- :	Ì	variant 2, mRNA /cds=(119,871)		121	1.
	٦	/gb=NM_004206 /gi=21536310			
		/ug=Hs.12942 /len=1519	*	,	
5600	0.018694	ADP-ribosylation factor 5 (ARF5), mRNA	NM_001662	Hs.430657	NP_001653
		/cds=(37,579) /gb=NM_001662			
		/gi=6995999 /ug=Hs.430657 /len=978			
5612	0.007388	MAP-kinase activating death domain	NM_003682	Hs.82548	NP_569832
		(MADD), transcript variant 4, mRNA			-
111		/cds=(192,5135) /gb=NM_003682		1	
	*	/gi=18860876 /ug=Hs.82548 /len=6016			
5616	0.011929	solute carrier family 31 (copper	NM_001859	Hs.380728	NP 001850
		transporters), member 1 (SLC31A1),		,	
	-	mRNA /cds=(153,725) /gb=NM_001859	÷ .	*	
•	I "	/gi=4507014 /ug=Hs.380728 /len=1804			

		nding To Differentially Expressed Gener			
Spot	p-value	D scription	Gene	Unigene	Protein
	1 .	**	Accession No.	Accession	Accession
		*		No.	No.
5620	0.026596	solute carrier family 25 (mitochondrial	NM_001636	Hs.407372	NP_001627
		carrier; adenine nucleotide translocator),			
		member 6 (SLC25A6), nuclear gene			- 10 a
• • •	).	encoding mitochondrial protein, mRNA			
		/cds=(93,989) /gb=NM 001636	•		
		/gi=27764862 /ug=Hs.407372 /len=1455			
: *		""			
5632	0.0068	macrophage migration inhibitory factor	NM 002415	Hs.407995	NP_002406
0002	0.0000	(glycosylation-inhibiting factor) (MIF),	14101_002-10	113.407333	141 _002400
	10	mRNA /cds=(98,445) /gb=NM_002415		9.7	
					1
5000	0.000007	/gi=4505184 /ug=Hs.407995 /len=561	NINA 420022	1110 2000	ND COCCO
5639	0.008697	mitogen-activated protein kinase 7	NM_139033	Hs.3080	NP_620603
		(MAPK7), transcript variant 1, mRNA		*	
•		/cds=(355,2805) /gb=NM_139033		* * * * * * * * * * * * * * * * * * * *	- 00
	1-1-1-1	/gi=20986500 /ug=Hs.3080 /len=3113		2 2 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
5644	0.003712	integrin, beta 1 (fibronectin receptor, beta	NM_002211	Hs.287797	NP_596867
		polypeptide, antigen CD29 includes	- 00		
	1 1 1	MDF2, MSK12) (ITGB1), transcript			•
		variant 1A, mRNA /cds=(127,2523)			, .
		/gb=NM_002211 /gi=19743812	* .		): **
		/ug=Hs.287797 /len=3700			
	·				
5654	0.042212	Tis11d	U07802		
5655	0.0068	clone MGC:43116 IMAGE:5260824,	BC038670	Hs.98508	NP_055932
		mRNA, complete cds /cds=(13,2859)	8.7		=
		/gb=BC038670 /gi=24217448			
		/ug=Hs.98508 /len=3268		÷	-
5662	0.009055	collagen, type XV, alpha 1 (COL15A1),	NM_001855	Hs.83164	NP 001846
0002	0.00000	mRNA /cds=(166,4332) /gb=NM_001855	11111_001000	110.00101	141 _001040
		/gi=18641349 /ug=Hs.83164 /len=5222			
		1004 1040 1dg=113.00 104 Nc11=5222		00	
5666	0.022154	KND 12 (-1153007 CT225)	D86061	<del>                                     </del>	ND 004640
5666	0.023131	KNP-la (=U53007 GT335)		110 225 422	NP_004640
0/18	0.034/84	ribosomal protein L14 (RPL14), mRNA	NM_003973	Hs.235422	NP_003964
		/cds=(38,688) /gb=NM_003973	ļ	α.	
	0.04:55	/gi=16753224 /ug=Hs.235422 /len=843	NA 000000	1	ND SOCIE
5723	0.04496	cytoskeleton-associated protein 4	NM_006825	Hs.74368	NP_006816
		(CKAP4), mRNA /cds=(85,1893)			1
		/gb=NM_006825 /gi=19920316	,		
	÷ .	/ug=Hs.74368 /len=2913		-	
5749	0.034784	up-regulated gene 4 (URG4), mRNA	NM_017920	Hs.5131	NP_060390
		/cds=(14,2782) /gb=NM_017920		<u> </u>	
		/gi=19923541 /ug=Hs 5131 /len=3606			
5769	0.018694	cDNA: FLJ21561 fis, clone COL06415.	AK025214	Hs.96918	
	*	/gb=AK025214 /gi=10437681			
		/ug=Hs.96918 /len=1641			
5789	0.012883	ribosomal protein L31 (RPL31), mRNA	NM_000993	Hs.184014	NP_000984
	0.012000	/cds=(28,405) /gb=NM_000993	1.1.1000000	1.13.107017	1.11 _000904
		/gi=15812219 /ug=Hs.184014 /len=442			1

		nding To Differentially Expressed Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
			0.0	No.	No.
5794	0.010203	xd87d05.x1 Soares_NFL_T_GBC_S1	AW104522	Hs.230403	
		cDNA clone IMAGE:2604585 3', mRNA			
	:	sequence /clone=IMAGE:2604585	*•	<b>,</b>	
		/clone_end=3' /gb=AW104522		<b>!</b>	
		/gi=6075257 /ug=Hs.230403 /len=459			*
5814	0.003097	ribosomal protein L36a-like (RPL36AL),	NM_001001	Hs.419465	NP 000992
<b>901.</b> 1	1 0.000007	mRNA /cds=(95,415) /gb=NM_001001	1	11.0.110100	
		/gi=16306559 /ug=Hs.419465 /len=537			
5826	0.018694	ribosomal protein L13a (RPL13A), mRNA	NM 012423	Hs.389335	NP 036555
0020	0.010054	/cds=(23,634) /gb=NM_012423	14,01_012,420,	113.000000	
		/gi=14591905 /ug=Hs.389335 /len=1142	. A.	1	
ē.		/gi= 1459 1905 /ug=115.569555 /iefi= 1 142	· ·		
5861	0.005746	mRNA for KIAA0338 gene, partial cds.	AB002336	Hs.26395	NP 818932
2001	0.003746		AB002330	F15.20393	147_010932
•		/cds=(1,2807) /gb=AB002336			- 18
5070	0.04700	/gi=2224616 /ug=Hs.26395 /len=6263	NIM 004270	11- 000504	ND 540070
5876	0.01/38	COX15 cytochrome c oxidase assembly	NM_004376	Hs.226581	NP_510870
		protein (yeast) (COX15), nuclear gene			
	-8-	encoding mitochondrial protein, transcript			
		variant 2, mRNA /cds=(52,1218)			i)
	14	/gb=NM_004376 /gi=17921986	7 7		
		/ug=Hs.226581 /len=2841			
	*			<u> </u>	
5900	0.006254	DCHT (=AF030403 Ste20-like protein	AF017635		NP_037365
	. 7.6.7	kinase)			
5901	0.001304	lipin 1 (LPIN1), mRNA /cds=(68,2740)	NM_145693	Hs.81412	NP_663731
		/gb=NM_145693 /gi=22027647		· ·	
		/ug=Hs.81412 /len=5363			
5905	0.039603	protein phosphatase 2 (formerly 2A),	NM_002718	Hs.28219	NP_002709
		regulatory subunit B", alpha (PPP2R3A),			<u> </u>
:.		mRNA /cds=(505,3957) /gb=NM_002718	: .	ļ.	
		/gi=19923228 /ug=Hs.28219 /len=5217	9	-	1
		g			·
5914	0.011929	ribosomal protein S20 (RPS20), mRNA	NM_001023	Hs.8102	NP_001014
JJ Inf	3.3020	/cds=(128,487) /gb=NM_001023		1	
	}	/gi=14591915 /ug=Hs.8102 /len=539		1	1
5915	0.004050	SH3-domain binding protein 5 (BTK-	NM 004844	Hs.109150	NP_004835
3313	0.004033	associated) (SH3BP5), mRNA	14141_004044	113.100100	111 _004000
	1	/cds=(64,1341) /gb=NM 004844	į .	1	
	Ī		)		3
E000	0.005740	/gi=4759057 /ug=Hs.109150 /len=2570	NIM 002227	Un 011	ND 002220
5928	0,005/46	ubiquitin-conjugating enzyme E2B (RAD6	NIVI_UU333/	Hs.811	NP_003328
		(UBE2B), mRNA /cds=(422,880)	, r	1.	Ì
		/gb=NM_003337 /gi=4507770		1 .	
		/ug=Hs.811 /len=2591	100 100 100	11. 04000	LUD 000=0=
5937	0.042212	mitogen-activated protein kinase 9	NM_139069	Hs.246857	NP_620709
		(MAPK9), transcript variant 3, mRNA	-	(*	
		/cds=(50,1198) /gb=NM_139069			[
		/gi=21237741 /ug=Hs.246857 /len=1947		1	-
	1 1	1	1	1	I

Spot	p-value	orresponding To Differentially Expressed Genes value Description		Unigene	Protein	
opo.	وهابت م		Gene Accession No.	Accession	Accession	
			Accession No.			
6001	0.037120	KIAA0441 gene product (KIAA0441),	NM 014797	No. Hs.32511	NP_055612	
0001	0.037 128		14101-014797	115.32311	INP_000012	
		mRNA /cds=(169,2262) /gb=NM_014797			,	
		/gi=7662127 /ug=Hs 32511 /len=5597	*-		-	
6006	0.000007	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	NIA 000004	11 440'400	115 000075	
6006   0	0.008697	ribosomal protein L23a (RPL23A), mRNA	NM_000984	Hs.419463	NP_000975	
		/cds=(22,492) /gb=NM_000984		7		
		/gi=17105393 /ug=Hs.419463 /len=546				
6026	0.024824	fibromodulin (FMOD), mRNA	NM_002023	Hs.230	NP_002014	
	* + :	/cds=(21,1151) /gb=NM_002023				
		/gi=5016093 /ug=Hs.230 /len=2863				
6042	0.028474	laminin, gamma 1 (formerly LAMB2)	NM_002293	Hs.432855	NP_002284	
		(LAMC1), mRNA /cds=(300,5129)			. *	
	e (	/gb=NM_002293 /gi=9845497			1	
	1	/ug=Hs.432855 /len=7923		23.		
6049	0.003097	chromobox 1 (HP1 beta Drosophila )	NM 006807	Hs.77254	NP 006798	
, i		(CBX1), mRNA /cds=(292,849)			-	
	900	/gb=NM_006807 /gi=21359877				
		/ug=Hs.77254 /len=2242				
6052	0.010203	thioredoxin (TXN), mRNA /cds=(64,381)	NM 003329	Hs.432922	NP 003320	
<b>0002</b>	0.010200	/gb=NM_003329 /gi=4507744	111111_000020	113.402022	111 _000020	
,		/ug=Hs.432922 /len=501		*		
6071	0.034784	hook3 protein (HOOK3), mRNA	NM 032410	Hs.130707	NP_115786	
0071	0.004704	/cds=(164,2320) /gb=NM_032410	NIVI_032410	113.130707	110700	
	1 8				.]	
		/gi=14165273 /ug=Hs.130707 /len=2648		. ,		
6090	0.004929	anlestene 1 phoephote	NINA 147121	110 75C44	ND 667242	
6090	0.004636	galactose-1-phosphate	NM_147131	Hs.75641	NP_667343	
	1 1	uridylyltransferase (GALT), transcript				
		variant 2, mRNA /cds=(68,448)				
	- 2	/gb=NM_147131 /gi=22165417				
·		/ug=Hs.75641 /len=2603	\		1	
6095	0.002342	immediate early protein (ETR101),	NM_004907	Hs.737	NP_004898	
		mRNA /cds=(101,772) /gb=NM_004907				
		/gi=4758313 /ug=Hs.737 /len=1811				
6096	0.001935	neuroblastoma RAS viral (v-ras)	NM_002524	Hs.260523	NP_002515	
		oncogene (NRAS), mRNA				
•		/cds=(254,823) /gb=NM_002524	}			
	* .	/gi=6006027 /ug=Hs.260523 /len=1963			1	
6102	0.021575	homer 2 (Drosophila) (HOMER2), mRNA	NM 004839	Hs.93564	NP_004830	
		/cds=(1,1065) /gb=NM_004839	_			
		/gi=4758547 /ug=Hs.93564 /len=1800		*		
6106	0.039603	EST (ym17h04.s1 clone 48282 3')	H11657		1:	
6146		mitochondrial precursor receptor	D63411	<del></del>	-	
3.10	3.33 1, 34	(=D13641 Human KIAA0016)		*		
6150	0.003343	poly(rC) binding protein 1 (PCBP1),	NM_006196	Hs.2853	NP_006187	
0100	0.002042	mRNA /cds=(178,1248) /gb=NM_006196	14141-000 180	113.2003	1111 _000 107	
			, ** · · · · · · · · · · · · · · · · · ·		1	
	•	/gi=14141164 /ug=Hs.2853 /len=1634		1.		

		nding To Differentially Expressed Gener			
Spot	p-value	Description	Gene	Unigene	Protein
	,		Accession No.	Accession	Accession
				No.	No.
6183	0.034784	actin related protein 2/3 complex, subunit	NM_005720	Hs.433506	NP_005711
J		1B, 41kDa (ARPC1B), mRNA		ļ	
		/cds=(90,1208) /gb=NM_005720			
		/gi=22907055 /ug=Hs.433506 /len=1520		• •	100
		, g,			
6192	0.037120	TNFAIP3 interacting protein 1 (TNIP1),	NM 006058	Hs.109281	NP 006049
0132	0.007 129	mRNA /cds=(258,2168) /gb=NM_006058	14141_000000	113.103201	_000043
		/gi=21361267 /ug=Hs.109281 /len=2921			
0405	0 00 10 10	,	10047040		<del></del>
6195	0.024048	myoM [Dictyostelium	AB017910	*	3.
	٠,	discoideum](38%ORF)	<u> </u>	· ·	
6239	0.028474	Similar to RD RNA-binding protein, clone	BC011600	Hs.356818	,
	}	MGC:2263 IMAGE:3050953, mRNA,		+ .	
		complete cds /cds=(34,1035)			-30
	.00	/gb=BC011600 /gi=15079543			
		/ug=Hs.356818 /len=2478			· ·
6248	0.001064	tumor differentially expressed 1 (TDE1),	NM_006811	Hs.272168	NP 006802
		mRNA /cds=(78,1499) /gb=NM_006811	-		
•		/gi=5803192 /ug=Hs.272168 /len=1892		<b>'</b>	.]
6272	0.047854	cDNA, 5' end /clone=IMAGE:4148900	BF342391	Hs.30469	NP_055313
0212	0.047034	/clone_end=5' /gb=BF342391	DI 342331	113.50403	-00000 10
				-	:
0075	0.000007	/gi=11289392 /ug=Hs.30469 /len=803	NIN 047040	11- 57000	ND 00000
6275	0.008697	hypothetical protein FLJ20432	NM_017819	Hs.57898	NP_060289
		(FLJ20432), mRNA /cds=(603,1361)		*	•
		/gb=NM_017819 /gi=8923404			
		/ug=Hs.57898 /len=1654			
6337	0.005746	adaptor-related protein complex 2, mu 1	NM_004068	Hs.152936	NP_004059
		subunit (AP2M1), mRNA	• 1		
	·	/cds=(136,1443) /gb=NM_004068	* **		
		/gi=14917108 /ug=Hs.152936 /len=1936			
•				·	•
6391	0.002467	GABA(A) receptor-associated protein like	NM 031412	Hs.336429	NP 113600
		1 (GABARAPL1), mRNA /cds=(282,635)			
		/gb=NM_031412 /gi=13899218	- "		
		/ug=Hs.336429 /len=1933		ľ	
		1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935   1935			1
6409	0.024704	protein phosphatase 2 (formerly 2A),	NM_002715	Hs.91773	NP_002706
0403	0.034764	1	NIVI_0027 13	115.51775	NF_002700
		catalytic subunit, alpha isoform		. ~ .	
		(PPP2CA), mRNA /cds=(210,1139)	***		
		/gb=NM_002715 /gi=4506016			
		/ug=Hs.91773 /len=2181			1 222 2 2 2 2 2 2 2 2
6422	0.032563	soc-2 suppressor of clear (C. elegans)	NM_007373	Hs.104315	NP_031399
		(SHOC2), mRNA /cds=(278,2026)		0.7	
		/gb=NM_007373 /gi=6677944			
		/ug=Hs.104315 /len=3872	3		
6428	0.007388	serologically defined colon cancer	NM_004713	Hs.388584	NP_004704
		antigen 1 (SDCCAG1), mRNA	_		_
				1	1
	ł	/cds=(183,1271) /gb=NM_004713			

Spot	p-value	nding To Differentially Expressed Genes Description	Gene	Unigene	Protein
opot	p-value		Accession No.	Accession	Accession
			Accession No.	No.	No.
6439	0.037120	protein phosphatase 1, catalytic subunit,	NM 002709	Hs.21537	NP 002700
0400	0.037 123	beta isoform (PPP1CB), mRNA	14141_002703	113.21,007	_002700
- 1		/cds=(259,1242) /gb=NM_002709		0.0	i
	}	/gi=4506004 /ug=Hs.21537 /len=3590		1	
		/gi=4300004 /dg=11s.2 1337 /ieii=3330	·	1	
6442	0.037129	6-phosphofructo-2-kinase/fructose-2,6-	NM 004566	Hs.195471	NP 004557
		biphosphatase 3 (PFKFB3), mRNA			
		/cds=(115,1677)/gb=NM 004566			
		/gi=4758899 /ug=Hs.195471 /len=4322			
6446	0.018694	CAR (RFP2) gene, complete cds; DLEU2	AF279660		
		and DLEU1 genes, complete sequence;			
		and RPL18 and p48/Hip pseudogenes,			<b>∤</b> ′
		complete sequence	· ·	. At	
6461	0.001179	zinc finger protein 175 (ZNF175), mRNA	NM 007147	Hs.119014	NP 009078
Q:10 1	0.001110	/cds=(346,2481) /gb=NM_007147	0077		
		/gi=6005969 /ug=Hs.119014 /len=3734			
6465	0.04496	KIAA0761 protein, partial cds	AB018304	<u> </u>	NP 055942
6468		reverse transcriptase related protein	1207289A	<del>                                     </del>	1207289A
6471		hydroxysteroid (11-beta) dehydrogenase	NM_005525	Hs.275215	NP 005516
· · · ·	0.010001	1 (HSD11B1), mRNA /cds=(95,973)		1.0.2.02.0	
	į.	/gb=NM 005525 /gi=5031764	, ,		
	* .	/ug=Hs.275215 /len=1375		* 1	
6478	0.023151	I-kappa-B-interacting Ras-like protein 1	XM_053030		
	0.020,01	(KBRAS1), mRNA			.:
6488	0.028474	oncostatin M receptor (OSMR), mRNA	NM 003999	Hs.238648	NP_003990
0.00	0.02017	/cds=(368,3307) /gb=NM_003999			
€	1	/gi=4557039 /ug=Hs.238648 /len=4171			
6513	0.023151	uncharacterized hematopoietic	NM_018464	Hs.43549	NP 060934
0010	0.020101	stem/progenitor cells protein MDS029	1111_010101	1.0.100.10	1.100040 :
•	1 (1)	(MDS029), mRNA /cds=(112,438)			·
	9	/gb=NM 018464 /gi=8923929		,	
	}	/ug=Hs.43549 /len=636			0.
6514	0.023151	cDNA FLJ11796 fis, clone	AK021858	Hs.284186	
0017	0.020101	HEMBA1006158, highly similar to	1 11 10 2 1 9 0 0	1	
-)-		transcription factor forkhead-like 7			
	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	(FKHL7) gene. /gb=AK021858		1	
•	4	/gi=10433135 /ug=Hs.284186 /len=1551		1	-0.0
		1			
6525	0.024824	cyclin I (CCNI), mRNA /cds=(545,1678)	NM_006835	Hs.79933	NP_006826
3-L.		/gb=NM_006835 /gi=17738314			, -
		/ug=Hs.79933 /len=1890		,	
6527	0.042212	hypothetical protein (HSPC016), mRNA	NM_015933	Hs.397853	NP_057017
3041		/cds=(39,233) /gb=NM_015933			
		/gi=7705430 /ug=Hs.397853 /len=384			*
6540	0.042212	LIM and SH3 protein 1 (LASP1), mRNA	NM_006148	Hs.334851	NP_006139
5540	0.042212	/cds=(76,861) /gb=NM_006148	1111   111	1.10.00,1001	
	1	/gi=5453709 /ug=Hs.334851 /len=3846	-	1	1

Genes	Correspon	nding To Differentially Express d Genes	s in Figur 15 - F	lyperlipidemia	3
	p-value	Description	Gene	Unig ne	Protein
1			Accession No.	Accession	Accession
	*		,	No.	No.
6550	0.04496	t-complex-associated-testis-expressed 1-	NM 006519	Hs.266940	NP 006510
		like 1 (TCTEL1), mRNA /cds=(1,342)		0.	-
	,	/gb=NM_006519 /gi=5730084			
		/ug=Hs.266940 /len=713			* '
6554	0.032563	mitochondrial ribosomal protein L13	NM 014078	Hs.333823	NP 054797
		(MRPL13), nuclear gene encoding	-		
		mitochondrial protein, mRNA	* *		160
f.		/cds=(287,823) /gb=NM_014078		*,	* 1 1.05
		/gi=21265072 /ug=Hs.333823 /len=1086			***
		, g., = . = . =			
6563	0.042212	cytochrome c oxidase subunit Va	NM_004255	Hs.323834	NP 004246
	0.012212	(COX5A), nuclear gene encoding	1	110.020001	141 _00 12 10
		mitochondrial protein, mRNA			,
1	*	/cds=(18,470) /gb=NM_004255			
		/gi=17017986 /ug=Hs.323834 /len=645		*	
6565	0.032563	PTK9 protein tyrosine kinase 9 (PTK9),	NM_002822	Hs.82643	NP 002813
0000	0.002500	mRNA /cds=(61,1113) /gb=NM_002822		113.02043	1002013
91		/gi=4506274 /ug=Hs.82643 /len=3000			
6566	0.01738	RAB11A, member RAS oncogene family	NM 004663	Hs.75618	NP 004654
0300	0.01730	(RAB11A), mRNA /cds=(104,754)	NIVI_004003	i iż. 1 20 10	NF_004034
1		/gb=NM_004663 /gi=20149549	1.5		
		/gg=Hs.75618 /len=2474			
6590	0.04406	mRNA for KIAA0981 protein, partial cds.	AB023198	Hs.158135	1
0390	0.04490	/cds=(1,1738) /gb=AB023198	AB023190 .	115.150,155	
1	in An	/gi=4589605 /ug=Hs.158135 /len=5182			
6592	0.033563	methylene tetrahydrofolate	NM_006636	Hs.154672	NP_006627
0092	0.032303	dehydrogenase (NAD dependent),	14M_000030	ITIS. 104072	NF_000027
		methenyltetrahydrofolate cyclohydrolase	0		* .
	* :	(MTHFD2), nuclear gene encoding			
		mitochondrial protein, mRNA		-8	
		/cds=(77,1111) /gb=NM 006636			
		/gi=13699869 /ug=Hs.154672 /len=2154	*		
6646	0.004433	protein phosphatase 1, regulatory	NM 002480	Hs.16533	NP 002471
0040	0.004433	(inhibitor) subunit 12A (PPP1R12A),	14141_002400	113.10333	- UU24/1
	-	mRNA /cds=(1,3093) /gb=NM 002480			
		/gi=4505316 /ug=Hs 16533 /len=4613			†
6654	0.04406	pM5 protein (PM5), mRNA /cds=(1,3669)	NM 014287	Hs.439182	NP_055102
0054	0.04496	, , , , , , , , , , , , , , , , , , , ,	14101_01420/	1115,438102	NF_000102
ĺ		/gb=NM_014287 /gi=10947030		1	
		/ug=Hs.439182 /len=4182			
GGEO	0.000424	host shock 70kDa protoin 9 (USDA9)	NM 006597	Hs.180414	ND 604004
6659	0.009424	heat shock 70kDa protein 8 (HSPA8),	NAINI_00009/	175. 1004 14	NP_694881
	<b>1</b> .	transcript variant 1, mRNA			110
		/cds=(79,2019) /gb=NM_006597			
	-	/gi=24234684 /ug=Hs.180414 /len=2276	* *		
6667	0.011020	H4 history familia mambas C (H4EC)	NIM 003540	Hs.46423	ND 003533
6664	0.011929	H4 histone family, member G (H4FG),	NM_003542	1115.40423	NP_003533
1		mRNA /cds=(1,312) /gb=NM_003542		1	
L.,,,,	Ļ	/gi=21071024 /ug=Hs.46423 /len=390	<del></del>	L	Ļ <u></u>

	p-value	nding To Differ ntially Expressed General Description	Gene	Unigene	Protein
			Acc ssion No.	Accession	Accession
			7.00 001011 110.	No.	No.
6673	0.004059	cAMP responsive element binding protein	NM 006368	Hs.287921	NP_006359
7 7 7		3 (luman) (CREB3), mRNA			
		/cds=(439,1554) /gb=NM_006368			
		/gi=22219461 /ug=Hs.287921 /len=1837			
•		1 222 10 10 1749 115.201021 71611: 1001		m .	
6683	0.004433	lamin A/C (LMNA), transcript variant 1,	NM_170707	Hs.377973	NP_733822
0000	0.001100	mRNA /cds=(213,2207) /gb=NM_170707	17.07.07	113.577575	141 _733022
(9)		/gi=27436945 /ug=Hs.377973 /len=3181			
	,				
6708	0.026596	erythroid differentiation-related factor 1	AF040247		<u> </u>
6713		cDNA FLJ23648 fis, clone COL04718.	AK074228	Hs.375782	
07-13	0.004400	/gb=AK074228 /gi=18676772	/////#220	115.57.57.62	
		/ug=Hs.375782 /len=2295			
6749	0.01720	histidyl-tRNA synthetase 2 (HARS2),	NM_080820	Hs.352419	ND 542040
0/49	0.01736		NNI_U0U02U	ITIS.352419	NP_543010
		mRNA /cds=(111,752) /gb=NM_080820			
		/gi=21361784 /ug=Hs.352419 /len=2396			· ·
0750	0.004575	ABB 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1114 01000	10000	1 ·
6750	0.021575	ADP-ribosylation-like factor 6 interacting	NM_016638	Hs.103561	NP_061164
		protein 4 (ARL6IP4), mRNA			. 14
.1		/cds=(63,719) /gb=NM_016638		÷ 11	
		/gi=7706183 /ug=Hs.103561 /len=952			
6752	0.037129	tumor endothelial marker 6 (TEM6),	NM_022748	Hs.12210	NP_073585
		mRNA /cds=(93,3710) /gb=NM_022748			, -
		/gi=17511208 /ug=Hs.12210 /len=6702			
6770	0.021575	FK506 binding protein 1A, 12kDa	NM_000801	Hs.380080	NP_463460
		(FKBP1A), transcript variant 12B, mRNA		*	
		/cds=(104,430) /gb=NM_000801			
		/gi=17149837 /ug=Hs.380080 /len=1578			
6773	0.024824	hypothetical protein FLJ14834	NM_032849	Hs.62905	NP_116238
•	1 2	(FLJ14834), mRNA /cds=(326,1237)			
		/gb=NM_032849 /gi=21361885			
•		/ug=Hs.62905 /len=2342			
6800	0.030461	tumor necrosis factor, alpha-induced	NM_021137	Hs.76090	NP_066960
		protein 1 (endothelial) (TNFAIP1), mRNA			- 1
		/cds=(212,1162) /gb=NM_021137			
	-	/gi=26051238 /ug=Hs.76090 /len=3571	,		
	· _ ·				-
6809	0.030461	eukaryotic translation initiation factor 4A,	NM_001967	Hs.173912	NP_001958
		isoform 2 (EIF4A2), mRNA			
		/cds=(16,1239) /gb=NM_001967			1
		/gi=9945313 /ug=Hs.173912 /len=1864			-
C011	0.026596	pleckstrin domain interacting protein	NM_017934	Hs.10177	NP 060404
6811					ı <del></del>
		(PHIP), mRNA /cds=(306.2429)			
	·	(PHIP), mRNA /cds=(306,2429) /gb=NM_017934 /gi=20149647		1	

Spot	p-value	Description	Gene	Unigene	Protein
	P		· ·	Accession	Accession
			Accession No.	No.	No.
6873	0.01738	coated vesicle membrane protein	NM 006815	Hs.75914	NP 006806
		(RNP24), mRNA /cds=(24,629)			
		/gb=NM_006815 /gi=21314646		•	· · .
		/ug=Hs.75914 /len=2060		- 20	
3875	0.012883	cDNA FLJ12924 fis, clone	AK022986	Hs.38034	14.1 · ja - 14.1
	1,5 , 5	NT2RP2004709. /gb=AK022986	, <del></del>		
•		/gi=10434694 /ug=Hs.38034 /len=2667	1,50		
880	0.004059	cytochrome c oxidase subunit VIIa	NM 001864	Hs.421621	NP 001855
7		polypeptide 1 (muscle) (COX7A1),			
		nuclear gene encoding mitochondrial			
		protein, mRNA /cds=(463,702)			
		/gb=NM_001864 /gi=18105034	*		
-		/ug=Hs.421621 /len=783	* .		
8889	0.003712	clone MGC:9929 IMAGE:3873001,	BC040341	Hs.314169	
		mRNA, complete cds /cds=(142,3333)			
		/gb=BC040341 /gi=25955484		11	<i>i</i>
		/ug=Hs.314169 /len=5328	0 2		
	0.026596	metaxin 1 (MTX1), mRNA /cds=(1,954)	NM_002455	Hs.247551	NP 002446
	, 0.020000	/gb=NM_002455 /gi=4505280	11111_002 100	110.217001	111 _002 110
	*	/ug=Hs.247551 /len=1065			
920	0.021575	thioredoxin (TXN), mRNA /cds=(64,381)	NM 003329	Hs.432922	NP_003320
	0.021070	/gb=NM_003329 /gi=4507744		113. 102022	111 _000020
		/ug=Hs.432922 /len=501			
3935	0.003712	FtsJ 3 (E. coli) (FTSJ3), mRNA	NM_017647	Hs.257486	NP_060117
3000	0.000112	/cds=(72,2615) /gb=NM_017647	11111_017047	113.237 400	111 _000117
	<b>.</b>	/gi=17017990 /ug=Hs.257486 /len=2999			
	÷ ,		* *		
5942	0.030461	eukaryotic translation elongation factor 1	NM_001402	Hs.422118	NP_001393
		alpha 1 (EEF1A1), mRNA /cds=(63,1451)	55	1,0.122.10	100.000
		/gb=NM_001402 /gi=25453469		<b>1</b>	1
	:	/ug=Hs.422118 /len=1837		34	
		7 dg - 1 (6:1122 1 10 /101) 1 1 0 0 /	*		
6954	0.011037	phospholipid transfer protein (PLTP),	NM_006227	Hs.283007	NP_006218
		mRNA /cds=(88,1569) /gb=NM_006227	, ,		
		/gi=5453913 /ug=Hs.283007 /len=1750			
5958	0.032563	origin recognition complex, subunit 5-like	NM_002553	Hs.153138	NP 002544
		(yeast) (ORC5L), mRNA /cds=(89,1396)	, <del>-</del>		7
		/gb=NM 002553 /gi=4505524			
		/ug=Hs.153138 /len=1901		•	,
3973	0.010203	mRNA; cDNA DKFZp313P0434 (from	AL832702	Hs.125019	
		clone DKFZp313P0434) /gb=AL832702			1
		/gi=21733281 /ug=Hs.125019 /len=2995			
	1 .				
7004	0.026596	FLJ30431 fis, clone BRACE2008968,	AK054993	Hs.173737	NP 061485
		highly similar to RAS-RELATED C3			
		BOTULINUM TOXIN SUBSTRATE 1	1 *	3	
		/cds=UNKNOWN /gb=AK054993	* .	100	*-
		/gi=16549633 /ug=Hs.173737 /len=2315			*
				1	

		nding T Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
		***	Accession No.	Accession	Accession
		× × × × × × × × × × × × × × × × × × ×		No.	No
7022	0.013901	ribosomal protein S29 (RPS29), mRNA	NM_001032	Hs.539	NP_001023
•		/cds=(31,201) /gb=NM_001032			
		/gi=13904868 /ug=Hs.539 /len=346	*		
7023	0.01738	activated RNA polymerase II transcription	NM 006713	Hs.349506	NP_006704
		cofactor 4 (PC4), mRNA /cds=(57,440)		**	_
	*	/gb=NM 006713 /gi=19923783	20		
		/ug=Hs.349506 /len=1336		. X *	
	]	199			
7025	0.037129	PKU-beta (=D50927 KIAA0137)	AB004885		
7026		density-regulated protein (DENR), mRNA	NM 003677	Hs.22393	NP_003668
1020	0.020474	/cds=(111,707) /gb=NM_003677	11111_000077	113.22,000	_000000
	: .	/gi=27501445 /ug=Hs.22393 /len=2766	*	· .	
7043	0.030603	platelet-activating factor acetylhydrolase,	NM_000430	Hs.77318	NP 000421
1043	0.008000	isoform Ib, alpha subunit 45kDa	14W_000430	113.77310	1115 _000421
,			}		
		(PAFAH1B1), mRNA /cds=(556,1788)			
		/gb=NM_000430 /gi=6031206	Ŷ.		
<del></del>	100000	/ug=Hs.77318 /len=5581	N. 1 040440	11 00704	ND 444044
7050	0.037129	cyclin D-type binding-protein 1	NM_012142	Hs.36794	NP_411241
		(CCNDBP1), transcript variant 1, mRNA			
		/cds=(158,1240) /gb=NM_012142			
		/gi=16554565 /ug=Hs.36794 /len=1615			
7099	0.011929	cell division cycle 42 (GTP binding	NM_001791	Hs.146409	NP_426359
•		protein, 25kDa) (CDC42), transcript			,
		variant 1, mRNA /cds=(105,680)		*	
		/gb=NM_001791 /gi=16357470		•	
		/ug=Hs.146409 /len=2183			×
7,107	0.023151	ectonucleotide	NM_014936	Hs.54037	NP_055751
		pyrophosphatase/phosphodiesterase 4	-		
		(putative function) (ENPP4), mRNA		*	
	)	/cds=(49,1410) /gb=NM_014936			
		/gi=7662357 /ug=Hs.54037 /len=4312		*	
7109	0.04496	hypothetical protein (KIAA1102)	AB029025	,	
7111		hypothetical protein LOC51234	NM_016454	Hs.250905	NP 057538
		(LOC51234), mRNA /cds=(72,623)	_		
		/gb=NM 016454 /gi=24475963			-
	· ·	/ug=Hs.250905 /len=1013			
7126	0.039603	ribosomal protein S18 (RPS18), mRNA	NM_022551	Hs.275865	NP_072045
	5.55555	/cds=(46,504) /gb=NM_022551		]	]
		/gi=14165467 /ug=Hs.275865 /len=549	- ×		4
7141	0.011020	ELK1, member of ETS oncogene family	NM_005229	Hs.181128	NP_005220
7 14 1	0.011929	(ELK1), mRNA /cds=(234,1520)	14141_009223	113.101120	_000220
		/gb=NM 005229 /gi=11496880	4	1	* * *
			. C		
		/ug=Hs.181128 /len=2828		I	1

		nding To Differentially Expressed Gener	Gene		
Spot	p-value	Description		Unigene Accession No.	Protein Accession No.
7147	0.042212	UI-1-BB1p-aki-h-05-0-UI.s1 NCI_CGAP_Pl6 cDNA clone UI-1-BB1p- akl-h-05-0-UI 3', mRNA sequence /clone=UI-1-BB1p-akl-h-05-0-UI	BQ022477	Hs.424771	
1		/clone_end=3' /gb=BQ022477 /gi=19757756 /ug=Hs.424771 /len=1598			
7166	0.012883	transducer of ERBB2, 1 (TOB1), mRNA /cds=(36,1073) /gb=NM_005749 /gi=22035666 /ug=Hs.178137 /len=1830	NM_005749	Hs.178137	NP_005740
7175	0.026596	AGENCOURT_6853421 NIH_MGC_99 cDNA clone IMAGE:5926418 5', mRNA sequence /clone=IMAGE:5926418 /clone_end=5' /gb=BQ064669	BQ064669	Hs.380699	
7178	0.023151	/gi=19893520 /ug=Hs.380699 /len=969 supervillin (SVIL), transcript variant 2, mRNA /cds=(754,7398) /gb=NM_021738 /gi=11496981 /ug=Hs.154567 /len=8300	NM_021738	Hs.154567	NP_068506
7184	0.009424	nucleosome assembly protein 1-like 1 (NAP1L1), transcript variant 1, mRNA /cds=(125,1300) /gb=NM_139207 /gi=21327707 /ug=Hs.302649 /len=3582	NM_139207	Hs.302649	NP_631946
7210	0.009424	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) (DCI), mRNA /cds=(9,917) /gb=NM_001919 /gi=4503266 /ug=Hs.403436 /len=1017	NM_001919	Hs.403436	NP_001910
7235	0.001442	SOCS box-containing WD protein SWiP- 1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243		Hs.187991	NP_599027
7288	0.028474	KIAA0800 gene product (KIAA0800), mRNA /cds=(169,4692) /gb=NM_014703 /gi=7662315 /ug=Hs.118738 /len=5984	NM_014703	Hs.118738	NP_055518
7306	0.009424	golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 (GOLGB1), mRNA /cds=(127,9906) /gb=NM_004487 /gi=4758453 /ug=Hs.7844 /len=10300	NM_004487	Hs.7844	NP_004478
7313	0.011929	translocation protein 1 (TLOC1), mRNA /cds=(613,1812) /gb=NM_003262 /gi=14602425 /ug=Hs.8146 /len=3091	NM_003262	Hs.8146	NP_003253

		nding To Differentially Express d Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	· · · · · · · · · · · · · · · · · · ·			No.	No.
7314	0.014988	chromosome 11 open reading frame 10	NM 014206	Hs.90918	NP 055021
	*	(C11orf10), mRNA /cds=(56,295)			
	5	/gb=NM_014206 /gi=7656933	• .		
		/ug=Hs.90918 /len=418			
7316	0.013901	integral membrane protein 2B (ITM2B),	NM_021999	Hs.239625	NP_068839
		mRNA /cds=(171,971) /gb=NM_021999	_		<del>-</del>
•	· e	/gi=11527401 /ug=Hs.239625 /len=1843	* )(7		
		3			*
7332	0.024824	a disintegrin-like and metalloprotease	NM 006988	Hs.8230	NP 008919
	<u> </u>	(reprolysin type) with thrombospondin			
	0.	type 1 motif, 1 (ADAMTS1), mRNA			
		/cds=(294,3146) /gb=NM_006988			
		/gi=11038653 /ug=Hs.8230 /len=4459			
7342	0.011929	KIAA0874 protein (KIAA0874), mRNA	NM 015208	Hs.27973	NP 056023
7072	0.011925	/cds=(1,6189) /gb=NM_015208		110.27070	
		/gi=14140237 /ug=Hs.27973 /len=6189		÷	
7349	0.002342	dermatopontin (DPT), mRNA	NM_001937	Hs.80552	NP_001928
1349	0.002542	/cds=(7,612) /gb=NM_001937	14141_001001	1.13.00332	_001320
٠,		/gi=4755134 /ug=Hs.80552 /len=717			
7350	0.012001	UI-H-DH0-aul-p-19-0-UI.s1	BM994422	Hs.289721	<del>                                     </del>
7300	0.013901		DIVI334422	HS.209721	
1		NCI_CGAP_DH0 cDNA clone			
	٠.	IMAGE:5871234 3', mRNA sequence			· . · .
		/clone=IMAGE:5871234 /clone_end=3'	7	30	
		/gb=BM994422 /gi=19719323		·	
7054	0.047054	/ug=Hs.289721 /len=2081	1114 000047	112 4000	ND 000000
7351	0.047854	replication protein A3, 14kDa (RPA3),	NM_002947	Hs.1608	NP_002938
		mRNA /cds=(1182,1547)			
•		/gb=NM_002947 /gi=19923751			
		/ug=Hs.1608 /len=1622	100105	11 105010	ND 040404
7359	7.78E-04	hypothetical protein BC009925	NM_138425	Hs.405913	NP_612434
• •	\ \ .	(LOC113246), mRNA /cds=(92,472)			1
	:	/gb=NM_138425 /gi=19923950			
	212 12 12	/ug=Hs.405913 /len=583		1	ND 00000
7361	0.016146	SWI/SNF related, matrix associated,	NM_003072	Hs.78202	NP_003063
		actin dependent regulator of chromatin,			
		subfamily a, member 4 (SMARCA4),		0	
	10	mRNA /cds=(277,5220) /gb=NM_003072	·		
		/gi=21071055 /ug=Hs.78202 /len=5681			
10				1	<del> </del>
7387	0.032261	ribosomal protein L4 (RPL4), mRNA	NM_000968	Hs.286	NP_000959
		/cds=(57,1340)/gb=NM_000968			
		/gi=16579884 /ug=Hs.286 /len=1449			
7390	0.028474	peptidylprolyl isomerase A (cyclophilin A)	NM_021130	Hs.401787	NP_066953
,		(PPIA), mRNA /cds=(45,542)			
		/gb=NM_021130 /gi=10863926	<u> </u>		,
	i '	/ug=Hs.401787 /len=753	<b>,</b>	$\Gamma$	1

Spot	p-value	Description	Gene	Unigene	Protein
			Acc ssion No.	Accession No.	Accession No.
7431	0.01738	ionized calcium binding adapter molecule	NM_031426	Hs.4944	NP_113614
		2 (IBA2), mRNA /cds=(89,541)			
٠		/gb=NM_031426 /gi=13899240			
		/ug=Hs.4944 /len=3381			
7439	0.024824	pleiotrophin (heparin binding growth	NM 002825	Hs.44	NP 002816
		factor 8, neurite growth-promoting factor			
		1) (PTN), mRNA /cds=(396,902)			
		/gb=NM_002825 /gi=27552761			-
	8	/ug=Hs.44 /len=1029		**	,
7452	0.042212	hypothetical protein PRO1051	NM 018572	Hs.326548	NP 061042
	0.012212	(PRO1051), mRNA /cds=(755,1003)	1.111_0 10012	110.020010	" _ 00 10 12
		/gb=NM_018572 /gi=8924004		*	
		/ug=Hs.326548 /len=1393	*	*	
7463	0.030461	early growth response 1 (EGR1), mRNA	NM 001964	Hs.326035	NP 001955
1,400	0.000401	/cds=(271,1902) /gb=NM_001964	1401_001304	13.520055	145 -00 1900
		/gi=4503492 /ug=Hs.326035 /len=3132		we.	
		/gi=4505492 /ug=ns.526055 /ieii=5152			
7464	0.047854	collagen, type XVIII, alpha 1 (COL18A1),	NM 030582	Hs.78409	NP 569712
. 101	0.017001	transcript variant 1, mRNA	11111_000002	1.10.10.100	
		/cds=(22,4572) /gb=NM_030582			
		/gi=18765744 /ug=Hs.78409 /len=5910			
7492	0.004433	ni59g06.s1 NCI_CGAP_Ov2 cDNA clone	AA526325	Hs.404464	
7 102	0.00.1100	IMAGE:981178 similar to contains Alu	701020020	1,0.101,101	
		repetitive element;, mRNA sequence		j ·	
		/clone=IMAGE:981178 /gb=AA526325		,-	
,		/gi=2268394 /ug=Hs.404464 /len=503			
-	*	 			
7508	0.030461	mRNA for RCC1-like protein (TD-60	AJ421269	Hs.284146	NP_061185
		gene) /cds=(236,1804) /gb=AJ421269			
	~	/gi=27526612 /ug=Hs 284146 /len=4114			
7515	0.021575	FLJ11708 fis, clone HEMBA1005123	AK021770	-24	NP 803882
7547		lipase, hormone-sensitive (LIPE), mRNA		Hs.95351	NP_005348
		/cds=(278,3508) /gb=NM 005357			
i	1	/gi=21328445 /ug=Hs.95351 /len=3806			1
		1.525.10749 110.0005171011 0000			
7548	0.001756	methionine adenosyltransferase II, beta	NM_013283	Hs.54642	NP_037415
		(MAT2B), mRNA /cds≃(73,1077)		, , ,	1 -
		/gb=NM_013283 /gi=20127525			1
		/ug=Hs.54642 /len=2054			
7551	0.047854	hypothetical protein FLJ11021 similar to	NM 023012	Hs.81648	NP_075388
		splicing factor, arginine/serine-rich 4			
		(FLJ11021), mRNA /cds=(767,1375)	*		1
		/gb=NM_023012 /gi=20127619			
		/ug=Hs.81648 /len=1878		1	

	p-value	nding To Differentially Expressed Genes Description	Gene	Unigene Accession No.	Protein Accession No.
7564	0.012883	paired basic amino acid cleaving system 4 (PACE4), transcript variant 1, mRNA /cds=(315,3224) /gb=NM_002570 /gi=20336178 /ug=Hs.170414 /len=4553	NM_002570	Hs 170414	NP_612198
7584		hypothetical protein FLJ10307 (FLJ10307), mRNA /cds=(78,1265) /gb=NM_018053 /gi=24431976 /ug=Hs 55024 /len=2179	NM_018053	Hs.55024	NP_060523
7587	0.037129	XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(25,1149) /gb=NM_007266 /gi=14149628 /ug=Hs.18259 /len=1829	NM_007266	Hs.18259	NP_009197
7604	0.024824	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 1, mRNA /cds=(197,4792) /gb=NM_004996	NM_004996	Hs.89433	NP_063957
7608	0.004059	/gi=9955961 /ug=Hs.89433 /len=5927 WW45 protein (WW45), mRNA /cds=(339,1490) /gb=NM_021818 /gi=18860913 /ug=Hs.288906 /len=3031	NM_021818	Hs.288906	NP_068590
7619	0.014988	mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA /cds=(443,2404) /gb=NM_005907 /gi=24497518 /ug=Hs.25253 /len=4139	NM_005907	Hs.25253	NP_005898
7663		cDNA FLJ10131 fis, clone HEMBA1003041. /gb=AK000993 /gi=7021996 /ug=Hs.274128 /len=2065	AK000993	Hs.274128	
7665	0.024824	putatative 28 kDa protein (LOC56902), mRNA /cds=(21,779) /gb=NM_020143 /gi=10047139 /ug=Hs.193384 /len=1194	NM_020143	Hs. 193384	NP_064528
7666	0.042212	FLJ14102 fis, clone MAMMA1000940 /cds=UNKNOWN /gb=AK024164 /gi=10436477 /ug=Hs.301811 /len=1878	AK024164	Hs.301811	, *
7668	0.005275	mitogen-activated protein kinase kinase 1 interacting protein 1 (MAP2K1IP1), mRNA /cds=(250,624) /gb=NM_021970 /gi=21614526 /ug=Hs.6361 /len=1416	NM_021970	Hs.6361	NP_068805
7691	0.039603	hypothetical protein FLJ10498 (FLJ10498), mRNA /cds=(37,1920) /gb=NM_018115 /gi=8922466 /ug=Hs.109045 /len=2755	NM_018115	Hs.109045	NP_060585
7697	0.04496	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463

		nding To Differentially Expressed G nes	s in Figure 15 - F	lyp rlipidemi	a
Spot	p-value	D scription	Gene	Unigene	Protein
		* • · · · · · · · · · · · · · · · · · ·	Accession No.	Accession	Accession
	-			No.	No.
7698	0.030461	CGG triplet repeat binding protein 1	NM 003663	Hs.86041	NP 003654
		(CGGBP1), mRNA /cds=(357,863)		*	· · · ·
		/gb=NM_003663 /gi=21361098			
1.	-	/ug=Hs.86041 /len=4279		. "	
7716	0.047854	IFNAR gene (HSIFNAR) for interferon	X60459		
	0.0 () 00 (	alpha/beta receptor	7,00,100		
7722	0.012883	Similar to hypothetical protein MGC4707,	BC013988	Hs.348323	
1122	0.012003	clone MGC:19860 IMAGE:3349493,	DC013300	113.040020	
1			0		
	-00	mRNA, complete cds /cds=(38,1051)		:	
		/gb=BC013988 /gi=15559264		~ 0	*
•		/ug=Hs.348323 /len=1684	-2.		
			Elizabeth de la company	1	
7726	0.030461	UI-H-DF1-auj-l-12-0-UI.s1	BM991698	Hs.355489	
		NCI_CGAP_DF1 cDNA clone		*	
		IMAGE:5870363 3', mRNA sequence	, ,		
	l ·	/clone=IMAGE:5870363 /clone_end=3'			
		/gb=BM991698 /gi=19711087		-,	
	14	/ug=Hs.355489 /len=1105			
7728	0.013901	Down syndrome critical region gene 5	NM 016430	Hs.408790	NP 710149
	-,-,-	(DSCR5), transcript variant 3, mRNA			
		/cds=(342,668) /gb=NM_016430	,		
		/gi=24497594 /ug=Hs.408790 /len=875			
7729	0.011020	protein phosphatase 1, regulatory	NM 006241	Hs.267819	NP_006232
1129	0.011929		NIVI_00024	HS.20/019	1117_000232
* **		(inhibitor) subunit 2 (PPP1R2), mRNA			6 .
	٠.	/cds=(235,852) /gb=NM_006241			٠.
	,	/gi=19923357 /ug=Hs.267819 /len=3355			
				1	
7746	0.0215/5	PHD finger protein 3 (PHF3), mRNA	NM_015153	Hs.78893	NP_055968
		/cds=(28,6147) /gb=NM_015153			
		/gi=7662017 /ug=Hs.78893 /len=6948			
7775		fibronectin gene ED-A region	X07718		
7789	0.007388	EST (DKFZp564A043 clone	AL050007		
	_•	DKFZp564A043)			
7825	0.030461	retinol dehydrogenase 14 (all-trans and 9-	NM_020905	Hs.288880	NP_065956
		cis) (RDH14), mRNA /cds=(64,1074)		ii e	
		/gb=NM_020905 /gi=10190745			
		/ug=Hs.288880 /len=1538		1	
7828	0.047854	BX101939 Soares infant brain 1NIB	BX101939	Hs.269499	<u> </u>
1020	0.047004	cDNA clone IMAGp998C11163, mRNA	DX 10 1000	113.200400	
					.=
		sequence			
	. ′	/clone=IMAGp998C11163_;_IMAGE:363	÷		
	***	64 /gb=BX101939 /gi=27831516			
		/ug=Hs.269499 /len=493		·	
7835	0.032563	EST (wr43e11.x1 NCI_CGAP_Pr28	AI972789		
<u> </u>		IMAGE:2490476 3')			
7843	0.013901	EST(qu23h09.x1 NCI_CGAP_Br12 clone	Al284640		
		IMAGE:1965665 contains Alu repeat)	7		
	ı		8	1	1

		nding To Differentially Expressed G n			
Spot	p-value	Description	Gene	Unigene	Protein
		y. * *	Accession No.	Accession	Accession
				No.	No.
7851	0.039603	capillary morphogenesis protein 2	NM_058172	Hs.5897	NP_477520
		(CMG2), mRNA /cds=(46,783)			
		/gb=NM_058172 /gi=17158002			
		/ug=Hs.5897 /len=2026	•		
7854	0.014988	EST fetal brain (TFujiwara) Human	D81944		NP_079215
		sapiens cDNA clone GEN-425D02 5'			
7855	0.04496	EST(tz31e10.x1 NCI_CGAP_Ut2 cDNA	Al630897		NP_008993
*		clone IMAGE:2290218 3')			
7857	0.001935	EST(PM4-SN0016-030400-002-c05	AW864432		119 c
		SN0016)	× .	,	111
7869	0.01738	hypothetical protein FLJ20534	NM_017867	Hs.44344	NP_060337
	8.5	(FLJ20534), mRNA /cds=(21,1061)	7		
·	, ,	/gb=NM_017867 /gi=8923502		2	
		/ug=Hs.44344 /len=1188	• •		
7886	0.002824	EST(zv79f07.s1 Soares total fetus	AA423871		
7000	0.00202	Nb2HF8 9w clone 759877 3')	7 0 (4200) 1		
7895	0.012883	EST(zw54g08.r1	AA463590		
1000	0.012003	Soares_total_fetus_Nb2HF8_9w clone	77403330	79	
		IMAGE:773918 5' contains Alu and			You are
-		MER22 repeat)			
7902	0.042212	cDNA FLJ40622 fis, clone	AK097941	11- 274250	
7902	0.042212		AKU9/941	Hs.374352	
		THYMU2013779. /gb=AK097941			· -
		/gi=21757847 /ug=Hs.374352 /len=1754			
7000	0.04400	DNIA for IZIA A 4005 masteria	AD075045	11-74700	
7903	0.04496	mRNA for KIAA1965 protein.	AB075845	Hs.71730	
		/cds=(1,1699) /gb=AB075845		* 1	
7007	0.04.4000	/gi=18916817 /ug=Hs.71730 /len=4299			
7927	0.014988	UI-H-EZ1-bca-n-05-0-UI.s1	BQ774356	Hs.43227	
		NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-		2	
		bca-n-05-0-UI 3', mRNA sequence			
·	·	/clone=UI-H-EZ1-bca-n-05-0-UI			
		/clone_end=3' /gb=BQ774356			
		/gi=21982825 /ug=Hs.43227 /len=1083			
7938	0.023151	UI-H-EU1-bai-b-07-0-UI.s1	BQ448117	Hs.8705	
	*	NCI_CGAP_Ct1 cDNA clone UI-H-EU1-	,		
		bai-b-07-0-UI 3', mRNA sequence			V
		/clone=UI-H-EU1-bai-b-07-0-UI			·
-		/clone_end=3' /gb=BQ448117 .			
		/gi=21251229 /ug=Hs.8705 /len=1171		(	
7939	0.023151	EST (IL-BT003-221198-003 BT003)	AI902209	/	
7947		EST (AV690707 GKC H.sapiens cDNA	AV690707		NP_004577
7951		EST (am59f03.x1 Johnston frontal	Al124626		-
7960		RAB5B, member RAS oncogene family	AF267863	Hs.77690	NP_002859
		(=DC43 mRNA, complete cds			
	I	(AF267863.1))			
	• (		<del>                                     </del>	<del> </del>	1
7962	0.037129	hypothetical protein MGC2941	NM 024297	IHs.288217	INP 077273
7962	0.037129	hypothetical protein MGC2941 (MGC2941) mRNA /cds=(172,969)	NM_024297	Hs.288217	NP_077273
7962	0.037129	hypothetical protein MGC2941 (MGC2941), mRNA /cds=(172,969) /gb=NM_024297 /gi=13236519	NM_024297	Hs.288217	NP_077273

Genes	Correspon	nding To Differentially Expressed Gener	s in Figure 15 - H	lyperlipidemi	a _
	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
7966	0.047854	cDNA: FLJ23165 fis, clone LNG09846.	AK026818	Hs.279898	
*		/gb=AK026818 /gi=10439763			
		/ug=Hs.279898 /len=2117		*	
7968	0.005746	low density lipoprotein receptor-related	NM_002335	Hs.6347	NP_002326
		protein 5 (LRP5), mRNA /cds=(49,4896)	_		_
	1	/gb=NM_002335 /gi=4505018			
	*	/ug=Hs.6347 /len=5100	·	*	
7975	0.009424	cDNA: FLJ22050 fis, clone HEP09454.	AK025703	Hs.173705	
		/gb=AK025703 /gi=10438305		111	
		/ug=Hs.173705 /len=1990			. 7
7984	0.024824	hypothetical protein FLJ11126	NM 018332	Hs.226396	NP 060802
	,	(FLJ11126), mRNA /cds=(81,1517)			
90		/gb=NM_018332 /gi=20070297			
	٠.	/ug=Hs.226396 /len=2927		· · · · · · · · · · · · · · · · · · ·	*
8020	0.011037	phosphoribosylglycinamide	NM 000819	Hs.82285	NP_780294
5525	3.9.100/	formyltransferase,		.,5.52250	
		phosphoribosylglycinamide synthetase,			
,,,,,		phosphoribosylaminoimidazole	*		
,	=	synthetase (GART), mRNA			
	-	/cds=(79,3111) /gb=NM_000819		8	
		/gi=24475881 /ug=Hs.82285 /len=3291	101		*
8036	0.032563	mitogen-activated protein kinase kinase	NM 003188	Hs.7510	NP 663306
0000	0.002000	kinase 7 (MAP3K7), transcript variant A,	14141_005100	113.7510	141 _003300
		mRNA /cds=(306,2045) /gb=NM_003188			
		/gi=21735560 /ug=Hs.7510 /len=2912			÷
		/gi=21/33300/ug=113.7310/left=2912			
8045	0.04496	hydrolase-like 1 (AHCYL1), mRNA	NM 006621	Hs.4113	NP_006612
00-10	0.94400	/cds=(369,1961) /gb=NM_006621	14141_000021	113.4110	141 _000012
		/gi=21361646 /ug=Hs.4113 /len=2677		* * , 0.,	
8071	0.01738	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM 001356	Hs.380774	NP 076829
007	0.01730	polypeptide 3 (DDX3), transcript variant	14141_00 1000	113.500774	JNI _070029
		2, mRNA /cds=(857,2845)	*	-	
				. 9	
		/gb=NM_001356 /gi=13514812 /ug=Hs.380774 /len=5322	•	· ·	×100m
8095	0.020091	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM 004728	Hs.169531	NP 004719
0033	0.020031	polypeptide 21 (DDX21), mRNA	14141_004728	118.109931	NF_004719
1		/cds=(266,2413) /gb=NM_004728			· V
		/gi=13787208 /ug=Hs.169531 /len=3319	•	-	
/		1376720674g=118.16933171e11=3319	*	•	-2-
8124	0.042242	hypothetical protein MGC9084	NM 033418	Hs.33922	NP_219486
0124	0.042212	(MGC9084), mRNA /cds=(279,1397)	14141_000410	113.33822	NF_2 19400
	9	/gb=NM_033418 /gi=15553096			
	ii .	, – •	• (()	- · ·	
8168	0.014000	/ug=Hs.33922 /len=1445	NIM 024570	Un 10207	ND 0700EE
0 100	0.014988	hypothetical protein FLJ23221	NM_024579	Hs.18397	NP_078855
	<b>l</b> .	(FLJ23221), mRNA /cds=(24,419)		1	
		/gb=NM_024579 /gi=13375757			*
<u> </u>	<u>L</u>	/ug=Hs.18397 /len=519	<u> </u>	I:	L

Accession No.   Accession No.   Accession No.   Rossion No.   Accession No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.			nding To Differentially Expressed Genes	s in Figure 15 - I	- lyperlipidemi	a
8191   0.047854   downstream neighbor of SON   NM_017613   Hs.17834   NP_66573i   CDONSON), transcript variant 1, mRNA   /cds=(68,1768) /gb=NM_017613   /gi=22035582 /ug=Hs.17834 /len=2189   /gb=NM_017810 /gi=22035582 /ug=Hs.17834 /len=2189   NM_017910   Hs.32356   NP_06038i /gb=NM_017910 /gi=134353382   /ug=Hs.32356 /len=1846   NP_06038i /gb=NM_017910 /gi=134353382   /ug=Hs.32356 /len=1846   NP_06038i /gb=NM_017910 /gi=134353382   /ug=Hs.32356 /len=1846   NP_06038i /gb=NM_017910 /gi=134353382   /ug=Hs.32356 /len=1846   NP_06038i /gb=Sit_yh89c04_r1 clone 136902_5)   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R39720   R3972	Spot	p-value	Description	Gene	Unigene	Protein
8191   0.047854   downstream neighbor of SON (DNSON), transcript variant 1, mRNA /cds-(68,1768) /gb=NM_017613   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834   ms. 17834				Accession No.	Accession	Accession
(DONSON), transcript variant 1, mRNA   /cds=(68, 1768) /gb=NM /017613   /gi=2035582 /ug=Hs 17834 /len=2189   NM_017910   Hs.32356   NP_06038( FL)20628, mRNA /cds=(23,1456)   /gb=NM_017910 /gi=13435382   /ug=Hs.32356 /len=1846   NP_06038( FL)20628   MRNA /cds=(23,1456)   /gb=NM_017910 /gi=13435382   /ug=Hs.32356 /len=1846   NP_06038( FL)20628   MRNA /cds=(23,1456)   NP_06038( FL)20628   MRNA /cds=(23,1456)   NP_06038( FL)20628   NR_0017910 /ms-1846   NP_06038( FL)20628   NR_0017910 /ms-1846   NP_06038( FL)20628   NR_001807 /ms-1846   NP_06038( FL)20628   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-1846   NR_001807 /ms-			1		No.	No.
/cds=(68,1768) /gb=NM, 017613   /gi=22035582 /ug=Hs.17834 /len=2189	8191	0.047854	downstream neighbor of SON	NM_017613	Hs.17834	NP_665738
Jgi=22035582 /ug=Hs. 17834 /len=2189		•	(DONSON), transcript variant 1, mRNA			_
8227   0.034784   hypothetical protein FLJ20628   NM_017910   Hs.32356   NP_06038(   FLJ20628)   mRNA /cds=(23,1456)   /qb=NM_017910 / (gb=13435382 / /ug=Hs.32356 /len=1846   NC_001807   /qb=NM_017910 / (gb=13435382 / /ug=Hs.32356 /len=1846   NC_001807   NC_001807   NC_001807   NC_001807   NC_003046   EST(ty24e09 x1 NCI_CGAP_Ut3 clone   Al758800   NAGE:2280040 3' contains Alu repeat)   NAGE:2280040 3' contains Alu repeat)   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_001807   NC_00180			/cds=(68,1768) /gb=NM_017613			
(FLJ20628), mRNA /cds=(23,1456) (gb=NM_017910 /gi=13435382 //ug=Hs.32356 /len=1846 8240			/gi=22035582 /ug=Hs.17834 /len=2189		<u>'.</u>	2
(FLJ20628), mRNA /ods=(23,1456)   /gb=NM_017910 /gi=13435382   /ug=Hs. 32356 /len=1846   8280   0.026596   EST(yh89c04 r1 clone 136902 5')   R39720   8308   0.030461   EST(yy24e09.x1 NCI_CGAP_Ut3 clone   Al758800   MAGE:2280040 3' contains Alu repeat)   Al758800   MAGE:2280040 3' contains Alu repeat)   Al758800   MAGE:2280040 3' contains Alu repeat)   Al758800   MAGE:2280040 3' contains Alu repeat)   Al758800   MAGE:2280040 3' contains Alu repeat)   Al758800   MAGE:2280040 3' contains Alu repeat)   Al758800   MAGE:2280040 3' contains Alu repeat)   Al758800   MAGE:228041, mRNA   BC043222   Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405455 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405253 /lg=Hs.405	8227	0.034784	hypothetical protein FLJ20628	NM_017910	Hs.32356	NP 060380
Aug=Hs 32356 /len=1846			(FLJ20628), mRNA /cds=(23,1456)		*	
8240         0.012481         mitochondrion, complete genome         NC 001807           8280         0.026596         EST(yh89c04.r1 clone 136902.5')         R39720           8308         0.030461         EST(yb24609.x1 NCL_CGAP_U3 clone IMAGE:2280040.3' contains Alu repeat)         Al758800           8311         0.001304         clone IMAGE:5295441, mRNA         BC043222         Hs.405253           // gb=BC043222 / gj=28175025         // yg=Hs.405253 / len=2712         BX118128         BX118128         Hs.15328           8326         0.042212         BX118128 Soares fetal liver spleen         NFLS cDNA clone IMAGP998L20388, mRNA sequence         // clone=IMAGP998L20388IMAGE:2017         63 //gb=BX118128 //gj=27840987         // yg=Hs.15328 // len=783           8359         0.013901         UI-H-BW1-amn-b-05-0-UI.s1         BF513064         Hs.446233           NCI_CGAP_Sub7 cDNA clone         IMAGE:3070401 // gi=11598243         // yg=Hs.446233 / len=777         BF513064         Hs.446233           8378         0.014988 601556349T1 NIH_MGC_58 cDNA clone         IMAGE:3826069 3', mRNA sequence         // clone=IMAGE:3826069 // clone_end=3'         // yg=BE739647 // yj=10153639         // yg=BE739647 // yj=10153639         // yg=BE739647 // yj=10153639         // yg=BE739647 // yj=10153639         // yg=BE739647 // yj=10153639         // yg=BE739647 // yj=10153639         // yg=BE739647 // yj=10153639         //	der.		/gb=NM_017910 /gi=13435382			
8280   0.026596   EST (yh8c04.r1 clone   136902.5')   R39720     8308   0.030461   EST (ty24e09.x1 NCI_CGAP_Ut3 clone   Al758800   MAGE:2280040.3' contains Alu repeat)     8311   0.001304   clone IMAGE:5295441, mRNA   (yb=BC043222 /gj=28175025   /ug=Hs.405253 /len=2712     8326   0.042212   BX118128   Soares fetal liver spleen   1NFLS cDNA clone IMAGp998L20388, mRNA sequence   /clone=IMAGp998L20388_iMAGE:2017   63 /gb=BX118128 /gj=27840987   /ug=Hs.15328 /len=783     8359   0.013901   Ul-H-BW1-amn-b-05-0-Ul.s1   NCI_CGAP_Sub7 cDNA clone   IMAGE:3070401 3', mRNA sequence   /clone=IMAGE:3070401 /clone_end=3' /gb=BF513064 /gj=11598243   /ug=Hs.486233 /len=777     8378   0.014988   601556349T1 NIH_MGC_58 cDNA clone   IMAGE:3826069 3', mRNA sequence   /clone=IMAGE:3826069 /clone_end=3' /gb=BF39647 /gj=10153639   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /		*	/ug=Hs.32356 /len=1846			
8280   0.026596   EST (yh8c04.r1 clone   136902.5')   R39720     8308   0.030461   EST (ty24e09.x1 NCI_CGAP_Ut3 clone   Al758800   MAGE:2280040.3' contains Alu repeat)     8311   0.001304   clone IMAGE:5295441, mRNA   (yb=BC043222 /gj=28175025   /ug=Hs.405253 /len=2712     8326   0.042212   BX118128   Soares fetal liver spleen   1NFLS cDNA clone IMAGp998L20388, mRNA sequence   /clone=IMAGp998L20388_iMAGE:2017   63 /gb=BX118128 /gj=27840987   /ug=Hs.15328 /len=783     8359   0.013901   Ul-H-BW1-amn-b-05-0-Ul.s1   NCI_CGAP_Sub7 cDNA clone   IMAGE:3070401 3', mRNA sequence   /clone=IMAGE:3070401 /clone_end=3' /gb=BF513064 /gj=11598243   /ug=Hs.486233 /len=777     8378   0.014988   601556349T1 NIH_MGC_58 cDNA clone   IMAGE:3826069 3', mRNA sequence   /clone=IMAGE:3826069 /clone_end=3' /gb=BF39647 /gj=10153639   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /	8240	0.012481	mitochondrion, complete genome	NC 001807		1.
IMAGE:2280040 3' contains Alu repeat)	8280				· ·	
IMAGE:2280040 3' contains Alu repeat)	8308			AI758800	-	1
8311   0.001304   clone IMAGE:5295441, mRNA						
/gb=BC043222 / gj=28175025   /ug=Hs_405253 / len=2712     8326   0.042212   BX118128 Soares fetal liver spleen   1NFLS cDNA clone IMACp998L20388, mRNA sequence   /clone=IMACp998L20388, imAGE:2017   63 /gb=BX118128 /gj=27840987   /ug=Hs_15328 /len=783     8359   0.013901   UI-H-BW1-amn-b-05-0-UI.s1   NCI_CGAP_Sub7 clone   IMAGE:3070401 3', mRNA sequence   /clone=IMAGE:3070401 3', mRNA sequence   /clone=IMAGE:3070401 /clone_end=3'   /gb=BF513064 /gj=11598243   /ug=Hs_446233 /len=777     8378   0.014986   60155634971 NIH_MGC_58 cDNA clone   IMAGE:3826069 3', mRNA sequence   /clone=IMAGE:3826069 /clone_end=3'   /gb=BE739647 (jg=10153639   /ug=Hs_88156 /len=692     8382   0.04496   hypothetical protein clone 23745 mRNA, complete cds   8402   0.026596   EST (wh75b01.x1 NCI_CGAP_CLL1   cDNA clone IMAGE:2386537 3' similar to   gb:X69392 60S RIBOSOMAL PROTEIN   L26 (HUMAN);contains L1.b3 L1   repetitive element;   mRNA, cDNA DKFZp586B1922 /from   clone DKFZp586B1922) /gb=AL049450   /gi=4500236 /ug=Hs_184779 /len=1433   8425   0.008019   EST yc14f05.s1 cDNA clone lenent.   8482   0.047805   EST (7q71c12.x1 NCI_CGAP_LU24   BF433956   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   BF433956   SFT (7q71c12.x1 NCI_CGAP_LU24   SFT (7q71c12.x1 NCI_CGAP_LU24   SFT (7q71c12.x1 NCI_CGAP_LU24   SFT (7q71c12.x1 NCI_CGAP_LU24   SFT (7q71c12.x1 NCI_CGAP_LU24   SFT (7q71c12.x1 NCI_CGAP_LU24   SFT (7q71c12.x1 NCI_CGAP_LU24   SFT (7q71c12.x1 NCI_CGAP_LU24   SFT (7q71c12.x1 NCI_CGAP_LU24   SF	8311	0.001304		BC043222	Hs.405253	4
Nug=Hs.405253 /len=2712	:				* 1 4 4	,
8326   0.042212   BX118128 Soares fetal liver spleen   1NFLS; cDNA clone   IMAGp998L20388, mRNA sequence   /clone=IMAGp998L20388_   IMAGE; 2017   63 /gb=BX118128 /gi=27840987   /ug=Hs.15328./len=783   8359   0.013901   UI-H-BW1-amn-b-05-0-UI.s1   BF513064   Hs.446233   NCI_CGAP_Sub7 cDNA clone   IMAGE; 3070401 3', mRNA sequence   /clone=IMAGE; 3070401 /clone_end=3' /gb=BF513064 /gi=11598243   /ug=Hs.446233 /len=777   8378   0.014988   601556349T1 NIH_MGC_58 cDNA clone   BE739647   Hs.88156   IMAGE; 3826069 3', mRNA sequence   /clone=IMAGE; 3826069 /clone_end=3' /gb=BE739647 /gi=10153639   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.88156 /len=692   /ug=Hs.8	, /		_			, and a
1NFLS cDNA clone IMAGp998L20388, mRNA sequence /clone=IMAGp998L20388IMAGE;2017 63 /gb=BX118128 /gi=27840987 /ug=Hs.15328 /len=783  8359	8326	0.042212		BX118128	Hs.15328	*
mRNA sequence /clone=IMAGp998L20388IMAGE:2017 63 /gb=BX118128 /gi=27840987 /ug=Hs.15328 /len=783  8359						
/clone=IMAGp998L20388,IMAGE;2017 63 /gb=BX118128 /gi=27840987 /ug=Hs.15328 /len=783  8359				* 1	;	a ,i a
63 /gb=BX118128 /gi=27840987 /ug=Hs.15328 /len=783	*					
Jug=Hs.15328 /len=783					- 7	
8359   0.013901   UI-H-BW1-amn-b-05-0-UI.S1   NCI_CGAP_Sub7 cDNA clone   IMAGE:3070401 3', mRNA sequence   /clone=IMAGE:3070401 /clone_end=3'   /gb=BF513064 /gi=11598243   /ug=Hs.446233 /len=777   8378   0.014988   601556349T1 NIH_MGC_58.cDNA clone   IMAGE:3826069 3', mRNA sequence   /clone=IMAGE:3826069 /clone_end=3'   /gb=BE739647 /gi=10153639   /ug=Hs.88156 /len=692   8382   0.04496   hypothetical protein clone 23745 mRNA, complete cds   end=3'   complete cds   end=3'   complete cds   end=3'   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4   end=4				*		7
NCI_CGAP_Sub7 cDNA clone   IMAGE:3070401 3', mRNA sequence   /clone=IMAGE:3070401 /clone_end=3'   /gb=BF513064 /gi=11598243   /ug=Hs.446233 /len=777     8378	8359	0.013901		BF513064	Hs.446233	
IMAGE:3070401 3', mRNA sequence						
/clone=IMAGE:3070401 /clone_end=3' /gb=BF513064 /gi=11598243 /ug=Hs.446233 /len=777  8378						
/gb=BF513064 /gi=11598243 /ug=Hs.446233 /len=777  8378  0.014988  601556349T1 NIH_MGC_58 cDNA clone IMAGE:3826069 3', mRNA sequence /clone=IMAGE:3826069 /clone_end=3' /gb=BE739647 /gi=10153639 /ug=Hs.88156 /len=692  8382  0.04496  hypothetical protein clone 23745 mRNA, complete cds  8402  0.026596  EST (wh75b01.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2386537 3' similar to gb:X69392 60S RIBOSOMAL PROTEIN L26 (HUMAN);contains L1.b3 L1 repetitive element;  8419  0.023151  mRNA, cDNA DKFZp586B1922 (from clone DKFZp586B1922) /gb=AL049450 /gi=4500236 /ug=Hs.184779 /len=1433  8425  0.008019  EST yc14f05.s1 cDNA clone 80673 3' contains L1 repetitive element.  8482  0.047805  EST (7q71c12.x1 NCI_CGAP_Lu24 BF433956					3	
Nug=Hs.446233 /len=777			l : : : : : : : : : : : : : : : : : : :			
8378	,		1			
IMAGE:3826069 3', mRNA sequence   /clone=IMAGE:3826069 /clone_end=3'   /gb=BE739647 /gi=10153639   /ug=Hs.88156 /len=692	8378	0.014988		BE739647	Hs.88156	
/clone=IMAGE:3826069 /clone_end=3' /gb=BE739647 /gi=10153639 /ug=Hs.88156 /len=692  8382	-	,				-7-
/gb=BE739647 /gi=10153639 /ug=Hs.88156 /len=692  8382				·		*
Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=Hs.88156 /len=692   Nug=						
8382		7.	"			
Complete cds   S402   0.026596   EST (wh75b01.x1 NCI_CGAP_CLL1   CDNA clone IMAGE:2386537 3' similar to gb:X69392 60S RIBOSOMAL PROTEIN   L26 (HUMAN); contains L1.b3 L1   repetitive element;   S419   0.023151   mRNA, cDNA DKFZp586B1922 (from clone DKFZp586B1922) /gb=AL049450   /gi=4500236 /ug=Hs.184779 /len=1433   S425   0.008019   EST yc14f05.s1 cDNA clone 80673 3'   contains L1 repetitive element.   S482   0.047805   EST (7q71c12.x1 NCI_CGAP_Lu24   BF433956   S7825   CONTAINS L1 REPETITION   BF433956   S7825   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   CONTAINS L1 REPETITION   C	8382	0.04496		U79260		
8402 0.026596 EST (wh75b01.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2386537 3' similar to gb:X69392 60S RIBOSOMAL PROTEIN L26 (HUMAN); contains L1.b3 L1 repetitive element;  8419 0.023151 mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922) /gb=AL049450 /gi=4500236 /ug=Hs.184779 /len=1433  8425 0.008019 EST yc14f05.s1 cDNA clone 80673 3' contains L1 repetitive element.  8482 0.047805 EST (7q71c12.x1 NCI_CGAP_Lu24 BF433956	1-2					
CDNA clone IMAGE:2386537 3' similar to gb:X69392 60S RIBOSOMAL PROTEIN L26 (HUMAN);contains L1.b3 L1 repetitive element;  8419  0.023151 mRNA, cDNA DKFZp586B1922 (from clone DKFZp586B1922) /gb=AL049450 /gi=4500236 /ug=Hs.184779 /len=1433  8425  0.008019 EST yc14f05.s1 cDNA clone 80673 3' contains L1 repetitive element.  8482  0.047805 EST (7q71c12.x1 NCI_CGAP_Lu24 BF433956	8402	0.026596	EST (wh75b01.x1 NCI_CGAP_CLL1	AI809166		
L26 (HUMAN); contains L1.b3 L1 repetitive element;  8419  0.023151 mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922) /gb=AL049450 /gi=4500236 /ug=Hs.184779 /len=1433  8425  0.008019 EST yc14f05.s1 cDNA clone 80673 3' contains L1 repetitive element.  8482  0.047805 EST (7q71c12.x1 NCI_CGAP_Lu24 BF433956					9	* x0 x
L26 (HUMAN); contains L1.b3 L1 repetitive element;  8419  0.023151 mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922) /gb=AL049450 /gi=4500236 /ug=Hs.184779 /len=1433  8425  0.008019 EST yc14f05.s1 cDNA clone 80673 3' contains L1 repetitive element.  8482  0.047805 EST (7q71c12.x1 NCI_CGAP_Lu24 BF433956	7.4	· ·	gb:X69392 60S RIBOSOMAL PROTEIN		. "	
repetitive element;  8419			1 7	· .		*
8419 0.023151 mRNA, cDNA DKFZp586B1922 (from clone DKFZp586B1922) /gb=AL049450 /gi=4500236 /ug=Hs.184779 /len=1433  8425 0.008019 EST yc14f05.s1 cDNA clone 80673 3' contains L1 repetitive element.  8482 0.047805 EST (7q71c12.x1 NCI_CGAP_Lu24 BF433956				•		3
clone DKFZp586B1922) /gb=AL049450  /gi=4500236 /ug=Hs.184779 /len=1433   8425   0.008019   EST yc14f05.s1 cDNA clone 80673 3'   T57825   contains L1 repetitive element.   8482   0.047805   EST (7q71c12.x1 NCI_CGAP_Lu24   BF433956	8419	0.023151		AL049450	Hs.184779	0.000
/gi=4500236 /ug=Hs.184779 /len=1433  8425		,	l '			· [
8425     0.008019     EST yc14f05.s1 cDNA clone 80673 3'     T57825       contains L1 repetitive element.     EST (7q71c12.x1 NCI_CGAP_Lu24     BF433956		,	, ,			***
	8425	0.008019		T57825		
8482 0.047805 EST (7q71c12.x1 NCI_CGAP_Lu24 BF433956		- 2				
	8482	0.047805		BF433956		
			cDNA clone IMAGE:3703702 3')			
8483 0.0068 EST (IL3-CT0219-271099-022-B11) AW376891	8483	0.0068		AW376891		

Spot p-value	nding To Differentially Expr ss d Genes Description	Gene	Unigene	Protein	
			Accession No.	Accession No.	Accession No.
8489	0.042212	CLK4 mRNA sequence /cds=(154,1515)	AF212224	Hs.406557	
	*	/gb=AF212224 /gi=9437514 /ug=Hs.406557 /len=1865			
8495	· · ·	EST(ws08g04.x1 NCI_CGAP_Kid11	Al985577		
8501		cDNA clone IMAGE:2496630 3') hypothetical protein FLJ40137	NM 173478	Hs.412708	NP 775749
0001	0.00210	(FLJ40137), mRNA /cds=(149,1141)	110470	113.412700	_//3/49
• 0		/gb=NM 173478 /gi=27735056	**	*	
	:	/ug=Hs.412708 /len=2241			
8544	0.037129	clone IMAGE:5285272, mRNA	BC041413	Hs.101615	·
	, , , ,	/gb=BC041413 /gi=27370619		110.1010	
		/ug=Hs.101615 /len=2656			
8559	0.034784	clone MGC:5564, mRNA, complete cds	BC003697	Hs.188757	
	,	/cds=(227,304) /gb=BC003697			
		/gi=13277575 /ug=Hs.188757 /len=2145	V : -	*	-
	,	is the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of th			
8563	0.04496	UI-E-EJ1-ajx-j-20-0-UI.r1 UI-E-EJ1 cDNA	BQ188931	Hs.334233	1.
,,,,,	0.0100	clone UI-E-EJ1-ajx-j-20-0-UI 5', mRNA		1.10.00.1200	
		sequence /clone=UI-E-EJ1-ajx-j-20-0-UI		- *	
	Ĭ .	/clone_end=5' /gb=BQ188931			
		/gi=20364482 /ug=Hs.334233 /len=1116	S. 15	* :	
		19, 2000 102 /dg 110.00 1200 110.11 1110			
8587	0.037129	UI-H-BI2-agk-g-09-0-UI.s1	AW291592	Hs.445096	
		NCI_CGAP_Sub4 cDNA clone			
		IMAGE:2724688 3', mRNA sequence			
	- 2	/clone=IMAGE:2724688 /clone_end=3'			
•		/gb=AW291592 /gi=6698228	0)		1
		/ug=Hs 445096 /len=680	3		K.
8593	0.026596	cs26g08.y1 Retinal pigment	CA392625	Hs.389253	
		epithelium/choroid cDNA (Un-normalized,			
		unamplified): cs cDNA clone cs26g08 5',		• • •	
		mRNA sequence /clone=cs26g08			
		/clone_end=5' /gb=CA392625		1	
	-	/gi=24725520 /ug=Hs.389253 /len=648			
	±	.g,g		•	
8598	0.024441	EST(cDNA clone IMAGE:3313792 3')	BF001617		<del></del>
8602	+	clone IMAGE:5217034, mRNA	BC041468	Hs.434746	
	V	/gb=BC041468 /gi=27370762			
	- 46	/ug=Hs.434746 /len=1884	71	i	
8606	0.004059	hypothetical protein DKFZp451G182	NM 153610	Hs.50794	NP 705838
- r. x =		(DKFZp451G182), mRNA /cds=(99,4049)			
		/gb=NM_153610 /gi=23957703	* .		1.
		/ug=Hs.50794 /len=4678	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	*	] .
8631	0.018694	clone IMAGE:4615963, mRNA	BC017826		- *
8634	+	mRNA; cDNA DKFZp564B033 (from	AL049241	Hs.296484	1
	3.500 101	clone DKFZp564B033) /gb=AL049241			
	1	/gi=4499975 /ug=Hs.296484 /len=2228	l·	1	1.00

C==4		nding To Differentially Expressed Gene		<del>,</del>	
Spot	p-value	•   • •	Gene	Unigen	Protein
			Accession No.	Accession	Acc ssion
				No.	No.
8635 0	0.028474	ESTs, cDNA, 3' end /clone_end=3'	BI789108	Hs.304928	
	4.1	/gb=BI789108 /gi=15816833			
		/ug=Hs.304928 /len=529	- 4		0.00
8642	0.020091	EST375384 MAGE resequences, MAGH	A1A(0C2244	116 202704	
0042	0.020091		Avvaossii	Hs.323791	
		cDNA, mRNA sequence /gb=AW963311			
	40.	/gi=8153147 /ug=Hs.323791 /len=608			
	14.5			<u>.</u>	
8644	0.012883	proteasome (prosome, macropain) 26S	NM_002802	Hs.4745	NP 002793
		subunit, ATPase, 1 (PSMC1), mRNA			
		/cds=(49,1371) /gb=NM_002802	4.1.10	. "	
	,	/gi=24430150 /ug=Hs.4745 /len=1586	*	=	
8646	0.042212	cDNA FLJ39413 fis, clone	AK006722	110 404220	
0040	0.042212		AK096732	Hs.194339	
		PLACE6015729. /gb=AK096732			:
		/gi=21756291 /ug=Hs.194339 /len=1957			
					, , , , , , , , , , , , , , , , , , ,
8660	0.018694	nk74h02.s1 NCI_CGAP_Sch1 cDNA	AA551072	Hs.368624	**************************************
	V	clone IMAGE:1019283 3' similar to			2 ·
		contains Alu repetitive element contains			, .
, i			,	*	
. "	•	element LTR5 repetitive element ;,		* .	
	11 10	mRNA sequence		· · · · · · (	
		/clone=IMAGE:1019283 /clone_end=3'			•
		/gb=AA551072 /gi=2321324	· · · · · · · · · · · ·		
		/ug=Hs.368624 /len=477			
8672	0.004838	FLJ22781 fis, clone KAIA1958	AK026434	Hs.213236	,
	*	/cds=UNKNOWN /gb=AK026434			•
	<b>.</b>	/gi=10439298 /ug=Hs.213236 /len=2599	· ·		,
		/gi=10459290 /ug=115.215250 /lef1=2599			
0070	0.000004	(50/00 4.0 ) 1/5/ 7 000 04	41000004		
8679	0.020091	wf59f02.x1 Soares_NFL_T_GBC_S1	AI809904	Hs.369826	
*	* (	cDNA clone IMAGE:2359899 3', mRNA		10	e.
		sequence /clone=IMAGE:2359899			
		/clone end=3' /gb=Al809904			
•		/gi=5396470 /ug=Hs.369826 /len=533	7		
0602	0.004704		AL 702014	Hs.372944	
	1 0 034/84	II IK EZ DOKOG 1317 - FILOKO (SVOGOVO)			
8683	0.034784	DKFZp686G1317_r1 686 (synonym:	AL702914	113.572544	
0003	0.034784	hlcc3) cDNA clone DKFZp686G1317 5',	AL702914	113.572544	
0003	0.034784	hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence	AL702914	113.072544	
0003	0.034784	hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5'	AC702914	/	
0003	0.034784	hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence	AC702914	,	
0003	0.034784	hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5'	AC702914	/	
		hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557	* - 30	,	NP 006292
8688		hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557 mitogen-activated protein kinase kinase	NM_006301	Hs.211601	NP_006292
		hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557 mitogen-activated protein kinase kinase kinase 12 (MAP3K12), mRNA	* - 30	,	NP_006292
		hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557 mitogen-activated protein kinase kinase kinase 12 (MAP3K12), mRNA /cds=(99,2678) /gb=NM_006301	* - 30	,	NP_006292
		hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557 mitogen-activated protein kinase kinase kinase 12 (MAP3K12), mRNA	* - 30	,	NP_006292
8688	0.001756	hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557 mitogen-activated protein kinase kinase kinase 12 (MAP3K12), mRNA /cds=(99,2678) /gb=NM_006301 /gi=21735551 /ug=Hs.211601 /len=3365	NM_006301	Hs.211601	
	0.001756	hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557 mitogen-activated protein kinase kinase kinase 12 (MAP3K12), mRNA /cds=(99,2678) /gb=NM_006301 /gi=21735551 /ug=Hs.211601 /len=3365 protein kinase, cAMP-dependent,	* - 30	,	NP_006292 NP_002725
8688	0.001756	hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557 mitogen-activated protein kinase kinase kinase 12 (MAP3K12), mRNA /cds=(99,2678) /gb=NM_006301 /gi=21735551 /ug=Hs.211601 /len=3365	NM_006301	Hs.211601	
8688	0.001756	hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557 mitogen-activated protein kinase kinase kinase 12 (MAP3K12), mRNA /cds=(99,2678) /gb=NM_006301 /gi=21735551 /ug=Hs.211601 /len=3365 protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific	NM_006301	Hs.211601	
8688	0.001756	hlcc3) cDNA clone DKFZp686G1317 5', mRNA sequence /clone=DKFZp686G1317 /clone_end=5' /gb=AL702914 /gi=19686269 /ug=Hs.372944 /len=557 mitogen-activated protein kinase kinase kinase 12 (MAP3K12), mRNA /cds=(99,2678) /gb=NM_006301 /gi=21735551 /ug=Hs.211601 /len=3365 protein kinase, cAMP-dependent,	NM_006301	Hs.211601	

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
,	4			No.	No.
8699	0.024824	clone IMAGE:3909623, mRNA, partial	BC015894	Hs.33264	more and the control of the control
		cds /cds=(1,178) /gb=BC015894			
	7	/gi=16198445 /ug=Hs.33264 /len=2980		0	
8707	0.006254	tc93c11.x1 NCI_CGAP_CLL1 cDNA	Al475669	Hs.309348	6-1 Page 111 - 11 - 44
		clone IMAGE:2073716 3' similar to			
		contains Alu repetitive element;, mRNA			*
		sequence /clone=IMAGE:2073716			
		/clone_end=3' /gb=Al475669		1	•
		/gi=4328714 /ug=Hs.309348 /len=487	*.		
8708	0.030461	BX111624 NCI CGAP Lu5 cDNA clone	BX111624	Hs.184840	
9,00	0.000401	IMAGp998D244068, mRNA sequence	BX111024	113.104040	
	- 1	/clone=IMAGp998D244068_;_IMAGE:16			
• 1		04327 /gb=BX111624 /gi=27837123		•	2-1
		/ug=Hs.184840 /len=808		* 0	
8728	0.027120	DKFZp547N166_r1_547 (synonym: hfbr1)	VI 134600	Hs.272048	
0120	0.037 129	cDNA clone DKFZp547N166 5', mRNA	AL 134096	IDS.272040	
		· · · · · · · · · · · · · · · · · · ·			- 1
		sequence /clone=DKFZp547N166			
	· ·	/clone_end=5' /gb=AL134698		1	
		/gi=6602885 /ug=Hs.272048 /len=586		. •	
8754	0.026506	602072454F1 NCI_CGAP_Brn67 cDNA	BF530944	Hs.319823	*
0134	0.020390	clone IMAGE:4215325 5', mRNA	DF330944	IUS.219052	1.
		sequence /clone=IMAGE:4215325			
		l •	<u>.</u>		
		/clone_end=5' /gb=BF530944			1
0755	0.04720	/gi=11618307 /úg=Hs.319823 /len=686	DO003400	11- 200402	
8755	0.01738	UI-H-EI1-azd-I-09-0-UI.s1	BQ003406	Hs.269493	
0		NCI_CGAP_EI1 cDNA clone	1)):		s •
	*	IMAGE:5847320 3', mRNA sequence		in '	
		/clone=IMAGE:5847320 /clone_end=3'			
		/gb=BQ003406 /gi=19728306		-	
070 :	0.01.00	/ug=Hs.269493 /len=1055	11.407534	11. 000 170	
8764	0.04496	mRNA; cDNA DKFZp761G241 (from	AL137501	Hs.306470	
		clone DKFZp761G241) /gb=AL137501	-		
<u> </u>		/gi=6808146 /ug=Hs.306470 /len=3018		11. 10==:=	<u> </u>
8766	0.028474	BX107527 Soares_testis_NHT cDNA	BX107527	Hs.187615	
		clone IMAGp998E231862, mRNA			
		sequence			1.
		/clone=IMAGp998E231862_;_IMAGE:75		, '.	÷
		7246 /gb=BX107527 /gi=27847429			
		/ug=Hs.187615 /len=775			1
8767	0.021575	UMP-CMP kinase (UMP-CMPK), mRNA	NM_016308	Hs.11463	NP_057392
		/cds=(31,717) /gb=NM_016308	*		
		/gi=7706496 /ug=Hs.11463 /len=2836	0.0	Ι'	

		nding To Differentially Expr ssed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
	• •		Accession No.	Accession	Accession
				No.	No.
8773	0.030461	nn16d07.s1 NCI_CGAP_Co12 cDNA	AA593988	Hs.270630	
	*	clone IMAGE:1084045 3' similar to			
		contains Alu repetitive element;contains	* *		,*
		element MER26 repetitive element ;,		,	
		mRNA sequence	. *		* .
		/clone=IMAGE:1084045 /clone_end=3'			
		/gb=AA593988 /gi=2409338	<u>.</u>	, *	•
	a	/ug=Hs.270630 /len=560		•	
8791	0.00213	tg51b06.x1 Soares_NFL_T_GBC_S1	Al419722	Hs.161220	
		cDNA clone IMAGE:2112275 3', mRNA			
*	-	sequence /clone=IMAGE:2112275		, '	-0
•		/clone_end=3' /gb=Al419722	*		
	:.	/gi=4265653 /ug=Hs.161220 /len=484			
8810		EST(cDNA clone IMAGE:2432925 3')	AI869557	9	NP_689744
8826	0.018694	cDNA FLJ25058 fis, clone CBL04608.	AK057787	Hs.350624	
•	n	/cds=(139,639) /gb=AK057787		. *	
		/gi=16553726 /ug=Hs.350624 /len=1808			
		×			
8827	0.030461	ob11d04.s1 NCI_CGAP_Kid3 cDNA	AA872730	Hs.125229	
		clone IMAGE:1323367 3' similar to	÷ .		
		contains Alu repetitive element;contains			
		element LTR5 repetitive element ;,			
	,	mRNA sequence	· · ·		
		/clone=IMAGE:1323367 /clone_end=3'			,
		/gb=AA872730 /gi=2968852	9		*
		/ug=Hs.125229 /len=586			
8833		no significant match, No orf	SEQ.ID.No.1		3.00
8837		no significant match	SEQ.ID.No.39		
8839		No significant match, ORF-1(3~472)	SEQ.ID.No.49		-
8845		No significant match	SEQ.ID.No.82		
8869		Novel, No orf	SEQ.ID.No.4	ν	
8918		EST EST72587 Ovary II cDNA 5' end	AA362818		NP_057226
8925	0.034784	EST TCBAP1D1176 Pediatric pre-B cell	BE244548		
•	9	acute lymphoblastic leukemia Baylor-		<u>.</u>	
		HGSC project=TCBA cDNA clone		· .	
		TCBAP1176			2002
8962	0.013901	UI-H-BW0-ajq-g-03-0-UI.s1	AW298806	Hs.438211	
		NCI_CGAP_Sub6 cDNA clone	. •	*	· .
		IMAGE:2732740 3', mRNA sequence		= -	
		/clone=IMAGE:2732740 /clone_end=3'			
,	'	/gb=AW298806 /gi=6705442			
		/ug=Hs.438211 /len=615			
8963	0.042212	EST(IL2-HT0433-020200-041-F07_1	BE161204	¥)	
		HT0433)			
8995	0.026596	EST1000 HEV PCR-select cDNA clone	BM956063	Hs.390155	
		HEV#2154, mRNA sequence			<b>I</b> `
	· · · · ·	/clone=HEV#2154 /gb=BM956063	4.	*	
	1	/gi=23346294 /ug=Hs.390155 /len=664			

Spot	p-value	Description	Gene	Unigene	Protein
epe.		2000p.1101.	,	Accession	Accession
•,		*.	Accession No.	No.	No.
9018	0.028474	EST382162 MAGE resequences, MAGK	AW970081	Hs.325603	INO.
,,,,	0.02011	cDNA, mRNA sequence /gb=AW970081	/ ( ( ) ( ) ( )	113.02000	
*,		/gi=8159926 /ug=Hs.325603 /len=423	, ,		
		/gi=0100920/ug=113.020000/ieii=420			-
9052	0.0068	yy73h08.s1	N46879	Hs.397476	
-	, 5,555,5	Soares multiple sclerosis 2NbHMSP			•
		cDNA clone IMAGE:279231 3', mRNA	•	. "	
		sequence /clone=IMAGE:279231		Ì	
		/clone_end=3' /gb=N46879 /gi=1188045		F	
	*	/ug=Hs.397476 /len=539		+:	
9057	0.003097	gycosyltransferase (LOC83468), mRNA	NM 031302	Hs.159993	NP_112592
		/cds=(408,1457) /gb=NM_031302	00.002		1.1
	- 20	/gi=21314737 /ug=Hs.159993 /len=1908		ļ	
					1
9061	0.013494	cDNA FLJ33960 fis, clone	AK091279	Hs.126465	
		CTONG2018843. /gb=AK091279	,		•
		/gi=21749612 /ug=Hs.126465 /len=2849			
	·	7g. 21. 100 12. ag 110. 120 100 11011 2010			
9067	0.04496	xs46d07.x1 NCI_CGAP_Kid11 cDNA	AW271316	Hs.371210	: * **
		clone IMAGE:2772685 3' similar to			
	3.5	contains Alu repetitive element; contains		1	1
		element MER12 MER12 repetitive			
		element ;, mRNA sequence		,	
	ļ	/clone=IMAGE:2772685 /clone end=3'	2		
		/gb=AW271316 /gi=6658346			
		/ug=Hs.371210 /len=496	0	·	
9077	0.047805	ty83h04.x1 NCI_CGAP_Kid11 cDNA	AI758933	Hs.292921	V
		clone IMAGE:2285719 3', mRNA			
	٠	sequence /clone=IMAGE:2285719	. 0		
		/clone end=3'/gb=Al758933		· ·	
		/gi=5152658 /ug=Hs.292921 /len=487		*	
9087	0.034784	EST370944 MAGE resequences, MAGE	AW958874	Hs.403977	1.
		cDNA, mRNA sequence /gb=AW958874			1
		/gi=8148558 /ug=Hs.403977 /len=504			-
9150	0.034784	EST, cDNA, 3' end	BE503107	Hs.281951	
	*	/clone=IMAGE:3214604 /clone_end=3'		,	
	*	/gb=BE503107 /gi=9705515	*		•
		/ug=Hs.281951 /len=368			
9151	0.016146	mRNA; cDNA DKFZp564A2164 (from	AL117611	Hs.19150	<u> </u>
		clone DKFZp564A2164) /gb=AL117611			
	-	/gi=5912187 /ug=Hs.19150 /len=1908			1 1
9152	0.028474	cDNA FLJ31610 fis, clone	AK056172	Hs.196379	
	0.020 ()	NT2RI2002865. /gb=AK056172	· · · · · · · · · · · · · · · · · · ·		*
		/gi=16551502 /ug=Hs.196379 /len=2194			
		1	· · ·	1	

		nding To Differentially Expressed Gener			<del></del>
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
9153	0.034784	AGENCOURT_8584280	BQ876563	Hs.346743	
		Lupski_sympathetic_trunk cDNA clone			* * * <u>*</u>
	*	IMAGE:6192820 5', mRNA sequence	1		
		/clone=IMAGE:6192820 /clone_end=5'	*		-, ·
	-	/gb=BQ876563 /gi=22268571			
		/ug=Hs.346743 /len=925			
9156	0.04496	AV700727 GKC cDNA clone GKCGRD12	AV700727	Hs.446006	
	V.,	3', mRNA sequence /clone=GKCGRD12	+(): -	-	,
	0	/clone_end=3' /gb=AV700727			
	• =	/gi=10302698 /ug=Hs.446006 /len=494			
			, v	,	
9192	0.036892	mRNA full length insert cDNA clone	AJ420453	Hs.351834	NP 006435
•		EUROIMAGE 1271944 /cds=UNKNOWN			
	·	/gb=AJ420453 /gi=17066317		* *	
		/ug=Hs.351834 /len=1186		*	
		<u> </u>			
9197	0.047854	EST(603060869F1 NIH_MGC_122 cDNA	BI767635		NP 689605
	0.011001	clone IMAGE:5210201 5')	B11 01 000	: E	141 _000000
9214	0.04496	602646211F1 NIH_MGC_76 cDNA clone	BG618829	Hs. 164064	
	0.011400	IMAGE:4767747 5', mRNA sequence	00010020	113.104004	•
		/clone=IMAGE:4767747 /clone end=5'	Ţ		r,
	* 1	/gb=BG618829 /gi=13670200			·
,		/ug=Hs.164064 /len=628	· `	2014	
9233	0.002573	AGENCOURT_10227215	BU536672	Hs.380933	
9233	0.002573	NIH_MGC_141 cDNA clone	D0330072	IUS.200922	
		IMAGE:6565196 5', mRNA sequence			
	. :		. ,		
		/clone=IMAGE:6565196 /clone_end=5'			,
: •		/gb=BU536672 /gi=22847113		· .	.•
0222	0.004540	/ug=Hs.380933 /len=1275	A E 4 E 00 7 E	11- 40470	
9333	0.034512	AF150275 mRNA from cd34 stem cells	AF150275	Hs.40173	
٠.		cDNA clone CBFBNE09, mRNA			
		sequence /clone=CBFBNE09	:		
		/gb=AF150275 /gi=5133711			
		/ug=Hs.40173 /len=1823			
9341		No significant match	SEQ.ID.No.43		115
9443	0.011929	synapse associated protein 1, SAP47	NM_032796	Hs.47334	NP_116185
		(Drosophila) (SYAP1), mRNA		9	-
		/cds=(94,1152) /gb=NM_032796			
	<u> </u>	/gi=19923854 /ug=Hs.47334 /len=2030			
9459	0.021575	ubiquinol-cytochrome c reductase binding	NM_006294	Hs.131255	NP_006285
	0	protein (UQCRB), mRNA /cds=(54,389)			,
		/gb=NM_006294 /gi=20070231			
• 1		/ug=Hs.131255 /len=965			
9460	0.04496	FLJ10254 (FLJ10254), mRNA	NM_018041	Hs.326551	
		/cds=(172,993) /gb=NM_018041			
		/gi=8922314 /ug=Hs.326551 /len=2134	_		L
9482	0.042212	mRNA for KIAA1367 protein, partial cds.	AB037788	Hs.224961	VI.
	:	/cds=(1,1741) /gb=AB037788			
		/gi=7243114 /ug=Hs.224961 /len=4196	- di-		

Spot	p-value	onding To Differentially Expressed Genes Description	Gene	Unigene	Protein
		× ×		Accession	Accession
	r		7.0000010111101	No.	N .
9485	0.009424	mRNA; cDNA DKFZp434K1412 (from	AL137753	Hs.12144	1
		clone DKFZp434K1412) /gb=AL137753			-)(-
	* * * * *	/gi=6808455 /ug=Hs.12144 /len=5448			
9513	0.008019	hypothetical gene supported by	XM 046853		1
:		AY007122 (LOC92719), mRNA	, Y.,	· r	
9529	0.032563	GTP-binding protein Sara (LOC51128),	NM_016103	Hs.279582	NP_057187
		mRNA /cds=(151,747) /gb=NM_016103		,	
	4	/gi=7705826 /ug=Hs.279582 /len=1280	**************************************		-
9532	0.037129	likely ortholog of rat V-1 protein (V-1),	NM_145808	Hs.21321	NP 665807
		mRNA /cds=(229,585) /gb=NM_145808	<del>-</del> ,		<del>-</del>
		/gi=21956644 /ug=Hs.21321 /len=3770			
9540	7.78E-04	translation factor sui1 (GC20), mRNA	NM_005875	Hs.21756	NP 005866
	. *	/cds=(242,583) /gb=NM_005875	<del>-</del> .	. "	
		/gi=5031710 /ug=Hs 21756 /len=992	*		
9601	0.008697	hypothetical protein FLJ20625	NM 017907	Hs.109773	NP_060377
		(FLJ20625), mRNA /cds=(53,538)	: <del>"</del>		_
		/gb=NM_017907 /gi=8923578	100	*	
•		/ug=Hs.109773 /len=1112			
9618	0.020091	protein phosphatase 1A (formerly 2C),	NM 021003	Hs.57764	NP_808821
		magnesium-dependent, alpha isoform			· -
		(PPM1A), mRNA /cds=(358,1506)		00.00	<i>t</i>
		/gb=NM_021003 /gi=10337594		. *	,
, .		/ug=Hs.57764 /len=2346			) - a
9619	0.04496	hypothetical protein MGC14817	NM_032338	Hs.124813	NP 115714
	•	(MGC14817), mRNA /cds=(53,442)			_
•		/gb=NM_032338 /gi=14150123	1.8	•	
		/ug=Hs.124813 /len=1010		*	
9642	0.028124	FK506 binding protein 11, 19 kDa	NM_016594	Hs:24048	NP_057678
		(FKBP11), mRNA /cds=(73,678)			
	• • •	/gb=NM_016594 /gi=7706130			• **
		/ug=Hs.24048 /len=727	·		
9663	0.04496	DKFZP586G011 protein (LAP1B), mRNA	NM_015602	Hs.234265	NP_056417
		/cds=(56,1444) /gb=NM_015602		. *	*
		/gi=24308098 /ug=Hs.234265 /len=3275			
9680	0.021575	clone 114 tumor rejection antigen mRNA,	AF445027	Hs.24723	
		complete cds /cds=(3482,3544)		*	
	٠.	/gb=AF445027 /gi=17386079	•	•	
		/ug=Hs.24723 /len=3648	4.	- · · · · · · · · · · · · · · · · · · ·	
9721	0.013901	EST(yj01e06.r1 clone 147490 5')	R81297		NP_057707
9727	0.024824	mRNA; cDNA DKFZp586F0219 (from	AL049404	Hs.432818	1
*	7.1	clone DKFZp586F0219) /gb=AL049404	* 1	-	
		/gi=4500192 /ug=Hs.432818 /len=2451			
9733	0.013901	hypothetical protein LOC92597	NM_173468	Hs.31422	NP_775739
•		(LOC92597), mRNA /cds=(151,801)			
	* *	/gb=NM_173468 /gi=27735028			
		/ug=Hs.31422 /len=6956		*	

	p-value	nding To Differentially Expressed Genes Description	Gene .		Protein
Shor	h-saine	Describrion		Unigene	
			Accession No.		Accession
9765	0.047805	602299495F1 NIH_MGC_87 cDNA clone	BC030805	<b>No.</b> Hs.439128	No.
9103	0.047.005	IMAGE:4393919 5', mRNA sequence	DG030603	HS.439128	
`		/clone=IMAGE:4393919 /clone_end=5'	* = #		
1	:	/gb=BG030805 /gi=12420450	_		
		/gb=BG030605/gi=12420450 /ug=Hs.439128 /len=924	y		
9783	0.021172	EST(tx54b12.x1 NCI_CGAP_Lu24 clone	VIC30004		
9100	0.021173	IMAGE:2273375 3' contains L1.t2 L1	A1630964		*
		,			
9801	0.020124	repeat) UI-1-BB1-aio-d-05-0-UI.s1	PO026442	115 205002	
9001	0.026124		BQ026113	Hs.365663	
• • •		NCI_CGAP_PI5 cDNA clone UI-1-BB1-			
		aio-d-05-0-UI 3', mRNA sequence			٠,
		/clone=UI-1-BB1-aio-d-05-0-UI			
	• • •	/clone_end=3' /gb=BQ026113		. 00	<b>!</b> ,
0005	0.004704	/gi=19761392 /ug=Hs.365663 /len=626	A1040540		4,5
9805	0.034/84	EST (qh12h02.x1	Al240516		1 41
		Soares_NFL_T_GBC_S1			
0000	0.007400	IMAGE:1844499 3')	DE050070	11 40000	
9806	0.037129	7k03e02.x1 NCI_CGAP_GC6 cDNA	BF056273	Hs.188920	
		clone IMAGE:3443402 3', mRNA	* 10	•	
ė.	· .	sequence /clone=IMAGE:3443402		*	
•	*	/clone_end=3' /gb=BF056273		*	*
0040	0.000500	/gi=10810169 /ug=Hs.188920 /len=572	A1 000 400	11. 070050	
9812	0.032563	mRNA; cDNA DKFZp313C1042 (from	AL833436	Hs.376859	
. •		clone DKFZp313C1042) /gb=AL833436			
		/gi=21734078 /ug=Hs.376859 /len=2103			
0040	0.04700	FOT ( 40 - 05 - 4 C 5 - 4   1	D04007		
9819	0.01738	EST (yq42a05 r1 Soares fetal liver spleen	R94397		
0000	0.047054	ACENCOLIDE COCAGEZ NULL MCC. CO.	DO000407	115 440405	
9833	0.047854	AGENCOURT_6861057 NIH_MGC_99	BQ066467	Hs.446485	2
•		cDNA clone IMAGE:5931113 5', mRNA			
	ļ	sequence /clone=IMAGE:5931113			
		/clone_end=5' /gb=BQ066467			
		/gi=19895513 /ug=Hs.446485 /len=1029			
0005	0.020000	Similar to Book protein like E. slane	DC005102	Ho 22040	ND 004050
9905	0.039603	Similar to RecQ protein-like 5, clone	BC005103	Hs.33818	NP_004250
	1	IMAGE:3629492, mRNA, partial cds		3	
0007	0.000474	(BC005103.1)	NINA 000404	11- 400000	ND 000470
9907	0.028474	glucuronidase, beta (GUSB), mRNA	NM_000181	Hs.183868	NP_000172
+		/cds=(27,1982) /gb=NM_000181			
0000	0.04705 :	/gi=4504222 /ug=Hs 183868 /len=2191	D0000 40 4	116 000070	
9960	J U.U4/854	similar to weakly similar to glutathione	BC029424	Hs.283072	
	1	peroxidase 2, clone MGC:32677	90000		
		IMAGE:4285958, mRNA, complete cds			- X
		Uede=135 664\ Jab=RC020424	i	ĺ	1
* i		/cds=(35,664) /gb=BC029424 /gi=20810222 /ug=Hs.283072 /len=1398	~ ·		

		nding To Diff rentially Expressed Gene			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Acc ssion
	,			No.	No.
9990	0.030461	hypothetical protein FLJ23467	NM_024575	Hs.16179	NP_078851
•		(FLJ23467), mRNA /cds=(103,657)	St.		_
•	87	/gb=NM_024575 /gi=13375749			
	,	/ug=Hs.16179 /len=1196		0	
10012	0.04496	hypothetical protein FLJ22729	NM 024683	Hs.94891	NP_078959
	0.000	(FLJ22729), mRNA /cds=(603,1079)		1110:0:1001	-07.000
		/gb=NM 024683 /gi=13375953			
		/ug=Hs.94891 /len=1278		<b> </b>	
10040	0.020464		ALCO20274	115 000540 t	- ** - **
10049	0.030461	FLJ12209 fis, clone MAMMA1000962	AK022271	Hs.366548	1.1
		/cds=UNKNOWN /gb=AK022271			
		/gi=10433630 /ug=Hs.366548 /len=1239			
			· · · · · · · · · · · · · · · · · · ·		
10054	0.021575	similar to hypothetical protein FLJ10883	NM_052937	Hs.60293	NP_443169
		(LOC115294), mRNA /cds=(98,1171)		*	
		/gb=NM_052937 /gi=24308385	7	8	
	* *	/ug=Hs.60293 /len=3967	,		
10075	0.039603	anti-silencing function 1A	NM 014034	Hs.108110	NP 054753
		(DKFZP547E2110), mRNA		,	
		/cds=(193,807) /gb=NM 014034	,	-	
		, , , , <del>, , _</del> , , , , , , , , , , , , , , , , ,	*		
10004	0.020002	/gi=7661591 /ug=Hs.108110 /len=2367	NM_031453	H= 402270	ND 442644
10084	0.039603	hypothetical protein MGC11034	NINI_02 1455	Hs.103378	NP_113641
	* 1	(MGC11034), mRNA /cds=(246,641)			
	.0	/gb=NM_031453 /gi=13899290			
		/ug=Hs.103378 /len=3301			
10107	0.013901	chromosome 20 open reading frame 99,	AK025768		NP_149080
		cDNA: FLJ22115 fis, clone HEP18471			*
10112	0.028474	COP9 constitutive photomorphogenic	NM_006837	Hs.380969	NP_006828
		subunit 5 (Arabidopsis) (COPS5), mRNA	*	, .	19.
		/cds=(121,1125) /gb=NM_006837	,	- ,	
	200	/gi=5803045 /ug=Hs.380969 /len=1277	0.0		
10114	0.047854	early growth response 3 (EGR3), mRNA	NM 004430	Hs.74088	NP 004421
	0.017001	/cds=(358,1521) /gb=NM_004430	700 7.00	1.10.7 1000	
		/gi=4758251 /ug=Hs.74088 /len=4289			
		19 -47 3623   749-113.74000 /1611-4203		į	Į.
10116	0.040040	culiaina factor 1 (CE1); mDNA	NM 004630	Ha 190677	NP 004621
10116	0.042212	splicing factor 1 (SF1), mRNA	NIVI_004630	Hs.180677	INP_004621
•		/cds=(383,2254) /gb=NM_004630			
		/gi=4759339 /ug=Hs.180677 /len=3131		<u> </u>	(
10145	0.039603	EST(fi21a05.x1 Sugano Kawakami	AW116880		0. 0.
		zebrafish DRA clone 2601776 3')			
10166	0.018694	TPA regulated locus (TPARL), mRNA	NM_018475	Hs.236510	NP_060945
	•	/cds=(195,1169) /gb=NM_018475			
		/gi=8923860 /ug=Hs.236510 /len=1913	·		
10194	0.008019	hypothetical protein FLJ11101	NM 018322	Hs.58382	NP 060792
		(FLJ11101), mRNA /cds=(1,552)	-	*	-
		/gb=NM 018322 /gi=8922866	. *		
			1		P
	1 '	/ug=Hs.58382 /len=1920		1	l .

Genes	Correspon	nding To Differentially Expressed Genes			
	p-value	Description	Gene	Unig n	Protein
. *	,	* ***	Accession No.	Accession	Accession
1				No.	No.
10227	0.042212	mRNA; cDNA DKFZp586N2424 (from	AL157503	Hs.27552	
		clone DKFZp586N2424) /gb=AL157503		· (× )	
	***	/gi=7018553 /ug=Hs.27552 /len=2220			
10228	0.047854	hypothetical protein FLJ10342	NM 018064	Hs.101514	NP 060534
10220	0.041.004	(FLJ10342), mRNA /cds=(534,1145)	14111_010004	113.101014	111 _0000004
	10 T	/gb=NM_018064 /gi=14149717			
	*	/ug=Hs.101514 /len=1506			
10232	0.023151	BX094256	BX094256	Hs.407356	w .
10232	0.023131		DAU94250	ITS.407336	in the second
		Soares_fetal_heart_NbHH19W cDNA	0.0		m Mari
- 3		clone IMAGp998B20783, mRNA			
100	1	sequence			
j.		/clone=IMAGp998B20783_;_IMAGE:342			
		835 /gb=BX094256 /gi=27841884			
		/ug=Hs.407356 /len=477			7
10236	0.047854	hypothetical protein MGC4701	NM_024511	Hs.421054	NP_078787
		(MGC4701), mRNA /cds=(149,1585)		*	
	1995	/gb=NM_024511 /gi=24308290		i j	
		/ug=Hs.421054 /len=1686		1	
10269	0.028474	hypothetical protein PRO1546	NP 061055		<u> </u>
10272		EST yc21h02.r1 Stratagene lung	T63815		
	i.	(#937210) cDNA clone IMAGE:81363 5'			
10282	0.023151	EST (7o83a06.x1 NCI_CGAP_Kid11	BF197462		
		cDNA clone IMAGE:3642898 3')		*	
10287	0.024824	EST (ye08g06.r1 Stratagene lung	T87941		
	0.021021	(#937210) cDNA clone IMAGE:117178	107011		, in
		(1/307210) 65107 GIGHE HVI/ (GE 117 170		**	1
10310	0.007388	EST (oy95f11.x1	AI079513		<u> </u>
10010	0.007.000	Soares_fetal_liver_spleen_1NFLS_S1	71073313	*.	
		cDNA clone IMAGE:1673613 3'	, , ,		
			3-4		
,	- ×-	similar to contains OFR.t1 OFR repetitive			
40005	0.004444	element;	NIM 450000	11 000 400	NID COOFO
10335	0.024441	hypothetical protein MGC13024	NM_152288	Hs.333488	NP_689501
		(MGC13024), mRNA /cds=(196,1083)		.,.	
0	ii .	/gb=NM_152288 /gi=22748650			
		/ug=Hs.333488 /len=2239			
10363	0.010203	Similar to RIKEN cDNA 2310026P19	BC043352	Hs.35096	
		gene, clone MGC:49935			
		IMAGE:6175382, mRNA, complete cds	:		
		/cds=(288,3329) /gb=BC043352		1	
		/gi=27694113 /ug=Hs.35096 /len=5900			1
10369	0.034784	phosphatidylinositol 4-kinase type-II beta	NM_018323	Hs.23920	NP_060793
		(PI4K2B), mRNA /cds=(112,1557)			
		/gb=NM 018323 /gi=18874095			
*	. ,	/ug=Hs.23920 /len=3458	·	-	
10387	0.04496	RAD52B (RAD52B), mRNA	NM_145654	Hs.194411	NP_663629
.0001	0.04400	/cds=(28,882) /gb=NM_145654	140004	1.13.13.4411	
		/gi=21717825 /ug=Hs.194411 /len=1159			].
			N. "	. "	· .
	L		L	L	

Genes Corresponding To Differ ntially Expressed Genes in Figure 15 - Hyperlipidemia						
Spot	p-value		Gene	Unigene	Protein	
			Accession No.	Acc ssion	Accession	
	·	1		No.	No.	
0397	0.012883	maternal G10 transcript (G10), mRNA	NM_003910 <sup>*</sup>	Hs.380233	NP_003901	
		/cds=(380,814) /gb=NM_003910				
	• •	/gi=4503836 /ug=Hs.380233 /len=1003	·			
0405	0.030461	EST (AW893778 RC4-NN0025-150400-	AW893778	-1		
		012-c12 NN0025 cDNA)		7		
0418	0.039603	602152595F1 NIH_MGC_81 cDNA clone	BF672139	Hs.19479		
		IMAGE:4293719 5', mRNA sequence		187	· ·	
		/clone=IMAGE:4293719 /clone_end=5'				
		/gb=BF672139 /gi=11946034	# Y .	0		
		/ug=Hs.19479 /len=896	*			
0430	0.001935	EST(ha63a03.x1 NCl_CGAP_Pan1	AW338626		NP 006826	
		cDNA clone IMAGE:2878348 3')			_	
0437	0.034784	UI-H-EI1-aze-c-02-0-UI.s1	BQ003590	Hs.29698	1	
		NCI_CGAP_EI1 cDNA clone				
	]	IMAGE:5847481 3', mRNA sequence	+ .			
		/clone=IMAGE:5847481 /clone end=3'		1		
	· ·	/gb=BQ003590 /gi=19728490			} '	
		/ug=Hs.29698 /len=1051				
0466	0.026229	cDNA, 5' end /clone=IMAGE:4592424	BG400792	Hs.83286	NP_714916	
0.100	0.020220	/clone_end=5' /gb=BG400792	00702	110.00200	-   -   -   -	
		/gi=13294240 /ug=Hs.83286 /len=973		,		
0481	0.030603	UI-H-DF0-beu-n-17-0-UI.s1	BU617990	Hs.444822	19- 11 A	
0401	0.059005	NCI CGAP_DF0 cDNA clone UI-H-DF0-	D0017990	113.444022		
		beu-n-17-0-UI 3', mRNA sequence			, ,	
	-	/clone=UI-H-DF0-beu-n-17-0-UI				
	0	•				
		/clone_end=3' /gb=BU617990	*		,	
		/gi=23284205 /ug=Hs.444822 /len=1088			· I	
0404	0.024704	LILLI DUO avil i 40 0 LII a4	BM994461	Hs.434057	1	
0491	0.034784	UI-H-DH0-aul-j-10-0-UI.s1	BM994461	HS.434057		
		NCI_CGAP_DH0 cDNA clone			1	
		IMAGE:5871081 3', mRNA sequence		* -	3	
		/clone=IMAGE:5871081 /clone_end=3'				
		/gb=BM994461 /gi=19719362				
		/ug=Hs.434057 /len=2059				
0495	0.023151	7q35h07.x1 NCI_CGAP_GC6 cDNA	BF478238	Hs.356203		
		clone IMAGE:3700476 3' similar to				
		contains element MER4 MER4 repetitive				
		element ;, mRNA sequence				
		/clone=IMAGE:3700476 /clone_end=3'		*		
		/gb=BF478238 /gi=11549065				
	<u> </u>	/ug=Hs.356203 /len=400			·	
0499	0.026229	cDNA: FLJ21545 fis, clone COL06195.	AK025198	Hs.83623		
	1	/gb=AK025198 /gi=10437662				
		/ug=Hs.83623 /len=2176				
0503	0.039603	thymosin, beta 4, X chromosome	NM_021109	Hs.75968	NP_066932	
		(TMSB4X), mRNA /cds=(78,212)				
		/gb=NM_021109 /gi=11056060	-			
	1	/ug=Hs.75968 /len=556			1	

		nding To Differentially Expressed Gener			
Spot	p-value	Description	Gene	Unigene	Protein
1			Accession No.	Accession	Accession
•				No.	No.
10518	0.037129	Ul-H-El1-ayz-p-10-0-Ul.s1	BQ006715	Hs.29088	
		NCI_CGAP_EI1 cDNA clone			
		IMAGE:5845881 3', mRNA sequence	-35	:	, ,
		/clone=IMAGE:5845881 /clone_end=3'		: *	
		/gb=BQ006715 /gi=19731615		9 4	• 1
* = 1		/ug=Hs.29088 /len=1062			
10525	0.012883	UI-H-DF0-beq-g-04-0-UI.s1	BU617513	Hs.25566	
		NCI CGAP DF0 cDNA clone UI-H-DF0-	* *		
		beg-g-04-0-UI 3', mRNA sequence			- () · · · · ·
		/clone=UI-H-DF0-beq-g-04-0-UI			
		/clone_end=3' /gb=BU617513	7		
		/gi=23283728 /ug=Hs.25566 /len=1170	*	- i	
10544	0.024444	hypothetical protein LOC153339	NM 174909	Hs.374538	NP 777569
10044	0.024441	(LOC153339), mRNA /cds=(21,239)	1748U8	113.074000	- 11 1 30 9
	**			•	
	, :	/gb=NM_174909 /gi=28372532	* *		300
40500	0.000740	/ug=Hs.374538 /len=726	DV404004	11 007000	
10589	0.003712	BX104984 Soares placenta Nb2HP	BX104984	Hs.287980	
	) i	cDNA clone IMAGp998G22188, mRNA			
		sequence			
		/clone=IMAGp998G22188_;_IMAGE:133			
÷.		677 /gb=BX104984 /gi=27833283		* '	5.yz * *
		/ug=Hs.287980 /len=752			
10595	0.013901	FLJ14309 fis, clone PLACE3000221	AK024371	Hs.129013	
	-	/cds=UNKNOWN /gb=AK024371			1
		/gi=10436741 /ug=Hs.129013 /len=4964			
				1	
10619	0.028474	HepG2 3' region cDNA, clone hmd4e11.	D16932	Hs.434575	
		/gb=D16932 /gi=598823 /ug=Hs.434575		÷	·
-		/len=382			
10630	0.00213	UI-H-DF0-bet-j-17-0-UI.s1	BU626301	Hs.443120	*
,,,,,		NCI_CGAP_DF0 cDNA clone UI-H-DF0-			
		bet-j-17-0-UI 3', mRNA sequence		1 :	
		/clone=UI-H-DF0-bet-j-17-0-UI	•	.,	
	· ;	/clone_end=3' /gb=BU626301	7		
		/gi=23292516 /ug=Hs.443120 /len=1130	÷	1.	
		/gi-23292310/ug-H5.443120/len-1130			
10640	5 OF T 04	UCC2ICO24 normalized infant brain	E12060	<del>                                     </del>	
10642	J 5.U5E-U4	HSC3IC021 normalized infant brain	F13068		
4005 *	0.040040	cDNA cDNA clone c-3ic02	D11400000	No 050044	
10654	0.042212	AGENCOURT_7968233 NIH_MGC_67	BU189828	Hs.258214	
		cDNA clone IMAGE:6170681 5', mRNA	1		
	i .	sequence /clone=IMAGE:6170681			
		/clone_end=5' /gb=BU189828		ļ	
		/gi=22703812 /ug=Hs.258214 /len=956	<u> </u>	<b></b>	<del> </del>
10661	0.010203	ip18c02.y1 HR85 islet cDNA clone	CA777576	Hs.115779	180
		IMAGE:6217706 5', mRNA sequence			
	[	/clone=IMAGE:6217706 /clone_end=5'	1	1	•
		/gb=CA777576 /gi=26015451	ļ., .		
		/ug=Hs.115779 /len=700			

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
	- 12		Accession No.	Accession	Accession
10660	0.0060	EST(Hippocampus SN pool 1 cDNA	Al217038	No.	No.
10669	0.0000		A1217036		
		clone IMAGE:1948863 similar to contains	. "		**
10070	0.004575	L1.t2 L1 repetitive element;)	A1705400	11- 444400	
10676	0.021575	ESTs, cDNA, 3' end	AI735488	Hs.111436	
		/clone=IMAGE:2354884 /clone_end=3'		* =	·
		/gb=Al735488 /gi=5057012	• • •		
10701	0.040040	/ug=Hs.111436 /len=514	DE070000	10.407	
10704		602149995F1 NIH_MGC_81 cDNA clone	BF670902	Hs.19107	1
		IMAGE:4291390 5', mRNA sequence		() · · · · · ·	*
·; · ·		/clone=IMAGE:4291390 /clone_end=5'	. 0	· ·	
	*	/gb=BF670902 /gi=11944797			. 00
		/ug=Hs.19107 /len=846			
10705	0.037129	No significant match,			
		ORF+2(386~529),+3(3~107)	SEQ.ID.No.2		
10717		No significant match	SEQ.ID.No.83		
10773	0.014988	EST (RC3-CT0254-300800-022-g07	BE927223		
		CT0254)			*
10779	0.04496	EST (ADB cDNA clone ADBAKA02 5')	AV704531		
10790	0.018694	similar to zinc finger protein 22 (KOX 15)	NM_145291	Hs.94013	NP_660334
		(LOC166793), mRNA /cds=(1401,2147)	-		
	·1.	/gb=NM 145291 /gi=21686968			
		/ug=Hs.94013 /len=2634	* *		4
10792	0.021575	EST (hb87e12.x1 NCI CGAP Ut2 cDNA	AW439703		
	1 # 1	clone IMAGE:2890222 3' similar to			
		contains Alu repetitive element)	,		
10794	0.011037	FSHD region gene 1 (FRG1), mRNA	NM_004477	Hs.203772	NP_004468
,		/cds=(192,968) /gb=NM_004477			-
	F (*)	/gi=4758403 /ug=Hs.203772 /len=1042			
10801	0.026229	UI-H-BI4-apt-h-07-0-UI.s1	BF511971	Hs.439923	
10001	0.02022	NCI_CGAP_Sub8 cDNA clone		1.0.100020	
		IMAGE:3088741 3', mRNA sequence	9	. *	
		/clone=IMAGE:3088741 /clone_end=3'	e .		
	.*	/gb=BF511971 /gi=11595269			100
	- 4	/ug=Hs.439923 /len=1228	( x)		8 = .
10814	0.016066	UI-E-CI1-afo-o-08-0-UI.s1 UI-E-CI1	BU732338	Hs.99472	+
10014	0.010900	cDNA clone UI-E-CI1-afo-o-08-0-UI 3',	00732330	113.33412	/
				1 2	
		mRNA sequence /clone=UI-E-CI1-afo-o- 08-0-UI /clone end=3' /gb=BU732338			
	*			1	
40000	0.040000	/gi=23658133 /ug=Hs.99472 /len=1229	DE000700		<del> </del>
10829	0.016966	EST CM2-BT0693-210300-123-a08	BE088733		
40000	0.000471	BT0693 cDNA	4.4600000	<del>                                     </del>	· ·
10836	0.028474	EST (nj28d04.s1 NCI_CGAP_AA1 cDNA	AA600996		
	227	clone IMAGE:993799 3')		1. 44.55	1
10873	0.012883	601156470F1 NIH_MGC_21 cDNA clone	BE279006	Hs.444551	1
		IMAGE:3140104 5', mRNA sequence		*	1 .
		/clone=IMAGE:3140104 /clone_end=5'	1		} .
		/gb=BE279006 /gi=9153993	, ;		
		/ug=Hs.444551 /len=549	8		

		nding To Diff rentially Expressed Gener				
Spot p-va	p-value	· · · · · · · · · · · · · · · · · · ·	Gen	Unig ne	Protein	
			Accession No.	Accession	Accession	
	1, 1, 1	(		No.	No.	
10875	0.014988	cDNA FLJ39179 fis, clone	AK096498	Hs.104935		
		OCBBF2004147. /gb=AK096498			,	
		/gi=21756010 /ug=Hs.104935 /len=2760	v.,			
•		791 211 000 10 749 110. 10 10 00 71011 21 00				
10891	0.022562	EST(yh69b07.r1 Soares placenta Nb2HP	D21622		<del> </del>	
10091	0.032303		N3 1023	e e		
	- 0	cDNA clone IMAGE:134965 5' similar to				
		contains Alu repetitive element)	* * * * * * * * * * * * * * * * * * * *			
	ļ					
		EST (clone GKBACD08 3')	AV699636			
10898	0.037129	heat shock 70kDa protein 5 (glucose-	NM_005347	Hs.75410	NP_005338	
	•	regulated protein, 78kDa) (HSPA5),			÷.	
		mRNA /cds=(205,2169) /gb=NM_005347				
, .		/gi=21361242 /ug=Hs.75410 /len=3925				
		1 2 100 12 12 149 110.10 110 1011 0020		*		
10912	0.020461	cDNA FLJ34675 fis, clone	AK091994	Hs.380100	4 W	
10912	0.030401		ANU9 1994	IUS:300 100	*	
		LIVER2001608. /gb=AK091994				
		/gi=21750487 /ug=Hs.380100 /len=1725	• .	* 3		
				-		
10926	0.047854	EST(yp57a07.s1 Soares fetal liver spleen	H37798			
		1NFLS cDNA clone IMAGE:191508 3'	, .			
		similar to gb:X56411_rna1 ALCOHOL			49 95 9	
	, ° .	DEHYDROGENASE CLASS II PI CHAIN)			• :	
·.	٠.					
1				A -		
40004	0.047054	MD2 C10496 204400 040 -06 C10496	DE044E00	110 446504	-	
10931	0.047854	MR2-Cl0186-291100-010-a06 Cl0186	BF814502	Hs.446594		
-	. , -	cDNA, mRNA sequence /gb=BF814502				
		/gi=12147047 /ug=Hs.446594 /len=530	* 14			
10946	0.013901	of yeast long chain polyunsaturated fatty	NM_021814	Hs.250175	NP_068586	
		acid elongation enzyme 2 (HELQ1),				
		mRNA /cds=(345,1244) /gb=NM_021814	** *	*	,	
		/gi=21361903 /ug=Hs.250175 /len=3011		e :		
		g	*			
10959	0.030461	7p65g03.x1 NCI_CGAP_Pr28 cDNA	BF436898	Hs.213352	† · · · · · · · · ·	
10000	0.030401	clone IMAGE:3650861 3', mRNA	121 40000	113.210002		
	3 3					
		sequence /clone=IMAGE:3650861				
		/clone_end=3' /gb=BF436898	,			
		/gi=11449213 /ug=Hs.213352 /len=426				
10966	0.024824	mRNA; cDNA DKFZp586C1723 (from	AL050192	Hs.80285		
		clone DKFZp586C1723) /gb=AL050192				
		/gi=4884408 /ug=Hs.80285 /len=1797			8	
10973	0.01738	IL3-HT0619-280600-191-F06 HT0619	BQ357271	Hs.232093		
		cDNA, mRNA sequence /gb=BQ357271			1	
		/gi=21022994 /ug=Hs.232093 /len=580	· io			
		/g -2 1022994 /ug-115.232093  e  -560 				
4000			1114 000000	11 405045	ND COOCE	
10991	0.01738	ribosomal protein L12 (RPL12), mRNA	NM_000976	Hs.405042	NP_000967	
		/cds=(89,586) /gb=NM_000976			· · ·	
		/gi=15431291 /ug=Hs.405042 /len=632		<u> </u>	*	
11010	0.014000	mitochondrion, complete genome	NC 001807		100	

Snot	p-value	nding To Differentially Expr ssed General Description	Gene	Unigene	Protein
Shor	h-saine	Describuon			
$\mathcal{A}$			Accession No.	Accession No.	Accession
11021	0.030461	FLJ23302 fis, clone HEP11143	AK026955	Hs.367841	<b>No.</b> NP 115652
		/cds=UNKNOWN /gb=AK026955			
		/gi=10439937 /ug=Hs.287737 /len=2509			
		/gi=10455557 /dg=113.207757 /ieii=2505			
11035	0.001592	wa21h07.x1 NCI_CGAP_Kid11 cDNA	Al651329	Hs.160289	
		clone IMAGE:2298781 3, mRNA			
		sequence /clone=IMAGE:2298781	-	* *	-81
	,	/clone_end=3' /gb=Al651329		- 8	-
		/gi=4735308 /ug=Hs.160289 /len=482			( v
1049	0.037120	cs69c03.y2 Retinal pigment	CA395789	Hs.446106	
1043	0.037 129		CV3931.09	ITS.440100	
		epithelium/choroid cDNA (Un-normalized,			
,		unamplified): cs cDNA clone cs69c03 5',	*		
		mRNA sequence /clone=cs69c03	,		1
	,	/clone_end=5' /gb=CA395789			
		/gi=24731580 /ug=Hs.446106 /len=585			
1085	0.01738	EST(cDNA clone IMAGE 2126419 3')	Al435109	1	. =
1094	0.034784	602969052F1 NIH_MGC_12 cDNA clone	BI260728	Hs.201769	
		IMAGE:5108412 5', mRNA sequence			
		/clone=IMAGE:5108412 /clone_end=5'			
	,	/gb=Bl260728 /gi=14819291			
		/ug=Hs.201769 /len=667	.000	,	<b>.</b>
1097	0.003808	ESTs, cDNA, 3' end /clone=UI-E-EJ0-ahj-	PM674241	Hs.354662	
1091	0.003600		DIVIO 7.424 I	ITS.334002	-
	* *	f-02-0-UI /clone_end=3' /gb=BM674241		1	
	0	/gi=18984139 /ug=Hs.354662 /len=684	,		
1099	0.012481	UI-H-DT1-avz-g-14-0-UI.s1	BQ015869	Hs.353471	
1033	0.012401	NCI_CGAP_DT1 cDNA clone	DQ013009	1118.333471	
	· ·				
		IMAGE:5886373 3', mRNA sequence			l .
		/clone=IMAGE:5886373 /clone_end=3'			0
		/gb=BQ015869 /gi=19751146		•	'
		/ug=Hs.353471 /len=1192	,		
1113	0.047854	wy94a10.x1 NCI_CGAP_Brn23 cDNA	AW073130	Hs 370580	
		clone IMAGE:2556186 3', mRNA	· .		
		sequence /clone=IMAGE:2556186			
		/clone_end=3' /gb=AW073130		*	• •
		/gi=6028128 /ug=Hs.370580 /len=536			
1114	0.030461	UI-CF-FN0-aew-k-20-0-UI s1 UI-CF-FN0	BU608201	Hs.44404	
	5.555451	cDNA clone UI-CF-FN0-aew-k-20-0-UI 3',			
		mRNA sequence /clone=UI-CF-FN0-aew-	1 .		
			1		
•		k-20-0-UI /clone_end=3' /gb=BU608201	v .		8
		/gi=23274416 /ug=Hs.44404 /len=1157			
1132	0.030603	UI-H-CO0-aqz-b-03-0-UI.s1	BQ027621	Hs.442094	•
11132	0.039003		DUUZ/021	115.442094	
		NCI_CGAP_Sub9 cDNA clone	i X		
		IMAGE:3105700 3', mRNA sequence	· · ·)*	,	1
		/clone=IMAGE:3105700 /clone_end=3'		- 10	- 1
		/gb=BQ027621 /gi=19762900	38		1
	1	/ug=Hs.442094 /len=922	1 '	1	120

		sponding To Differentially Expressed G nes	Gene	Unigene	Protein
Opor	p-value	Description	Accession No.	_	Accession No.
11142	0.007388	cDNA: FLJ22447 fis, clone HRC09479.	AK026100	Hs.344000	110.
	0.9	/gb=AK026100 /gi=10438841			n o
		/ug=Hs.344000 /len=1659		•	6
11162	0.04496	cDNA FLJ33072 fis, clone	AK057634	Hs.348724	
	,	TRACH2000243. /gb=AK057634	, , , ,		
	1	/gi=16553392 /ug=Hs.348724 /len=2552	· / *		. *
		<b>9</b>			
11167	0.032563	cDNA FLJ31063 fis, clone	AK055625	1.4	
		HSYRA2001105			
11168	0.047854	hv66b12.x1 NCI CGAP Lu24 cDNA	BE220031	Hs.192491	- 30
		clone IMAGE:3178367 3', mRNA			
		sequence /clone=IMAGE:3178367			
		/clone_end=3' /gb=BE220031			
		/gi=8907349 /ug=Hs.192491 /len=379			
11218	0.047854	chromosome 3q clone CTD-2650N22,	AC108668		
		WORKING DRAFT SEQUENCE, 5	* ***		*
	* *	unordered pieces			
11234	0.006254	likely ortholog of mouse WD-40-repeat-	NM 018639	Hs.136644	NP 061109
		containing protein with a SOCS box 2	=		_
	eg .	(WSB2), mRNA /cds=(66,1280)			
٠		/gb=NM_018639 /gi=20149658	è		- 20
** *	1. 1. 1. 1.	/ug=Hs.136644 /len=2610	,		
11266	0.001304	B-cell translocation gene 1, anti-	NM_001731	Hs.77054	NP_001722
		proliferative (BTG1), mRNA	* ,		
•	- 0	/cds=(309,824) /gb=NM_001731			
	_	/gi=4502472 /ug=Hs.77054 /len=1783	*		
11318	0.016966	SAR1 protein (SAR1), mRNA	NM_020150	Hs.110796	
		/cds=(125,721) /gb=NM_020150			
		/gi=21361614 /ug=Hs.110796 /len=3003			~
•.					
11327	0.003392	low density lipoprotein receptor-related	NM 014045	Hs.3804	NP_054764
		protein 10 (LRP10), mRNA			31
		/cds=(566,1261) /gb=NM_014045			ı
	(	/gi=13027587 /ug=Hs.3804 /len=1833			
11333	0.003392	hypothetical protein FLJ13615	NM_025114	Hs.288715	NP_079390
	,	(FLJ13615), mRNA /cds=(345,2069)			
		/gb=NM_025114 /gi=13376688			
		/ug=Hs.288715 /len=2719		<u> </u>	
11368	0.005746	cofactor required for Sp1 transcriptional	NM_004268	Hs.22630	NP_004259
		activation, subunit 6, 77kDa (CRSP6),	);		
	0.7	mRNA /cds=(196,2151) /gb=NM_004268	,		
·. `		/gi=10835074 /ug=Hs.22630 /len=2546			· ·
11369	0.001304	clone IMAGE:5301545, mRNA	BC041951	Hs.177781	
	· 1x	/gb=BC041951 /gi=27469737	ŀ		*
-, ,		/ug=Hs.177781 /len=2155		4	

Genes Corresponding To Differentially Expressed Genes in Figure 15 - Hyperlipidemia						
		D scription	Gene	Unigene	Protein	
			Accession No.	Accession	Accession	
			1000	No.	No	
11382	0.039603	GTP cyclohydrolase 1 (dopa-responsivè	NM_000161	Hs.86724	NP 000152	
,		dystonia) (GCH1), mRNA /cds=(149,901)	_		_	
	-	/gb=NM 000161 /gi=4503948		:		
	· .	/ug=Hs.86724 /len=2921			1	
11391	0.011929	putative S1 RNA binding domain protein	NM_016505	Hs.54971	NP_057589	
	v.	(PS1D), mRNA /cds=(137,862)				
	·	/gb=NM_016505 /gi=21361575	, ,	<b>.</b>	0.4	
		/ug=Hs.54971 /len=1602				
11457	0.037129	fucose-1-phosphate guanylyltransferase	NM_003838	Hs.150926	NP_003829	
	•	(FPGT), mRNA /cds=(38,1822)				
'	* 40 '	/gb=NM_003838 /gi=4503776		· .		
		/ug=Hs.150926 /len=3144				
11470	0.018694	hypothetical protein MGC45400	NM_153333 '	Hs.389734	NP_699164	
		(MGC45400), mRNA /cds=(245,598)			-	
		/gb=NM_153333 /gi=23503246			1	
	·	/ug=Hs.389734 /len=1290				
11477	0.004838	mRNA for KIAA0626 protein, complete	AB014526	Hs.178121	NP_067679	
		cds /cds=(178,1407) /gb=AB014526		0		
		/gi=3327065 /ug=Hs.178121 /len=6184				
11498	0.04496	clone MGC:16614 IMAGE:4111344,	BC009313	Hs.193700		
		mRNA, complete cds /cds=(258,998)				
		/gb=BC009313 /gi=14424569	*			
		/ug=Hs.373515 /len=2052				
11534	0.006254	EST(ow60e12.x1	AI088021	1	NP_060823	
	10	Soares_NSF_F8_9W_OT_PA_P_S1				
		clone IMAGE:1651246 3')				
11537	0.007388	UI-H-DF1-auf-c-04-0-UI.s1	BM992029	Hs.358825		
j .		NCI_CGAP_DF1 cDNA clone				
ľ		IMAGE:5868603 3', mRNA sequence			1 .	
l		/clone=IMAGE:5868603 /clone_end=3'				
	,	/gb=BM992029 /gi=19711418				
<u> </u>		/ug=Hs.358825 /len=1052		,		
11546	0.028474	EST(PM3-NT0011-120400-001-b03	AW888715	1		
		NT0011)	1.00555	·		
11551	0.020091	EST(EST64315 Jurkat T-cells VI 5'	AA355853		NP_114107	
= -		ribosomal protein S21)	N. 100 0 1 = 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	<b>.</b>	lub os	
11554	0.012883	EST(df27f12.y1 Morton Fetal Cochlea	AW021741		NP_057485	
44505	0.00 105 1	clone IMAGE:2484646 5')	NIM 000444	11- 074000	ND 445547	
11569	0.024824	hypothetical protein DKFZp434K1421	NM_032141	Hs.374609	NP_115517	
ļ	Į	(DKFZP434K1421), mRNA	·		,	
c		/cds=(29,1705) /gb=NM_032141				
		/gi=14149806 /ug=Hs.374609 /len=2547				
11589	0.01738	EST(yl75h05.s1 clone 43989 3'	H05122		NP_000029	
1	3.31,30	gb:M73548 ADENOMATOUS				
ł						

		nding To Differentially Express d Genes			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
11605	0.026596	hypothetical protein PRO1051	NM_018572	Hs.326548	NP 061042
11000	0.020000	(PRO1051), mRNA /cds=(756,1004)	11111_010072	113.020040	141 _001042
	·		₹.	- );	
		/gb=NM_018572 /gi=8924004			
		/ug=Hs.326548 /len=1393	· · · · · · · · · · · · · · · · · · ·		
11621	0.039603		NM_005177	Hs.267871	NP_005168
		subunit a isoform 1 (ATP6V0A1), mRNA			*
		/cds=(168,2663) /gb=NM_005177			·
	1	/gi=19913417 /ug=Hs.267871 /len=4139		*	
		/g/ 10010111 /ug 110.20101 / //oil			."
11620	0.020464	cDNA FLJ30301 fis, clone	AK054863	110 005700	
11030	0.030461		ANU04003	Hs.285728	
		BRACE2003217. /gb=AK054863	**************************************		·:
		/gi=16549482 /ug=Hs.285728 /len=2186		. *	
		NC .		1 1	* *
11652	0.034784	EST(nf43h10.s1 NCI_CGAP_Pr2 cDNA	AA573636	A 91 1	
		clone IMAGE:916579 similar to contains			i
	- "	element MER22 repetitive element)	**		\$
		leiement wichtzz repetitive element)			
44074	0.047054	LULU BBO - I - 104 O LUL A	D0000707	11. 440050	
11671	0.04/854	UI-H-DP0-avb-p-04-0-UI.s1	BQ020727	Hs.446656	
	* "	NCI_CGAP_Fs1 cDNA clone		_	
	(ii)	IMAGE:5877363 3', mRNA sequence			
		/clone=IMAGE:5877363 /clone_end=3'			
		/gb=BQ020727 /gi=19756005			• (6)
		/ug=Hs.446656 /len=1208			
11000	0.046542		A A CC 2470		
11683	0.010043	EST (clone IMAGE:1218466 3' similar to	AA662478		
		contains			
11701	9.60E-04	of yeast long chain polyunsaturated fatty	NM_021814	Hs.250175	NP_068586
		acid elongation enzyme 2 (HELO1),			-
		mRNA /cds=(345,1244) /gb=NM_021814	A 40		
		/gi=21361903 /ug=Hs.250175 /len=3011			
0.0		1			1
11702	0.004939	eukaryotic translation elongation factor 1	NM 001402	Hs.422118	NP_001393
11/02	0.004636			1113.422110	INL _00 1292
		alpha 1 (EEF1A1), mRNA /cds=(63,1451)		ļ	
		/gb=NM_001402 /gi=25453469			
		/ug=Hs.422118 /len=1837			**
				·	
11747	0.04496	lysyl oxidase-like 1 (LOXL1), mRNA	NM_005576	Hs.65436	NP 005567
		/cds=(306,2030) /gb=NM_005576			_
		/gi=5031882 /ug=Hs.65436 /len=2328			^
44755	0.040000		NINA (000004	Un 04 45 4	ND 006470
11755	0.012883	ketohexokinase (fructokinase) (KHK),	NM_000221	Hs.81454	NP_006479
		transcript variant a, mRNA /cds=(9,905)			
	1	/gb=NM_000221 /gi=4557692			
	٠.	/ug=Hs.81454 /len=1899			
11766	0.013901	AV701088 ADA cDNA clone ADAAGB09	AV701088	Hs.419141	
, 55	0.010001	5', mRNA sequence /clone=ADAAGB09	1	1	
		1	_		
	4	/clone_end=5' /gb=AV701088			
		/gi=10717418 /ug=Hs.419141 /len=652		1	
	Í	1	·	1	100

		nding To Differentially Expr ssed Gene			
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
	*	*.	Addicasion No.	No.	No.
11770	0.01738	FLJ33160 fis, clone UTERU2000485	AK057722	Hs.124733	NO.
	0.01700	/cds=UNKNOWN /gb=AK057722	,	113.12-7700	
		/gi=16553641 /ug=Hs.124733 /len=2328		· ·	
• .			9		
11779	0.021575	chromosome 11 hypothetical protein	NM 020154	Hs.4245	NP_064539
11773	0.02 107 0	ORF3 (LOC56851), mRNA /cds=(14,742)	- 1	113.4240	141 _004559
		/gb=NM_020154 /gi=9910345			-
,		/ug=Hs.4245 /len=1072			
11803	0.04496		NM_006080	Hs.2414	NP_006071
11000	0.04430	(lg), short basic domain, secreted,	141W_000000	113.2414	147 _00007 1
		(semaphorin) 3A (SEMA3A), mRNA			
·		/cds=(16,2331) /gb=NM_006080			
* 's		/gi=5174672 /ug=Hs.2414 /len=2530		•-	
11822	0.005746	protein phosphatase 2, regulatory subunit	NM 002710	Hs.171734	NP 848703
11022	0.005740	B (B56), gamma isoform (PPP2R5C),	NIVI_0027 19	П5.17 17 34	INP_046703
×		mRNA /cds=(89,1633) /gb=NM_002719			
		/gi=4506022 /ug=Hs.171734 /len=4064			*
1100É	0.000454	protoin who on hotopo 2 (formowly 2D)	NM_000944	Hs.272458	ND 000025
11000	0.023151	protein phosphatase 3 (formerly 2B),	[NIVI_000944	IDS.272458	NP_000935
+ . •		catalytic subunit, alpha isoform	*		
	,	(calcineurin A alpha) (PPP3CA), mRNA	* *		-
		/cds=(407,1972) /gb=NM_000944			: '
		/gi=19923130 /ug=Hs 272458 /len=4425			
11869	0.042212	cDNA FLJ30649 fis, clone	AK055211	Hs.167700	<del></del>
11009	0.042212	CTONG2006562. /gb=AK055211	AKU55211	Ins. 167700	-
	)				-
		/gi=16549888 /ug=Hs.167700 /len=3061	-		
11887	0.012002	oral-facial-digital syndrome 1 (OFD1),	NM_003611	Uo 6492	ND 003603
11007	0.012003		NIVI_0036   1	Hs.6483	NP_003602
	,	mRNA /cds=(312,3350) /gb=NM_003611 /gi=4503178 /ug=Hs.6483 /len=3615			
	*	/gi-45051767ug-H5.64657lett-5615		*	
11004	0.034784	mitogon activated protein kingen	NM 004635	He 227780	ND: 004636
11904	0.034764	mitogen-activated protein kinase- activated protein kinase 3 (MAPKAPK3)	NM_004635	Hs.227789	NP_004626
		mRNA /cds=(119,1267) /gb=NM_004635			
، د		/gi=14589907 /ug=Hs.227789 /len=2509	*		* . `
-		/g =14369907 /ug=Hs.227769 /left=2309			
11911	0.030405	MSTP058 mRNA, complete cds	AF116728	Hs.434855	
וופוו	0.039405		\\rac{\rac{\rac{\rac{\rac{\rac{\rac	1115.434000	
		/cds=(930,1688) /gb=AF116728			
		/gi=27462073 /ug=Hs.434855 /len=2418			ļ
11921	0.00013	hypothetical protein DKFZp762O076	NIM 019710	He 21621	ND 061100
11921	0.00913		NM_018710	Hs.21621	NP_061180°
		(DKFZp7620076), mRNA /cds=(77,850)		0)-	
		/gb=NM_018710 /gi=24308164		•	1
	<u> </u>	/ug=Hs.21621 /len=2266	1.		<u> </u>

Genes	Corr spor	nding To Differentially Expressed Gene	s in Figure 15 - H	lyp rlipidemi:	a
	p-value	Description	Gene	Unigene	Protein
•			Accession No.	Accession	Accession
		<u></u>	7	No.	No.
11922	0.047854	Hypothetical protein MGC30022, cDNA	AK022894	Hs.179852	NP_689490
		FLJ12832 fis, clone NT2RP2003137			
		/cds=UNKNOWN /gb=AK022894		· .	-
		/gi=10434551 /ug=Hs.179852 /len=2540	'		100
٠.	10.	, g		1	
11944	0.011037	retinoic acid repressible protein (RARG-	NM 016167	Hs.106346	NP_057251
	*	1), mRNA /cds=(33,806)			
		/gb=NM_016167 /gi=15743546		1 .	
		/ug=Hs.106346 /len=896		* *	- ()-
11952	0.034784	SWI/SNF related, matrix associated,	NM_003601	Hs.9456	NP_003592
1,004	0.001701	actin dependent regulator of chromatin,		1.0.0 100	000002
	·	subfamily a, member 5 (SMARCA5),	•		
		mRNA /cds=(463,3621) /gb=NM_003601			
		/gi=21071057 /ug=Hs.9456 /len=3866			
11050	0.000500	-DNA EL 144420 Es alama	AK021501	116 207440	1 W 1/2
11956	0.032563	cDNA FLJ11439 fis, clone	AKUZ 15U I	Hs.287416	
0.0	* 12	HEMBA1001299. /gb=AK021501	- 14		
		/gi=10432697 /ug=Hs.287416 /len=1500	100		*
11960	0.039603	TNF-induced protein (GG2-1), mRNA	NM_014350	Hs.17839	NP_055165
		/cds=(198,770) /gb=NM_014350		. 01	
		/gi=7657123 /ug=Hs.17839 /len=2003			
11963	0.028474	proline rich 2 (PROL2), mRNA	NM_006813	Hs.75969	NP_006804
	war and a	/cds=(114,1097) /gb=NM_006813			
		/gi=5802981 /ug=Hs.75969 /len=2061	- /		
11980	0.009424	thyroglobulin gene, partial cds; and Src-	AF305872		
		like adapter protein gene, complete cds,			100
		complete sequence			4
11983	0.007323	RAS-like, estrogen-regulated, growth-	NM_032918	Hs.21594	NP_116307
*	<b>i</b> .	inhibitor (RERG), mRNA /cds=(291,890)			74.
	``	/gb=NM_032918 /gi=14249703	*		
		/ug=Hs.21594 /len=2240			
12017	0.016146	EST(EST382704 MAGE resequences,	AW970622		
		MAGK)			
12037	0.026596	EST(EST58819 Infant brain 3' contains	AA351153		
		Alu repeat)			
12062	0.021575	EST(wc78g04.x1 NCI_CGAP_Pan1	AI701086	· · · · · · · · · · · · · · · · · · ·	
		clone IMAGE:2324790 3')		-	
12119	0.021575	UI-H-BI2-agk-c-06-0-UI.s1	AW291541	Hs.446655	***************************************
	5.52 157 5	NCI_CGAP_Sub4 cDNA clone	, (442010-1	1.10.440000	* :
	*	IMAGE:2724490 3', mRNA sequence	· ·		:
		/clone=IMAGE:2724490 /clone_end=3'			-
		<u> </u>			
		/gb=AW291541 /gi=6698177	=	1	
40450	0.007400	/ug=Hs.446655 /len=783	D0004000	115 40000	
12153	0.03/129	clone IMAGE:4824086, mRNA	BC034996	Hs.406327	
	7	/gb=BC034996 /gi=23273314		1	*
		/ug=Hs.406327 /len=1818	<u> </u>		

		nding To Differentially Expressed Gene		lyperlipidemi	a
Spot	p-value	Description	Gene	Unig n	Protein
			Accession No.	Accession	Accession
	*			No.	No.
12156	0.042212	hypothetical protein FLJ11269	NM 018372	Hs.25245	NP 060842
. *		(FLJ11269), mRNA /cds=(197,1228)			_
,	*	/gb=NM_018372 /gi=8922961			
		/ug=Hs.25245 /len=2115		·	
12182	0.039603	Williams-Beuren Syndrome critical region	NM 145645	Hs.406306	NP 663620
	:	protein 20 copy B (WBSCR20B), mRNA			
		/cds=(984,1448) /gb=NM_145645	. *		*
		/gi=21717802 /ug=Hs.406306 /len=1634		. :	ľ ·
		3			- 4,
12197	0.019682	DKFZp586E2017_r1 586 (synonym:	AL046885	Hs.413463	
		hute1) cDNA clone DKFZp586E2017 5',			
		mRNA sequence	* *	1.0	
٧.	* :	/clone=DKFZp586E2017 /clone_end=5'			
12		/gb=AL046885 /gi=5936275	9 1		
		/ug=Hs.413463 /len=640			
12211		EST (te41e06.x1 Soares_NhHMPu_S1	Al381664	भागा े ना हा	
1	3.0-1-00	cDNA clone IMAGE:2089282 3')	,		- 4
12246	0.014988	EST (yo20f05.r1 Soares adult brain	H46503		· · · · · · · · · · · · · · · · · · ·
12270	0.01-300	N2b5HB55Y cDNA clone IMAGE:178497	11140000		. * .
		FY			
12247	0.042212	stress 70 protein chaperone, microsome-	NW 006048	Hs.352341	NP_008879
1224!	0.042212	associated, 60kDa (STCH), mRNA	14141_000948	1115.552541	NF_000079
		/cds=(37,1452) /gb=NM_006948		- ()	- 1 -
	, .	/gi=24431965 /ug=Hs.352341 /len=3998		•	
		/gi-24431903/ug-115.332341/lei1-3998		-	
12251	0.010203	AGENCOURT_10616002	BU963194	Hs.422374	
12231	0.010203	NIH_MGC_141 cDNA clone	D0903194	115.422574	.y. *
		IMAGE:6744199 5', mRNA seguence			
		/clone=IMAGE:6744199 /clone_end=5'			
		/gb=BU963194 /gi=24192766			
12271	0.020003	/ug=Hs.422374 /len=939	A A 40077C	1 11 1	~ · · · · · · ·
12271	0.039603	EST(ne86c04.s1 NCI_CGAP_Kid1 clone	AA480776		
,		IMAGE:911142 contains L1.t1 L1 repeat)			
10070	0.040403	ECT (DC4 MT0005 004000 044 -04	DE000454		
12273	0.012481	EST (RC4-MT0235-061200-011-e04	BF900451		
40001	0.000474	MT0235)	DV400750	115 040740	
12291	0.028474	BX100756 Soares_NFL_T_GBC_S1	BX100756	Hs.213748	
		cDNA clone IMAGp998G055863, mRNA		÷	
		sequence		I	
l ·		/clone=IMAGp998G055863_;_IMAGE:23	· .	y. 30	
1.		62012 /gb=BX100756 /gi=27844613		,	
	A	/ug=Hs.213748 /len=474			
12300	0.030461	hypothetical protein MGC32104	NM_144684	Hs.147025	NP_653285
		(MGC32104), mRNA /cds=(101,1651)			*
2		/gb=NM_144684 /gi=21389584			
	l i	/ug=Hs.147025 /len=4732	9 - 0		

		nding To Differentially Expr ssed G n			
Spot	p-value	D scription	Gene	Unigene	Protein
			Acc ssion No.	Accession	Accession
				No.	No.
12305	0.012883	AGENCOURT_6567049 NIH_MGC_88	BM561213	Hs.438146	2000/100/100/100/100/100
-		cDNA clone IMAGE:5739531 5', mRNA	*	,	**
		sequence /clone=IMAGE:5739531	-6-		
		/clone_end=5' /gb=BM561213	4 5	-	
		/gi=18806283 /ug=Hs.438146 /len=954			
12311	0.030461	DKFZP566I1024 protein	NM 015411	Hs.279696	NP 056226
		(DKFZP566I1024), mRNA /cds=(48,953)			
		/gb=NM_015411 /gi=24308052			
		/ug=Hs.279696 /len=2005			
	-	749-113.27,5050 /1011-2005		)	
12351	0.005275	ESTs, cDNA /gb=AW979086	AW979086	Hs.314427	· · · · · · · · · · · · · · · · · · ·
	0.003273		1744919000	115,31442 <i>1</i>	
12352	0.04406	/gi=8170371 /ug=Hs.314427 /len=550 UI-H-BI2-ahm-d-05-0-UI.s1	A)A/2024E2	115 40000	
12352	0.04496		AW293452	Hs.16228	
		NCI_CGAP_Sub4_cDNA clone	·		
	. ,	IMAGE:2727224 3', mRNA sequence			
	·. ·	/clone=IMAGE:2727224 /clone_end=3'			
	i.	/gb=AW293452 /gi=6700088			
		/ug=Hs.16228 /len=634			
		EST(cDNA clone IMAGE:3645928 3')	BF436461		NP_003109
12400	0.028474	cyclin I (CCNI), mRNA /cds=(545,1678)	NM_006835	Hs.79933	NP_006826
	€ 1	/gb=NM_006835 /gi=17738314	• • •	• *	
		/ug=Hs.79933 /len=1890		*	
12403	0.021575	mRNA; cDNA DKFZp564D2071 (from	AL110232	Hs.279243	
		clone DKFZp564D2071) /gb=AL110232			1
		/gi=5817171 /ug=Hs.279243 /len=1077		*	
12422	0.024824	EST (clone EUROIMAGE 2120537	AJ420510	Hs.7759	NP 579866
		/cds=UNKNOWN /gb=AJ420510			
	1	/gi=17066374 /ug=Hs.7759 /len=4303			
12461	0.008019	ESTs, cDNA, 3' end	Al399637	Hs.292543	
	* -	/clone=IMAGE:2119566 /clone_end=3'			*
		/gb=Al399637 /gi=4242724	7 W		
		/ug=Hs.292543 /len=255			
12474	0.049694	clone RP11-350H1 from 7p14-15,	AC006195	10 - 1	1.
	1 0.0 1000 !	complete sequence	1,10000100		
12486	0.04496	cDNA FLJ31040 fis, clone	AK055602	Hs.98314	
12-100	0.04430	HSYRA2000224. /gb=AK055602	/110000002	113.00014	*
			-	İ	
12/02	0.042212	/gi=16550372 /ug=Hs.98314 /len=2467	A1146202	<del>                                     </del>	
12493	0.042212	EST (Soares_fetal_heart_NbHH19W clone IMAGE:1707091 3')	AI146302	"	
12501	0.030603	EST(cDNA clone IMAGE:4693130 5')	BG539987	7	NP 005397
					INF_009397
		EST(cDNA clone IMAGE:4724612 5'.)	BG573579	Un 274 472	
12517	0.007388	UI-H-DP0-avt-a-17-0-UI.s1	BQ000272	Hs.371473	
		NCI_CGAP_Fs1 cDNA clone			
		IMAGE:5883928 3', mRNA sequence	· ·		
		/clone=IMAGE:5883928 /clone_end=3'		-	
	-	/gb=BQ000272 /gi=19725172			
	Ī	/ug=Hs.371473 /len=1051	·	1	

	p-value	nding To Differentially Expressed General Description	G ne	Unig n Accession No.	Protein Acc ssion No.
12519	*	EST(cDNA clone IMAGE:1637714 3' similar to contains Alu repetitive element;contains L1.t1 L1 repetitive element;)	Al000800	-	
12577	0.047854	No significant match, No orf	SEQ.ID.No.3	,	
12593	0.030134	No significant match, ORF+2(71~409),+1(121~384)	SEQ.ID.No.94		
12630		No significant match	SEQ.ID.No.100	•	<u> </u>
12658	0.039603	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 (GNAI2), mRNA /cds=(124,1191) /gb=NM_002070 /gi=4504040 /ug=Hs.77269 /len=1702	NM_002070	Hs.77269	NP_002061
12679	0.004059	BX092629 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998P06398; IMAGE:205685, mRNA sequence /clone=IMAGp998P06398_;_IMAGE:205 685 /gb=BX092629 /gi=27822922 /ug=Hs.303022 /len=735	BX092629	Hs.303022	7
12719	0.006254	EST (xg72d04.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2633863 3')	AW167199		
12740	0.04496	EST (602153645F1 NIH_MGC_83 clone IMAGE:4294739 5')	BF679004		
12763	0.047854	UI-H-FG0-bct-g-21-0-UI.s1 NCI_CGAP_EN1_2 cDNA clone UI-H- FG0-bct-g-21-0-UI 3', mRNA sequence /clone=UI-H-FG0-bct-g-21-0-UI /clone_end=3' /gb=BU627064 /gi=23293278 /ug=Hs.85999 /len=1075	BU627064	Hs.85999	
12803	0.047854	EST (UI-R-A1-dy-b-07-0-UI.s1 UI-R-A1 cDNA clone UI-R-A1-dy-b-07-0-UI.s2 UI-R-A1-dy-b-07-0-UI.s2)	AA924425		, , ,
12833	0.009424	cDNA FLJ30547 fis, clone BRAWH2001439. /gb=AK055109 /gi=16549767 /ug=Hs.351021 /len=1830	AK055109	Hs.351021	*
12835	0.030461	AGENCOURT_8856629 Lupski_sciatic_nerve cDNA clone IMAGE:6200636 5', mRNA sequence /clone=IMAGE:6200636 /clone_end=5' /gb=BQ947179 /gi=22362657 /ug=Hs:356605 /len=1277	BQ947179	Hs.356605	
12843	0.028474	cDNA clone IMAGE:123789 3' similar to contains Alu repetitive element; contains THR repetitive element; Soares fetal liver spleen 1NFLS	R01434		<
12848	0.019682	cDNA: FLJ23165 fis, clone LNG09846. /gb=AK026818 /gi=10439763 /ug=Hs.279898 /len=2117	AK026818	Hs.279898	,

		nding To Differentially Expressed Genes			
Spot   p	p-value		Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
12866	0.030461	clone IMAGE:3882977, mRNA, partial	BC020516	Hs.350268	-
		cds /cds=(1,683) /gb=BC020516	*		
	ŀ	/gi=18088177 /ug=Hs.350268 /len=3562		',	
		9	٠.	· .	0
12884	0.005275	clone IMAGE:3454421, mRNA	BC010534	Hs.318887	
		/gb=BC010534 /gi=14714772	,		
		/ug=Hs.318887 /len=1507	-		
12898	0.032563	603395193F1 NIH MGC_90 cDNA clone	BI871283	Hs.443147	
12000	0.002000	IMAGE:5405278 5', mRNA sequence	5.0.1200	1.0.110117	100
·		/clone=IMAGE:5405278 /clone end=5'	,	· · ·	
		/gb=BI871283 /gi=16044958		0	(0)
		, <del>, , -</del>			**
12000	0.006506	/ug=Hs.443147 /len=845	AK095791	Hs.50150	
12909	0.020596	cDNA FLJ38472 fis, clone	AK095/91	HS.50150	
	* * * * *	FEBRA2022148. /gb=AK095791	4.	ix:	
10051	0.007400	/gi=21755125 /ug=Hs.50150 /len=2454	0.0005000	11 000101	
12951	0.03/129	UI-1-BB1p-auc-h-10-0-UI.s1	BQ025322	Hs.396161	
		NCI_CGAP_PI6 cDNA clone UI-1-BB1p-		2	
		auc-h-10-0-UI 3', mRNA sequence	12		2
		/clone=UI-1-BB1p-auc-h-10-0-UI			
•		/clone_end=3' /gb=BQ025322	*		,
		/gi=19760601 /ug=Hs.396161 /len=921		/* /	
12962	0.032261	UI-H-FH0-bco-e-02-0-UI.s1	CA420130	Hs.365560	
		NCI_CGAP_FH0 cDNA clone UI-H-FH0-	0	*	
		bco-e-02-0-UI 3', mRNA sequence	1.		. *
		/clone=UI-H-FH0-bco-e-02-0-UI			* .
	·	/clone_end=3' /gb=CA420130	i ·	`	
		/gi=24782785 /ug=Hs.365560 /len=716		1	
12970	0.030461	EST(yy21h08.s1 Soares melanocyte	N35259		NP_079229
0.0	0,000,000	2NbHM H sapiens cDNA clone			0. 0229
	,	IMAGE:271935 3')			-
12977	0.004433	ESTs, cDNA, 5' end	BG027813	Hs.344521	
12311	0.004433	/clone=IMAGE:4389132 /clone_end=5'	DG027013	113.544521	
•				·	
		/gb=BG027813 /gi=12416651	20		
10000	0.000404	/ug=Hs.344521 /len=1068	11/05/1000	11- 207004	<del> </del>
12980	0.030461	FLJ30434 fis, clone BRACE2009016	AK054996	Hs.367901	·
	a -	/cds=UNKNOWN /gb=AK054996			
		/gi=16549636 /ug=Hs.367901 /len=2738			
			,		
12985	0.030461	EST380762 MAGE resequences, MAGJ	AW968686	Hs.445373	
		cDNA, mRNA sequence /gb=AW968686	*		
	1	/gi=8158527 /ug=Hs.445373 /len=699			,
13073	0.007672	UI-H-BI4-aqa-c-02-0-UI.s1	BF508251	Hs.197875	
		NCI_CGAP_Sub8 cDNA clone			
		IMAGE:3089258 3', mRNA sequence			1
	, 4	/clone=IMAGE:3089258 /clone_end=3'	1		
	,	/gb=BF508251 /gi=11591549			
	1	/ug=Hs.197875 /len=1237		1	1

		nding To Differentially Expr ss d G ne			
Spot	p-value	Description	Gene	Unig ne	Protein
			Accession No.	Accession	Accession
			44.4	No.	No.
13110	0.021575	hypothetical protein P1 p373c6	NM_019110	Hs.44720	NP_061983
		(P1P373C6), mRNA /cds=(254,1891)	<del>_</del> · · · ·		
		/gb=NM_019110 /gi=17738284			
1	100	/ug=Hs.44720 /len=2316		7 ·	
13112	0.026596	glutathione S-transferase M4 (GSTM4),	NM_000850	Hs.348387	NP 671490
	0.0200,00	transcript variant 1, mRNA	1100 9000	110.0-10001	· · · · · · · · · · · · · · · · · · ·
*		/cds=(310,966) /gb=NM_000850			
, ,		/gi=23065554 /ug=Hs.348387 /len=1436		- 3	1 1
	j=	/gi=250000004 /dg=113.040007 /icit; 1400	, v		-
13113	0.018604	aldehyde dehydrogenase 2 family	NM 000690	Hs.195432	NP 000681
13113	0.010094		14141_000090	ITIS. 19040Z	NP_000001
	•	(mitochondrial) (ALDH2), nuclear gene		* 30	
	9 .	encoding mitochondrial protein, mRNA			
)	*	/cds=(442,1995) /gb=NM_000690	,	·, •	
		/gi=25777731 /ug=Hs.195432 /len=2445			*
				19	
3114	0.024824	eukaryotic translation initiation factor 2C,	NM_012199	Hs.14520	NP_036331
		1 (EIF2C1), mRNA /cds=(214,2787)			
		/gb=NM_012199 /gi=6912351			
		/ug=Hs.14520 /len=7478			
13134	0.021575	sine oculis homeobox 2 (Drosophila)	NM_016932	Hs.101937	NP_058628
•	,	(SIX2), mRNA /cds=(283,1158)	,		
		/gb=NM_016932 /gi=21314676			
		/ug=Hs.101937 /len=2141			
13140	0.016146	epithelial V-like antigen 1 (EVA1),	NM 005797	Hs.116651	NP_658911
	, , , , , ,	transcript variant 1, mRNA			<del>-</del>
		/cds=(142,789) /gb=NM_005797	.00	· · · · · ·	4
;		/gi=21536270 /ug=Hs.116651 /len=2634	* 6		
1	**	/gi-210002707dg-113.1100017ici1-2004		7.0	
13146	8 65E 04	UI-H-DH0-aul-p-19-0-UI.s1	BM994422	Hs.289721	
13140	0.000	NCI CGAP DH0 cDNA clone	DIVIDOTTE	113.203721	*
		IMAGE:5871234 3', mRNA sequence	v	10	300
				. 3.	- 0
		/clone=IMAGE:5871234 /clone_end=3'	•		· · · · · · · · · · · · · · · · · · ·
	1.0	/gb=BM994422 /gi=19719323	•		
		/ug=Hs.289721 /len=2081			N.D. 057044
13175	0.011929	chromosome 1 open reading frame 9	NM_016227	Hs.108636	NP_057311
		(C1orf9), mRNA /cds=(125,4342)			
•	1	/gb=NM_016227 /gi=7705321	***	Y.	
	<u> </u>	/ug=Hs.108636 /len=5919	*		
13183	0.00213	translocation related non-coding gene	AF044579	Hs.375632	
		(TNRG10) mRNA, complete sequence		44	
	1	/gb=AF044579 /gi=3095103		*	
		11 11. 075000 // 0700			f
		/ug=Hs.375632 /len=2726			
13195	0.022757	hypothetical protein HSPC210	NM_016472	Hs.4104	NP_057556
13195	0.022757	hypothetical protein HSPC210	NM_016472	Hs.4104	NP_057556
13195	0.022757	hypothetical protein HSPC210 (HSPC210), mRNA /cds=(138,605)	NM_016472	Hs.4104	NP_057556
13195	0.022757	hypothetical protein HSPC210 (HSPC210), mRNA /cds=(138,605) /gb=NM_016472 /gi=24475986	NM_016472	Hs.4104	NP_057556
-		hypothetical protein HSPC210 (HSPC210), mRNA /cds=(138,605) /gb=NM_016472 /gi=24475986 /ug=Hs.4104 /len=1152			- ÷
13195 13199		hypothetical protein HSPC210 (HSPC210), mRNA /cds=(138,605) /gb=NM_016472 /gi=24475986	NM_016472 NM_020197	Hs.4104 Hs.66170	NP_057556 NP_064582

Cmas		nding To Diff r ntially Express d G ne			
Spot	p-valu	Description	Gene	Unigene	Protein
		*	Acc ssion No.	Accession	Acc ssion
				No.	No.
13202	0.047854	hypothetical protein FLJ12806	NM_022831	Hs.107637	NP_073742
:		(FLJ12806), mRNA /cds=(158,1078)	g+ +		
	٠.	/gb=NM_022831 /gi=12383075			
		/ug=Hs.107637 /len=2485			·
13209	0.042059	zd62d11.s1	W72877	Hs.380971	
		Soares_fetal_heart_NbHH19W cDNA			
	. 0	clone IMAGE:345237 3', mRNA			
	,	sequence /clone=IMAGE:345237			
		/clone_end=3' /gb=W72877 /gi=1383090			
		/ug=Hs.380971 /len=588			
3235	0.026219	Myosin IB, FLJ20153 fis, clone	AK000160	Hs.121576	
3 — <del>- 7</del>		COL08656, highly similar to AJ001381		1.0.121010	
		Homo sapiens incomplete cDNA for a			
. :		mutated allele /cds=UNKNOWN			
٠.,		/gb=AK000160 /gi=7020066	* *	- 30	
•		/ug=Hs.121576 /len=4295			
3247	0.042212	phosphoserine phosphatase (PSPH),	NIM ODAEZZ	Ho 50407	ND 004500
3241	0.042212		NM_004577	Hs.56407	NP_004568
		mRNA /cds=(20,697) /gb=NM_004577			
2054	0.047054	/gi=21614545 /ug=Hs 56407 /len=1432			
3254	0.047854	FLJ14397 (FLJ14397), mRNA	NM_032779	Hs.270981	NP_116168
		/cds=(14,511) /gb=NM_032779		· · ·	
		/gi=14249437 /ug=Hs.270981 /len=1579		*	
. 17					-
3274	0.012883	TAF7 RNA polymerase II, TATA box	NM_005642	Hs 155188	NP_005633
		binding protein (TBP)-associated factor,			
		55kDa (TAF7), mRNA /cds=(741,1790)		*	
	3.	/gb=NM_005642 /gi=14717406			
		/ug=Hs.155188 /len=2310			
3281	0.037129	cDNA FLJ11379 fis, clone	AK021441	Hs.200113	
		HEMBA1000469. /gb=AK021441			*
		/gi=10432627 /ug=Hs.200113 /len=1672		14	
	, ,	3			. ,
3315	0.034784	partial RANBP7 gene for	AJ295844		
		RanBP7/importin7 and partial ZNF143	, 10200011		
		gene	* * * * * * * * * * * * * * * * * * * *		
3320	0.039603	cDNA FLJ23879 fis, clone LNG13743.	AK074459	Hs.352648	
. 5020	0.000000	/gb=AK074459 /gi=18677071	1,1101,4409	113.552046	
	,	/ug=Hs.352648 /len=1514			
13357	0.026506	mRNA; cDNA DKFZp451B1418 (from	AL 920GOO	Ho 446400	
13337	V.UZ0090		AL832622	Hs.446489	· ·
	* †	clone DKFZp451B1418) /gb=AL832622		F	
,	. :	/gi=21733197 /ug=Hs.446489 /len=5612	*	1 .	
10000	0.007000		NISA 00 100 5	10 2555	
13363	0.007388	vacuolar protein sorting 4B (yeast)	NM_004869	Hs.126550	NP_004860
	8 -	(VPS4B), mRNA /cds=(202,1536)			
	A +	/gb=NM_004869 /gi=17865801			
	1	/ug=Hs.126550 /len=3337			l <i>'</i>

Genes	Correspo	nding To Differentially Expressed Genes	s in Figure 15 - H	lyperlipidemia	1
Spot	p-value	Description	Gene	Unigene	Protein
-	,		Accession No.	Accession	Accession
•				No.	No.
13366	0.037129	hypothetical protein DKFZp434I1916	NM 032245	Hs.334641	NP_115621
	1	(DKFZp434l1916), mRNA	<del>-</del>		
		/cds=(144,563) /gb=NM_032245	* (*)	. 18	, -
		/gi=14149959 /ug=Hs.334641 /len=800		1	
13383	0.018694	cytochrome c oxidase subunit VIb	NM 001863	Hs.431668	NP 001854
	Ý.	(COX6B), nuclear gene encoding	<del>-</del>		. —
	<i>t</i> ,	mitochondrial protein, mRNA		ľ	* 1
		/cds=(163,423) /gb=NM_001863			
		/gi=17999530 /ug=Hs.431668 /len=578	***		•
13437	0.002882	nucleolar protein family 6 (RNA-	NM 022917	Hs.183253	NP 631981
. ,		associated) (NOL6), transcript variant	. ,,,,_===== ; .		
	4	alpha, mRNA /cds=(61,3501)			0
		/gb=NM 022917 /gi=22212928	6 .		
4		/ug=Hs.183253 /len=4854	•		-
13443	0.028474	unknown protein	AAA88036		
13456		EST(yx97d08.s1 Soares melanocyte	N26866		
10 100	0.0000	2NbHM clone IMAGE:269679 3' contains	N20000		* · · · · · · · · · · · · · · · · · · ·
1 39	*	Alu and MER22 repeat)	t e		
13471	0.037129	PHD zinc finger protein XAP135	NM_133325	Hs.7759	NP_579866
1.	0.007 120	(XAP135), transcript variant 2, mRNA	11111_100020 .	113.7700	141 _07 3000
		/cds=(222,1448) /gb=NM_133325			0.00
		/gi=19747275 /ug=Hs.7759 /len=1583		*	•
13557	0.001442	UI-E-DW0-agh-g-03-0-UI.s2 UI-E-DW0	BU737016	Hs.444375	
10007	0.001442	cDNA clone UI-E-DW0-agh-g-03-0-UI 3',	00707010	113.444070	·
		mRNA sequence /clone=UI-E-DW0-agh-			
		g-03-0-UI /clone_end=3' /gb=BU737016		40	
		/gi=23672027 /ug=Hs.444375 /len=757	,		
13570	0.002382	601445486F1 NIH MGC 65 cDNA clone	RE868854	Hs.314370	•
100.0	0.002002	IMAGE:3849740 5', mRNA sequence	DE00000#	110.014070	
		/clone=IMAGE:3849740 /clone_end=5'			
		/gb=BE868854 /gi=10317630			**
	·	/ug=Hs.314370 /len=754	:	1	
13584	0.042212	PTK7 protein tyrosine kinase 7 (PTK7),	NM_002821	Hs.90572	NP_690622
'5554	0.072212	transcript variant PTK7-1, mRNA		1.10.00072	
		/cds=(199,3411) /gb=NM_002821	, i	1	
	,	/gi=27886610 /ug=Hs.90572 /len=4249			
13595	0.01/088	zinc finger protein 274 (ZNF274),	NM_133502	Hs.83761	NP_598009
15535	0.014300	transcript variant ZNF274c, mRNA	14W_133302	113.03701	147 _590009
		/cds=(460,2421) /gb=NM 133502	-16-		
3					
13600	0.001170	/gi=19743800 /ug=Hs.83761 /len=2839	NM 015185	Hs.54697	NID OFFICE
13000	0.001179	Cdc42 guanine nucleotide exchange	NINI_U 10 100	115.54097	NP_056000
0 .		factor (GEF) 9 (ARHGEF9), mRNA		_	
		/cds=(802,2352) /gb=NM_015185	·		
12602	0.005075	/gi=7662107 /ug=Hs.54697 /len=5413	NIM 016494	He 0100	ND 057505
13603	0.005275	hypothetical protein HSPC219	NM_016481	Hs.9196	NP_057565
	i '-	(HSPC219), mRNA /cds=(78,1403)			ì
		/gb=NM_016481 /gi=13123781	0		
	<u></u>	/ug=Hs.9196 /len=1664	<u> </u>	I :	<u> </u>

Genes Corresponding To Diff rentially Expressed Genes in Figure 15 - Hyperlipidemia						
	p-valu	D scription	Gene Accession No.	Unigene Acc ssion	Protein Accession	
	, , , , , , , , , , , , , , , , , , ,			No.	No.	
13606	0.037129	phosphoribosylaminoimidazole	NM_006452	Hs.117950	NP 006443	
		carboxylase,	,—			
		phosphoribosylaminoimidazole		1		
		succinocarboxamide synthetase (PAICS),	٠.			
Y		mRNA /cds=(206,1483) /gb=NM_006452			*	
		/gi=17388802 /ug=Hs.117950 /len=3322		**.		
13612	0.039603	poly(rC) binding protein 2 (PCBP2),	NM_005016	Hs.63525	NP_114366	
-		transcript variant 1, mRNA	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \			
		/cds=(89,1189) /gb=NM_005016				
		/gi=14141167 /ug=Hs.63525 /len=1362		·		
13640	0.023151	FLJ20259 (FLJ20259), mRNA	NM_017730	Hs.9956	NP_598328	
		/cds=(24,1274) /gb=NM_017730		•		
		/gi=8923233 /ug=Hs.9956 /len=2022	<i></i>		9	
		(=IMPDH2)		-		
13644	0.04496	AGENCOURT_6497573 NIH_MGC_125	BM544964	Hs.406354	-	
		cDNA clone IMAGE:5588748 5', mRNA			* * * * * * * * * * * * * * * * * * * *	
*		sequence /clone=IMAGE:5588748	* * *			
į.		/clone_end=5' /gb=BM544964	<b> </b>			
, ,		/gi=18776658 /ug=Hs.406354 /len=1184	00	*		
					4.	
13655	0.039405	vacuolar protein sorting 29 (yeast)	NM_057180	Hs.69192	NP_476528	
		(VPS29) transcript variant 2, mRNA				
		/cds=(61,621) /gb=NM_057180			*	
42050	0.042000	/gi=17402911 /ug=Hs.69192 /len=1107	NII 4 00 400 4		NID 00 1055	
13658	0.012883	cyclin-dependent kinase inhibitor 1B	NM_004064	Hs.238990	NP_004055	
*		(p27, Kip1) (CDKN1B), mRNA		`		
		/cds=(466,1062) /gb=NM_004064 /gi=17978497 /ug=Hs.238990 /len=2422		Ì.		
		17976497		0.0		
13659	0.0068	hypothetical protein (HSPC016), mRNA	NM_015933	Hs.397853	NP_057017	
19900	0.0000	/cds=(39,233) /gb=NM_015933	14W_010900	1 13.337 003	MF_05/01/	
		/gi=7705430 /ug=Hs.397853 /len=384		-		
13702	0.047854	mRNA for KIAA0551 protein, partial cds.	AB011123	Hs.170204		
	0.017007	/cds=(192,4349) /gb=AB011123	1,0011120	113.170204		
•	4 4	/gi=20521082 /ug=Hs.170204 /len=5727		0		
		79. 2002 1002 10g (10.17 020 ( 71011 0727		,	70	
13713	0.028474	heterogeneous nuclear ribonucleoprotein	NM 019597	Hs.278857	NP_062543	
7		H2 (H') (HNRPH2), mRNA	*			
-		/cds=(79,1428) /gb=NM_019597	•.	1		
		/gi=14141155 /ug=Hs.278857 /len=2220			* *	
13736	0.042212	hypothetical protein DC50 (DC50),	NM_031210	Hs.324521	NP_112487	
		mRNA /cds=(37,366) /gb=NM_031210	344			
	,	/gi=24475712 /ug=Hs.324521 /len=442				
13748	0.023151	Similar to likely ortholog of yeast ARV1,	BC018945	Hs.290444		
		clone IMAGE:4106796, mRNA				
2.	.*	/gb=BC018945 /gi=17511970	,			
		/ug=Hs.290444 /len=3219	-2-	1		

		nding To Differentially Expressed Gene			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
13788	0.024824	programmed cell death 7 (PDCD7),	NM_005707	Hs.143253	NP 005698
	0.02.02.	mRNA /cds=(56,1513) /gb=NM_005707	,000707	110.110200	
	, , ,	/gi=22027540 /ug=Hs.143253 /len=2866			
		/gi-2202/540/ug-ns.145255/leii-2666		¥	
13794	0.013901	myosin VI (MYO6), mRNA	NM 004999	Hs.118483	NP 004990
× .		/cds=(140,3997) /gb=NM_004999			
		/gi=4826845 /ug=Hs.118483 /len=5212		=	9
13805		mRNA for KIAA1969	AB075849	Hs.373495	*
13003	0.030092	protein/cds=UNKNOWN /gb=AB075849	AD013049	Пэ.57 5495	* *
10000	0.005040	/gi=18916832 /ug=Hs.373495/len=3146	45055070		NE COSOS
13806	0.005942	short form transcription factor C-MAF(c-	AF055376	Hs.30250	NP_005351
		maf) mRNA, complete cds			
		/cds=(807,1928)	- X-	*	
	· · · · · · · · · · · · · · · · · · ·	/gb=AF055376/gi=3335147	*		1.
, -		/ug=Hs.30250 /len=4246	nă.		
13855	0.011929	calpastatin (CAST), transcript variant 2,	NM 173060	Hs.359682	NP_775085
,		mRNA /cds=(155,2215) /gb=NM_173060	1,-		
•		/gi=27765084 /ug=Hs.359682 /len=4296			. 4
	. :				
13888	0.001035	EST(wb25b05.x1 NCI_CGAP_GC6 clone	A1650654		1 13 13
13000	0.00 (933		A1000004		1 2
		IMAGE:2306673 3' contains Alu repeat)			- 20
10000	0.00000	FOT(: 104 107 - 4 NOL COAD LINE	44057000		
13909	0.039603	EST(oh94d07.s1 NCI_CGAP_HN4 clone	AA857009	~	
		IMAGE:1474669 3' contains L1.b1 L1	,,	-1-	
		repeat) 、		ļ	
13926	0.034784	wo08b04.x1 NCI_CGAP_Pan1 cDNA	Al927713	Hs.137546	
•		clone IMAGE:2454703 3', mRNA	-		
	171	sequence /clone=IMAGE:2454703			
		/clone_end=3' /gb=Al927713			
	· ·	/gi=5663677 /ug=Hs 137546 /len=509			*
13933	0.024824	EST(qx14c02.x1 NCI CGAP Lym12	Al358712		
.0000	0.024024	clone IMAGE:2001314 3' contains Alu	/110007 12		
42020	0.000500	and MER4 repeat)	NIM 007024	Î.I 44000	ND 000005
13938	0.026596	DnaJ (Hsp40) subfamily B, member 4	NM_007034	Hs.41693	NP_008965
	, .	(DNAJB4), mRNA /cds=(160,1173)			
	1	/gb=NM_007034 /gi=24431959			
		/ug=Hs.41693 /len=2250			
13946	0.016146	cDNA FLJ13536 fis, clone	AK023598	Hs.11493	
		PLACE1006521. /gb=AK023598		*	
		/gi=10435577 /ug=Hs.11493 /len=2132			·
13954	0.016966	EST nw48e08.s1 NCI_CGAP_Ew1	AA730589	· · · · · ·	
		IMAGE:1249862			
13957	0.003166	echinoderm microtubule associated	NM_019063	Hs.333555	NP 061936
10001	0.000100		11401_013003	1.13.333333	-001930
		protein like 4 (EML4), mRNA	<b>]</b> ,		
•	l .	/cds=(237,3182) /gb=NM_019063			
	<b>.</b>	/gi=19923496 /ug=Hs.333555 /len=5539	1	İ	1
105			1004/055	ļ	
13985	0.042212	EST (wd75h02.x1 NCI_CGAP_Lu24	Al914259	-	
		cDNA clone IMAGE:2337459 3')	1		

0.021575 0.042212	Description  EST(AV713804 DCB cDNA clone DCBAXA05 5') cDNA: FLJ20973 fis, clone ADSU01580, highly similar to HS222E13A Isoform 1 of a novel mRNA from chromosome 22. /gb=AK024626 /gi=10436944 /ug=Hs.334836 /len=3387	Gene Accession No. AV713804 AK024626	Unigene Accession No. Hs.334836	Protein Accession No. NP_004853 NP_835237
0.042212	DCBAXA05 5') cDNA: FLJ20973 fis, clone ADSU01580, highly similar to HS222E13A Isoform 1 of a novel mRNA from chromosome 22./gb=AK024626 /gi=10436944	1 C.		NP_004853
0.042212	DCBAXA05 5') cDNA: FLJ20973 fis, clone ADSU01580, highly similar to HS222E13A Isoform 1 of a novel mRNA from chromosome 22./gb=AK024626 /gi=10436944	1 C.	Hs.334836	
	highly similar to HS222E13A Isoform 1 of a novel mRNA from chromosome 22. /gb=AK024626 /gi=10436944	AK024626	Hs.334836	NP_835237
	a novel mRNA from chromosome 22. /gb=AK024626 /gi=10436944			
0.042212	/gb=AK024626 /gi=10436944			
0.042212				0.0
0.042212	/ug=Hs.334836 /len=3387		i .	13
0.042212				
0.042212	COT 07-42 -4 Cooks 4-45- NUIT	A A 4245 42	200	
	EST zu07e12.r1 Soares_testis_NHT	AA421543		
•	cDNA clone IMAGE:731182 5' similar to			
0.000454	contains L1.t3 L1 repetitive element;	1100151		1
0.023151	EST yt98a02.r1	H96454		1.
		,		
100111		2-2-1	, , , , , , , , , , , , , , , , , , , ,	*
		R26018	0.00	
		NM_012423	Hs.389335	NP_036555
	/gi=14591905 /ug=Hs.389335 /len=1142	0		
				1%.
0.047854	ox08a07.x1	AI023766	Hs.434976	
•	Soares_fetal_liver_spleen_1NFLS_S1	:		
* .	cDNA clone IMAGE:1655700 3', mRNA			i i
97.	sequence /clone=IMAGE:1655700			•
	/clone_end=3' /gb=AI023766	00		:
	/gi=3238810 /ug=Hs.434976 /len=432			
		AA572847		
			· .	
5.63E-04		BM712540	Hs.355827	
			,	÷
		*		
0 .				
				*
	791 10020100 749 110.000021 7011 1112			
0.003392	EST(vg06d08 s1 Soares fetal liver spleen	R91930		
0.000002		1101000		
1			12	
	Similar to contains Ald repetitive elementy		•	
0.047805	similar to CG3714 gene product	NM 145201	Hs 333388	NP 660202
J. 9 / 000		170201	1.15.000000	
		-*		
	/gb=NM_145201 /gi=24475828 /ug=Hs.333388 /len=1198	•		
()	0.021575 0.047854 0.028474 5.63E-04	cDNA clone IMAGE:132647 5')  0.021575 ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=NM_012423 /gi=14591905 /ug=Hs.389335 /len=1142  0.047854 ox08a07.x1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1655700 3', mRNA sequence /clone=IMAGE:1655700 /clone_end=3' /gb=Al023766 /gi=3238810 /ug=Hs.434976 /len=432  0.028474 EST (nf20b09.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:914297)  5.63E-04 UI-E-EJ0-ahh-k-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahh-k-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahh-k-20-0-UI /clone_end=5' /gb=BM712540 /gi=19025798 /ug=Hs.355827 /len=1172  0.003392 EST(yq06d08.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:196143 3' similar to contains Alu repetitive element)  0.047805 similar to CG3714 gene product (PP3856), mRNA /cds=(697,1098)	clone IMAGE:232298 5'  0.032563 EST(yh44h12.r1 Soares placenta Nb2HP cDNA clone IMAGE:132647 5')  0.021575 ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=NM_012423 /gi=14591905 /ug=Hs.389335 /len=1142  0.047854 ox08a07.x1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1655700 3', mRNA sequence /clone=IMAGE:1655700 /clone_end=3' /gb=Al023766 /gi=3238810 /ug=Hs.434976 /len=432  0.028474 EST (nf20b09.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:914297)  5.63E-04 UI-E-EJ0-ahh-k-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahh-k-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahh-k-20-0-UI /clone_end=5' /gb=BM712540 /gi=19025798 /ug=Hs.355827 /len=1172  0.003392 EST(yq06d08.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:196143 3' similar to contains Alu repetitive element)  0.047805 similar to CG3714 gene product (PP3856), mRNA /cds=(697,1098)	Clone IMAGE:232298 5'   C.032563   EST(yh44h12.r1 Soares placenta Nb2HP cDNA clone IMAGE:132647 5')   C.021575   ribosomal protein L13a (RPL13A), mRNA   NM_012423   /cds=(23,634) /gb=NM_012423   /gi=14591905 /ug=Hs.389335 /len=1142   Al023766   Hs.434976   Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1655700 3', mRNA sequence /clone=IMAGE:1655700 /clone_end=3' /gb=Al023766   /gi=3238810 /ug=Hs.434976 /len=432   C.028474   EST (nf20b09.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:914297)   E.63E-04   UI-E-EJ0-ahh-k-20-0-UI r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahh-k-20-0-UI f', mRNA sequence /clone=UI-E-EJ0-ahh-k-20-0-UI /clone_end=5' /gb=BM712540   /gi=19025798 /ug=Hs.355827 /len=1172   C.003392   EST(yq06d08.s1 Soares fetal liver spleen n1NFLS cDNA clone IMAGE:196143 3' similar to contains Alu repetitive element)   NM_145201   Hs.333388   C.047805   Similar to CG3714 gene product (PP3856), mRNA /cds=(697,1098)   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388   NM_145201   Hs.333388

	p-value	nding To Differentially Expressed General Description	Gene	Unigene	Protein
Spor	p-value	Description		T	
			Accession No.	Accession	Accession
44004	0.007000	05-44	A1740000	No.	No.
14231	0.007388	wg85c11.x1	AI743032	Hs.310364	0
		Soares_NSF_F8_9W_OT_PA_P_S1	00 a		· · · · · · · · · · · · · · · · · · ·
•		cDNA clone IMAGE:2371892 3' similar to			
	-	contains Alu repetitive element,, mRNA			*
	·	sequence /clone=IMAGE:2371892	**	\	
	e	/clone_end=3' /gb=AI743032			8 .
•		/gi=5111320 /ug=Hs.310364 /len=562		0	
14246	0.047854	mRNA; cDNA DKFZp564C2063 (from	AL117595	Hs.4055	
		clone DKFZp564C2063) /gb=AL117595			
	· ;*	/gi=5912159 /ug=Hs.4055 /len=1444		* )	*
14259	0.039603	BX109840	BX109840	Hs.269512	
		Soares_fetal_heart_NbHH19W.cDNA			
		clone IMAGp998M11793, mRNA			
		sequence	,, ,		
		/clone=IMAGp998M11793_;_IMAGE:346	,	*	
		930 /gb=BX109840 /gi=27877881	*	, ,	
		/ug=Hs.269512 /len=749	* *		
14266	0.009424	EST, cDNA /clone=IMAGE:1266535	AA729300	Hs.325555	
		/gb=AA729300 /gi=2750659			
		/ug=Hs.325555 /len=173	·	*	
14284	0.024824	hypothetical protein FLJ23751	NM 152282	Hs.37443	NP 689495
7	9.02 1021	(FLJ23751), mRNA /cds=(121,1563)	102202	113.07 110	111 _000-100
		/gb=NM 152282 /gi=22748648			,
		/ug=Hs.37443 /len=2994			
14332	0.023151	EST(cDNA clone IMAGE:1860591 3'	AI199593		
14002	0.020101	similar to contains MER30.b2 MER30	A1100000	x .	-
	÷	repetitive element;)			
14362	0.042212	EST(cDNA clone IMAGE:2446750 3')	AI891033		NP 079440
14377		601864909F1 NIH MGC 57 cDNA clone		Hs.323117	INP_0/9440
14911	0.02 10/0		DI-2404 IS	1115,343111	
• .	. Ο γ	IMAGE:4082978 5', mRNA sequence /clone=IMAGE:4082978 /clone end=5'			* **
•			*		2.
		/gb=BF245413 /gi=11159346	* * *		L
14200	0.000454	/ug=Hs.323117 /len=875	DV007000	11- 000004	
14390	0.023151	BX097880 NCI_CGAP_Thy1 cDNA clone	BY08\880	Hs.208961	
	1	IMAGp998F242841, mRNA sequence	*	l '	-
	1000	/clone=IMAGp998F242841_;_IMAGE:11	* 3		
	*	33207 /gb=BX097880 /gi=27829041			
		/ug=Hs.208961 /len=354	A 1.5.		*
6					
14401	0.01738	df28a02.w1 Morton Fetal Cochlea cDNA	BI492702	Hs.345492	0
	· ·	clone IMAGE:2484387 3', mRNA		<b>.</b>	
		sequence /clone=IMAGE:2484387		1	1
•		/clone_end=3' /gb=BI492702 .			
		/gi=15332046 /ug=Hs.345492 /len=678			
14407	0.028474	EST(HNC (Human Normal Cartilage)	BG928856		NP_598014
	1	Homo sapiens cDNA)			

Genes	Correspon	nding To Differentially Expr ssed Gene	s in Figure 15 - F	lyperlipidemi	a
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14439	0.012481	cDNA FLJ13571 fis, clone PLACE1008405. /gb=AK023633 /gi=10435617 /ug=Hs.116278 /len=2484	AK023633	Hs.116278	
14474	0.044857	EST(cDNA clone IMAGE:4850459 3')	BG745876		
14494	0.009424	No significant match	SEQ.ID.No.70		
14497	0.011929	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), mRNA /cds=(233,1489) /gb=NM_000295 /gi=21361197 /ug=Hs.297681 /len=1584	NM_000295	Hs.297681	NP_000286
14513	0.042212	EST(aj44d01.s1 Soares testis NHT clone 1393153 3' contains Alu and KER repeat)	AA813111		NP_057336
14527	0.014988	URB mRNA, complete cds /cds=(146,2998) /gb=AF506819 /gi=21039408 /ug=Hs.356289 /len=3320	AF506819	Hs.356289	
14543	0.039405	low density lipoprotein receptor-related	NM 002336	Hs.23672	NP_002327
-		protein 6 (LRP6), mRNA /cds=(78,4919) /gb=NM_002336 /gi=4505016 /ug=Hs.23672 /len=5301		*	
14546	0.005275	EST (601819273F1 NIH_MGC_58 cDNA clone IMAGE:4051098 5')	BF130672		NP_003655
14547	0.030134	cDNA FLJ11469 fis, clone HEMBA1001658. /gb=AK021531 /gi=10432731 /ug=Hs.224398 /len=1665	AK021531	Hs.224398	
14563	0.042212	df13e04.y1 Morton Fetal Cochlea cDNA clone IMAGE:2483406 5', mRNA sequence /clone=IMAGE:2483406 /clone_end=5' /gb=AW020719	AW020719	Hs.233140	
14639	0.028474	/gi=5874249 /ug=Hs.233140 /len=357 EST (no81g07.s1 NCI_CGAP_AA1	AA613881		
14664	0.021575	IMAGE:1113276 3') EST(ob01g03.s1 NCI_CGAP_Kid3 cDNA clone IMAGE:1322452 3')	AA740661	· · · · · · · · · · · · · · · · · · ·	NP_055459
14682	0.047854	clone IMAGE: 5227612, mRNA /gb=BC043650 /gi=27693174 /ug=Hs.378059 /len=3723	BC043650	Hs.378059	
14688	0.019682	cDNA FLJ34825 fis, clone NT2NE2008785, weakly similar to ANTER-SPECIFIC PROLINE-RICH PROTEIN APG. /gb=AK092144 /gi=21750666 /ug=Hs.376593 /len=2130	AK092144	Hs.376593	
14698	0.002382	EST(MR1-MT0282-191200-005-b11 MT0282 cDNA)	BF904004		

G nes	Corr spoi	nding To Differentially Express d Gene	s in Figure 15 - F	lyperlipidemi:	a
Spot	*	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14708	0.028474	FLJ11397 fis, clone HEMBA1000622 /cds=UNKNOWN /gb=AK021459 /gi=10432651 /ug=Hs.169068 /len=1512	AK021459	Hs.169068	
14781	0.020091	UI-1-BC1-ajq-h-10-0-UI.s1 NCI_CGAP_PI2 cDNA clone UI-1-BC1- ajq-h-10-0-UI 3', mRNA sequence /clone=UI-1-BC1-ajq-h-10-0-UI /clone_end=3' /gb=BQ010713 /gi=19735614 /ug=Hs.281575 /len=1108	BQ010713	Hs.281575	
14797	0.032563	EST (3' end clone=IMAGE:2540192) /clone_end=3' /gb=Bl495875 /gi=15335219./ug=Hs.347887 /len=354	BI495875	Hs.347887	NP_003109
<b>14804</b>	0.039603	splicing factor, arginine/serine-rich 12 (SFRS12), mRNA /cds=(342,1868) /gb=NM_139168 /gi=21040254 /ug=Hs.381165 /len=3811	NM_139168	Hs.381165	NP_631907
14819	0.012481	FLJ14036 fis, clone ( HEMBA1004709/cds=UNKNOWN /gb=AK024098 /gi=10436394 /ug=Hs.306663/len=2067	AK024098	Hs.306663	, , , , , , , , , , , , , , , , , , ,
14875	0.04496	RC1-NN0073-090500-012-f02 NN0073 cDNA, mRNA sequence /gb=AW898615 /gi=8062820 /ug=Hs 130729 /len=660	AW898615	Hs.130729	
14937					
14948		EST(Fetal Cochlea Homo sapiens cDNA clone IMAGE:2537435 5')	BI497119		NP_006826
		No significant match	SEQ.ID.No.38		
14962	0.037729	No significant match, ORF+3(30~140),+2(131~232)	SEQ.ID.No.72		

<u> </u>		TABLE 3 I			
		nding To Diff rentially Expressed Gen	es in Figure 16 -	LungDisease	
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
- ,,			100	No.	No.
1	0.010368	vacuolar protein sorting 28 (yeast)	NM_016208	Hs.339697	NP_057292
	1	(VPS28), mRNA /cds=(62,727)			
		/gb=NM_016208 /gi=7705884			
* *		/ug=Hs.339697 /len=928			
10	0.02571	JTV1 gene (JTV1), mRNA	NM_006303	Hs.301613	NP_006294
		/cds=(114,1076) /gb=NM_006303			
•		/gi=11125769 /ug=Hs.301613 /len=1221	1	,	
0					
18		histone H1 (0)	X03473		
22	0.025072	54TMp (54tm) (=S83365 RAB5-	AF004876		NP_065203
	14	interaction protein)		4.7	-
23	0.042048	1-aminocyclopropane-1-carboxylate	NM_032592	Hs.126706	NP_115981
		synthase (PHACS), mRNA			× .
	•	/cds=(396,1901) /gb=NM_032592	- * >		0
		/gi=14211920 /ug=Hs.126706 /len=2167			
					* =
65	0.012669	glycoprotein, synaptic 2 (GPSN2),	NM 138501	Hs.306122	NP 612510
•. •		mRNA /cds=(90,1016) /gb=NM 138501	· -		
	* .	/gi=24762237 /ug=Hs.306122 /len=1139	,		
					-
83	0.026766	angiotensin II receptor-like 2 (AGTRL2),	NM 005162	Hs.433156	NP 005153
	X	mRNA /cds=(1481,1696)	7		
		/gb=NM_005162 /gi=6031157			
* 4	• _	/ug=Hs.433156 /len=1816			
97	0.027356	hypothetical protein BC009925	NM 138425	Hs.405913	NP_612434
	-	(LOC113246), mRNA /cds=(92,472)			_
		/gb=NM_138425 /gi=19923950		·	
	*	/ug=Hs.405913 /len=583	0		
100	0.036684	gene predicted from cDNA with a	NM_004906		NP 690597
-		complete coding sequence			
9	-	(KIAA0105)= D14661.1	•	*. *	
101	0.048502	conserved gene amplified in	NM_005730	Hs.355816	NP_005721
		osteosarcoma (OS4), mRNA	0007.00		000 <u>/</u> 2 :
	•	/cds=(306,1157) /gb=NM_005730	,		=
	. *	/gi=19923329 /ug=Hs.355816 /len=4833		· .	
	15.	/gr 10020020 /ug 110.0000 10 /ioii 1000			
103	0.040325	supervillin (SVIL), transcript variant 2,	NM_021738	Hs.154567	NP_068506
,		mRNA /cds=(754,7398)			-====================================
		/gb=NM_021738 /gi=11496981		`` '	*
		/ug=Hs.154567 /len=8300	7		
132	0.046353	phosphatidylinositol glycan, class C	NM 153747	Hs.433030	NP_714969
102	J.U-0000	(PIGC), transcript variant 1, mRNA	14101-193747	11,3.40,000	1.14909
		/cds=(312,1205) /gb=NM_153747		·	
		/cds=(312,1203)7gb=NM_133747 /gi=24430185 /ug=Hs.433030 /len=1514	, '	,	
		/MI= /A/13(11)85 /HM=HE /1321/141 /A6=1514			

		nding To Differentially Expressed G n			
Spot	p-value		Gene	Unigene	Protein
		*	Accession No.	Acc ssion	Accession
				No.	No.
133	0.040325	phosphodiesterase 2A, cGMP-	NM_002599	Hs.154437	NP_002590
		stimulated (PDE2A), mRNA			-
		/cds=(162,2987) /gb=NM_002599	1.2		
		/gi=4505656 /ug=Hs.154437 /len=4240	. •		
			t		*
140	0.020104	yg33d08.s1 Soares infant brain 1NIB	R44968	Hs.412527	
		cDNA clone IMAGE:34540 3', mRNA		1.0.112027	
		sequence /clone=IMAGE:34540			
		/clone_end=3' /gb=R44968 /gi=824322	*		
:		/ug=Hs.412527 /len=453			
148	0.007267	wl84f02.x1 NCI_CGAP_Brn25 cDNA	Al884779	Hs.380770	<del> </del>
140;	0.007207	clone IMAGE:2431611 3', mRNA	7100 <del>4113</del>	1115.500770	
		sequence /clone=IMAGE:2431611	*	÷ ;	
		· ·		*	,
		/clone_end=3' /gb=AI884779			
400	0.040004	/gi=5589943 /ug=Hs.380770 /len=527	NIM 007405	11- 074000	NID COCAGE
186	0.016234	polymerase (DNA directed) iota (POLI),	NM_007195	Hs.271699	NP_009126
		mRNA /cds=(65,2212) /gb=NM_007195			
		/gi=6005847 /ug=Hs.271699 /len=2484	- *		
	L				```
208	0.005681	ubiquitin-like 3 (UBL3), mRNA	NM_007106	Hs.173091	NP_009037
	4 E .	/cds=(110,463) /gb=NM_007106	0)		
		/gi=6005927 /ug=Hs.173091 /len=3323			ľ
				- 00	
211	0.002965	Splicing factor, arginine/serine-rich,	NM_032102	Hs.155160	NP_115285
		46kD (SRP46), mRNA /cds=(283,1131)			
•	Ì	/gb=NM_032102 /gi=15055542		. *	•
		/ug=Hs.155160 /len=2186			
			•		
218	0.030215	mRNA for KIAA0650 protein, partial	AB014550	Hs.8118	
	*	cds. /cds=(1,2549) /gb=AB014550			
		/gi=3327113 /ug=Hs.8118 /len=5003			
229	0.024727	activating transcription factor 6 (ATF6),	NM_007348	Hs.5813	NP_031374
		mRNA /cds=(43,2055) /gb=NM_007348	_		
		/gi=6671584 /ug=Hs.5813 /len=2474		1	
		<u> </u>			<b>\</b>
244	0.048502	protocadherin 18 (PCDH18), mRNA	NM_019035	Hs.97266	NP 061908
		/cds=(388,3795) /gb=NM 019035			
	,	/gi=14589928 /ug=Hs.97266 /len=5157	,		:
247	0.042188	G protein-coupled receptor Edg-2	Y09479		NP_476500
248		hemoglobin, beta (HBB), mRNA	NM_000518	Hs.155376	NP_000509
		/cds=(51,494) /gb=NM_000518			
		/gi=28302128 /ug=Hs.155376 /len=626			-
	- 37			0	
254	0.033310	cytoplasmic FMR1 interacting protein 1	NM 014608	Hs.77257	NP_055423
204	0.000019	(CYFIP1), mRNA /cds=(53,3814)	   4000	113.77237	141 _000423
		1 ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '	· .		9
		/gb=NM_014608 /gi=24307968		1	
	1 .	/ug=Hs.77257 /len=4394	l	I .	i

Spot	Correspo p-value	Description	Gene	Unigene	Protein
Opor	p vuiue	Besonpagn	Accession No.	Accession	Acc ssion
264	0.048502	zinc finger protein 22 (KOX 15)	NM 006963	<b>No.</b> Hs.108642	<b>No.</b> NP_008894
	0.010002	(ZNF22), mRNA /cds=(90,779)	1111_000000	110.100012	
<i>i</i> *		/gb=NM_006963 /gi=5902159	.**		-
	- (X)	/ug=Hs.108642 /len=798		* *	
285	0.033319	torsin family 1, member B (torsin B)	NM 014506	Hs.252682	NP_055321
		(TOR1B), mRNA /cds=(61,1071)	<del>-</del>		
		/gb=NM_014506 /gi=14149652			
• .	, 3	/ug=Hs.252682 /len=2774			-27
311		Ankhzn mRNA,	AB011370		NP 033801
317	0.048502	J domain containing protein 1 (JDP1),	NM_021800	Hs.260720	NP 068572
		mRNA /cds=(154,750) /gb=NM 021800	· · · · · ·		_
		/gi=11141870 /ug=Hs.260720 /len=1203			
			*		*,
328	0.016234	EST(yj40f11.r1 clone 151245 5')	H02533	,	NP_705833
336	0.040325	mRNA for KIAA0570 protein, partial	AB011142	Hs.180948	
		cds. /cds=(480,10718) /gb=AB011142	*		
		/gi=20521084 /ug=Hs.180948		*	
		/len=11269			
422	0.040325	mRNA; cDNA DKFZp686C117 (from	AL832773	Hs.433512	
		clone DKFZp686C117) /gb=AL832773			
-		/gi=21733355 /ug=Hs.433512 /len=5984			
· <u> </u>			3	*	8
468		hypothetical protein (KIAA1333)	AB037754	W Y	NP_060239
480	0.044069	heparin-binding neurite outgrowth	S60110		
		promoting factor (genomic sequence)			· ·
483	0.035609	DXS8237E (=D50912 hypothetical	U35373		NP_690595
		protein (KIAA0122))	t.		
484	0.028538	troponin T1, skeletal, slow (TNNT1),	NM_003283	Hs.73980	NP_003274
	-	mRNA /cds=(149,904) /gb=NM_003283			
		/gi=21359857 /ug=Hs.73980 /len=1018			
485	0.036684	GNAS complex locus (GNAS),	NM_080425	Hs.374523	NP_536351
		transcript variant 3, mRNA	Φ.	÷ ,	-
		/cds=(1,2730) /gb=NM_080425	0		
		/gi=18426897 /ug=Hs.374523 /len=3091	,		
400	0.044000			1. 22 :	
489	0.044069	tyrosine 3-monooxygenase/tryptophan 5	NM_006761	Hs.79474	NP_006752
		monooxygenase activation protein,	,		·
		epsilon polypeptide (YWHAE), mRNA			*
,		/cds=(80,847) /gb=NM_006761			
		/gi=21328449 /ug=Hs.79474 /len=1776		<u> </u>	
400	0.027905	outoobromo o ovidose automit VIII.	NIM .004007	Un 400075	ND 004050
492	0.02/895	cytochrome c oxidase subunit VIIc	NM_001867	Hs.430075	NP_001858
		(COX7C), nuclear gene encoding			
•		mitochondrial protein, mRNA			∞
		/cds=(90,281) /gb=NM_001867	* •		
		/gi=18105039 /ug=Hs.430075 /len=448		i	ŀ

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	100			No.	No.
515	0.035609	ribosomal protein L13 (RPL13),	NM_033251	Hs.431392	NP_150254
		transcript variant 2, mRNA			٠.
	-	/cds=(238,873) /gb=NM_033251		*	
		/gi=15431294 /ug=Hs.431392 /len=1296			•
- 30 (				*	
519	0.030468	splicing factor (45kD) (SPF45), mRNA	NM 032905	Hs.107001	NP 116294
		/cds=(148,1353) /gb=NM_032905			
		/gi=14249677 /ug=Hs.107001 /len=1566			
*	300				
531	0.014265	tumor rejection antigen (gp96) 1	NM 003299	Hs.82689	NP_003290
ŲŪ,	0.014200	(TRA1), mRNA /cds=(106,2517)	14141_000239	113.02003	141 _000230
		/gb=NM_003299 /gi=4507676			
		/ug=Hs.82689 /len=2780			
522	0.027256		NM 000184	Un 206655	NP 000175
533	0.027330	hemoglobin, gamma G (HBG2), mRNA	NIVI_000104	Hs.386655	INP_000175
		/cds=(54,497) /gb=NM_000184	Species .		
		/gi=28302132 /ug=Hs.386655 /len=583		* . **	
560	0.017207	quiescin Q6 (QSCN6), mRNA	NM_002826	Hs.77266	NP_002817
*		/cds=(76,2319) /gb=NM_002826			
* .	-8.	/gi=13325074 /ug=Hs.77266 /len=3314		,	., -
		0.5	· ·		
602	0.020912	helicase with zinc finger domain	NM_014877	Hs.3085	NP_055692
		(HELZ), mRNA /cds=(146,5974)			
		/gb=NM_014877 /gi=7661883			- 1
		/ug=Hs.3085 /len=6274		* *	
647	0.046353	xu91a05.x1 NCI_CGAP_Ut2 cDNA	AW515080	Hs.180241	
ė		clone IMAGE:2809040 3', mRNA	,		
		sequence /clone=IMAGE:2809040			Ì
		/clone_end=3' /gb=AW515080			
		/gi=7153162 /ug=Hs.180241 /len=487			
651	0.030215	B lymphoma Mo-MLV insertion region	NM 005180	Hs.380403	NP_005171
<b>55</b> ,	3.0002,0	(mouse) (BMI1), mRNA	1000.00	1.10.000	
		/cds=(515,1495) /gb=NM_005180		, ,	*
		/gi=27883841 /ug=Hs.380403 /len=3260	_ /	3: 3	4
		/g -2700504174g=113.50040571e11-5200 			[
659	0.038336	mRNA; cDNA DKFZp564F053 (from	AL049265	Hs.71968	<del></del>
039	0.030330	clone DKFZp564F053) /gb=AL049265	AL049203	115.7 1300	ŀ
				. 1	
000	0.040000	/gi=4500013 /ug=Hs.71968 /len=2864	A5457500	· · · · · · · ·	N.D. 00440
682		alpha endosulfine	AF157509	11112	NP_004427
684	0.009227	tumor necrosis factor receptor	NM_001065	Hs.159	NP_001056
		superfamily, member 1A (TNFRSF1A),			1.
		mRNA /cds=(282,1649)	7		*
		/gb=NM_001065 /gi=23312372		· .	÷ .
		/ug=Hs.159 /len=2236			
689	0.016234	PTK2 protein tyrosine kinase 2 (PTK2),	NM_153831	Hs.740	NP_722560
	*	transcript variant 1, mRNA			ļ
	· ·	/cds=(231,3389) /gb=NM_153831		,	1
	1 .	/gi=27886591 /ug=Hs.740 /len=4453	1.00	l	1

		nding To Differentially Expressed Gen			
Spot	p-value	D scription	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
690	0.008196	mRNA for KIAA0518 protein, partial	AB011090	Hs.23763	+ 5
		cds. /cds=(1,1953) /gb=AB011090			
		/gi=3043559 /ug=Hs.23763 /len=4617	•		
697	0.020104	interferon, alpha-inducible protein (clone	NM 022873	Hs.265827	NP 07501
-2		IFI-6-16) (G1P3), transcript variant 3,	7		
÷	-	mRNA /cds=(108,524) /gb=NM 022873	÷		
Χ.		/gi=13259549 /ug=Hs.265827 /len=841		8	* .
**		/gi-13239349 /dg-113.203021 /icii-04 /		i .	
711	0.044250	NADU dobydrogopoo (whiguingpo) 1	NIM OOFOOD	Up 75007	ND 00400
711	0.044259	NADH dehydrogenase (ubiquinone) 1	NM_005002	Hs.75227	NP_00499
- 8-		alpha subcomplex, 9, 39kDa			1
	1.	(NDUFA9), mRNA /cds=(20,1153)		1	
	*	/gb=NM_005002 /gi=20127470		- 2	
	100	/ug=Hs.75227 /len=1343			
712		KIAA1224	AB033050		
730	0.044259	PTD016 protein (LOC51136), mRNA	NM_016125	Hs.30154	NP_057209
		/cds=(183,809) /gb=NM_016125		*	
		/gi=21361528 /ug=Hs.30154 /len=1917			*
747;	0.040325	stanniocalcin 1 (STC1), mRNA	NM_003155	Hs.25590	NP_00314
	5.0 15025	/cds=(285,1028) /gb=NM_003155	11000100	110.2000	
	) .	/gi=4507264 /ug=Hs.25590 /len=3901			1.
753	0.003960	aminoadipate-semialdehyde	NM 015423	Hs.64595	NP 05623
ି / ၁১	0.003669	1.	19191_015423	IU8'04090	NP_056236
	٠-	dehydrogenase-phosphopantetheinyl			8
	*	transferase (AASDHPPT), mRNA	· ·		i i
	*	/cds=(147,1076) /gb=NM_015423			
		/gi=20357567 /ug=Hs.64595 /len=2880	.'		]
(					
771	0.020104	zinc finger protein (ZFD25) (62% aa)	AB027251		NP_05730
775	0.018081	cofilin isoform 1	AF134802		NP_06873:
786	0.040325	syntaxin 8 (STX8), mRNA	NM_004853	Hs.380938	NP_004844
		/cds=(151,861) /gb=NM_004853			_
		/gi=4759187 /ug=Hs.380938 /len=979	0		
789	0.010368	LPS-responsive vesicle trafficking,	NM_006726	Hs.62354	NP 00671
	1.5,5,50	beach and anchor containing (LRBA),			
	. *	mRNA /cds=(245,8836)			,
	1				· · · · · · · · · · · · · · · · · · ·
		/gb=NM_006726 /gi=16904380		Į	-
044	000005	/ug=Hs.62354 /len=9909	104 000000	11 75700	ND 00007
. 811	0.002965	sterol carrier protein 2 (SCP2), mRNA	NM_002979	Hs.75760	NP_00297
		/cds=(22,1665) /gb=NM_002979			
	İ	/gi=19923232 /ug=Hs.75760 /len=2572			
				<u> </u>	
816	0.01302	X-ray repair complementing defective	NM_022550	Hs.150930	NP_07204
		repair in Chinese hamster cells 4			
		(XRCC4), transcript variant 3, mRNA		[ '	
		/cds=(176,1180) /gb=NM_022550	*		
		/gi=12408648 /ug=Hs.150930 /len=1707			1
		1/9. 12-1000-10 149-118. 100800 11611-1101	1.	1	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigen	Protein
			Accession No.	Accession	Accession
833	0.016234	NADH dehydrogenase (ubiquinone) 1	NM 002491	<b>No.</b> Hs.109760	<b>No.</b> NP_002482
000	0.010234	beta subcomplex, 3, 12kDa (NDUFB3),	NIVI_002491	ms. 109760	NP_002402 
	,	mRNA /cds=(253,549) /gb=NM_002491	• •		
		/gi=4505360 /ug=Hs.109760 /len=693			
		/gi=4505500 /dg=118.109700 /le11=095	*	*	
834	0.024727	tetraspan 3 (TSPAN-3), mRNA	NM_005724	Hs.100090	NP_005715
		/cds=(218,979) /gb=NM_005724		*	
		/gi=21264581 /ug=Hs.100090 /len=1842			
857	0.027356	mitochondrial carrier 1 (MTCH1),	NM 014341	Hs.279939	NP_055156
	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	nuclear gene encoding mitochondrial	11111_0 131041	113.273333	_000100
		protein, mRNA /cds=(1,1119)			. 2
		/gb=NM_014341 /gi=7657344			
		/ug=Hs.279939 /len=1890			
879	0.044259	laminin, beta 1 (LAMB1), mRNA	NM_002291	Hs.82124	NP_002282
		/cds=(336,5696) /gb=NM_002291	7.7		
		/gi=4504950 /ug=Hs.82124 /len=5831			
880	0.016234	mRNA; cDNA DKFZp667D087 (from	AL833217	Hs.348420	
		clone DKFZp667D087) /gb=AL833217		· ·	
		/gi=21733848 /ug=Hs.348420 /len=3440		95	* *
					· .
881	0.005008	CBF1 interacting corepressor (CIR),	NM_004882	Hs.89421	NP_004873
		mRNA /cds=(33,1388) /gb=NM_004882	_		_
		/gi=21361177 /ug=Hs.89421 /len=1519		, .	
			·	,	0.0
882	0.048502	hypothetical protein H41 (H41), mRNA	NM_017548	Hs.283690	NP_060018
		/cds=(324,1100) /gb=NM_017548			
	. '	/gi=24475997 /ug=Hs.283690 /len=3346			
<u> </u>					v
887	0.008196	polyadenylate binding protein-interacting	NM_006451	Hs.109643	NP_006442
		protein 1 (PAIP1), mRNA	•		7
		/cds=(188,1627) /gb=NM_006451			
		/gi=17511254 /ug=Hs 109643 /len=2764			,
900	0.040005		NIM 000070	11- 404000	ND coocs
892	0.040325		NM_003270	Hs.121068	NP_00326
		6 (TM4SF6), mRNA /cds=(104,841)	*		
		/gb=NM_003270 /gi=21265115		l	
016	0.014554	/ug=Hs.121068 /len=2069	NIM 004007		ND 004074
916	0.01 <del>4</del> 551	LIM and senescent cell antigen-like	NM_004987		NP_004978
		domains 1 (LIMS1) =U09284, PINCH protein			
918	0.024727	AGENCOURT_6456859 NIH_MGC_92	BM466169	Hs.439148	
510	0.024727	cDNA clone IMAGE:5576908 5', mRNA	I DINIHOO IOS	113.433140	
		sequence /clone=IMAGE:5576908			
		/clone_end=5' /gb=BM466169	•		
		/gi=18515211 /ug=Hs.439148 /len=1150			
	1	pg:= 100 102 1 1 10g=115.403 140 /1811- 1 150	1	1	

		nding To Differentially Expressed Gen			
Spot	p-value	D scription	Gen Accession No.	Unigene Accession No.	Protein Accession No.
919	0.044259	putative protein tyrosine phosphatase	U93051	Hs.356062	NP_000305
	# * · · · · · · · · · · · · · · · · · ·	(PTEN) mRNA, complete cds /cds=(1,1212) /gb=U93051 /gi=1916351 /ug=Hs.356062 /len=1212			
935	0.030215	Fc fragment of IgE, high affinity I,	NM_004106	Hs.433300	NP_004097
•	a .	receptor for; gamma polypeptide (FCER1G), mRNA /cds=(26,286) /gb=NM_004106 /gi=4758343 /ug=Hs.433300 /len=591			
963	0.048502	nucleoporin 153kDa (NUP153), mRNA /cds=(201,4628) /gb=NM_005124	NM_005124	Hs.211608	NP_005115
-		/gi=24430145 /ug=Hs.211608 /len=5687	- *	*	*
967	0.022315	hepatoma-derived growth factor (high-	NM_004494	Hs.89525	NP_004485
		mobility group protein 1-like) (HDGF), mRNA /cds=(316,1038)		7)	
		/gb=NM_004494 /gi=4758515 /ug=Hs.89525 /len=2376	v :		190
996	0.040325	mitochondrion, complete genome	NC 001807		
1001		RAD23 B (S. cerevisiae) (RAD23B), mRNA /cds=(352,1581) /gb=NM_002874 /gi=19924138	NM_002874	Hs.404283	NP_002865
		/ug=Hs.404283 /len=2943	1		
1005	0.020104	splicing factor (45kD) (SPF45), mRNA /cds=(148,1353) /gb=NM_032905	NM_032905	Hs.107001	NP_116294
٠,		/gi=14249677 /ug=Hs.107001 /len=1566			
1021	0.022315	tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA	NM_006290	Hs.211600	NP_006281
		/cds=(67,2439) /gb=NM_006290 /gi=26051241 /ug=Hs.211600 /len=4446			* .
1034	0.010368	N-myristoyltransferase 2 (NMT2), mRNA /cds=(47,1543) /gb=NM_004808	NM_004808	Hs.122647	NP_004799
		/gi=4758815 /ug=Hs.122647 /len=2838	,		:
1184	0.033319	mannosidase, alpha, class 1A, member 2 (MAN1A2), mRNA /cds=(521,2446)	NM_006699	Hs.367638	NP_006690
		/gb=NM_006699 /gi=5729912 /ug=Hs.367638 /len=2792	*	,	,
1193	0.011629	CGI-100 protein (CGI-100), mRNA /cds=(113,802) /gb=NM_016040 /gi=19923441 /ug=Hs.348996 /len=3635	NM_016040	Hs.348996	NP_057124

		nding To Differentially Expressed Gen			
Spot	p-value		Gene	Unigene	Protein
			Accession No.	Accession	Accession
	22.242.22			No.	No.
1213	0.044259	heat shock 10kDa protein 1 (chaperonin	NM_002157	Hs.1197	NP_002148
•		10) (HSPE1), mRNA /cds=(42,350)			
		/gb=NM_002157 /gi=4504522	* .	,	l
		/ug=Hs.1197 /len=538			
1278	0.027356	clone IMAGE:5311364, mRNA	BC042008	Hs.97093 ✓	
		/gb=BC042008 /gi=27469534			
		/ug=Hs.97093 /len=2520			
1307	0.033319	epithelial membrane protein 1 (EMP1),	NM_001423	Hs.79368	NP_001414
		mRNA /cds=(219,692) /gb=NM_001423			
		/gi=4503558 /ug=Hs.79368 /len=2786	*		
			* * * * * * * * * * * * * * * * * * * *	1.	· .
1314	0.00507	RAB, member of RAS oncogene family-	NM 006860	Hs.50267	NP 00685
		like 4 (RABL4), mRNA /cds=(364,921)			
		/gb=NM_006860 /gi=9257237	,	0 8	
		/ug=Hs.50267 /len=1021			
1408	0.016234	dihydrolipoamide dehydrogenase (E3	NM_000108	Hs.74635	NP_000099
1.120		component of pyruvate dehydrogenase	11000 100	1110.111000	
		complex, 2-oxo-glutarate complex,			
•	* *	branched chain keto acid	*.		*
		dehydrogenase complex) (DLD), mRNA		·	•
		/cds=(83,1612) /gb=NM_000108		'.	
	, (				
		/gi=5016092 /ug=Hs.74635 /len=2320		-	Ì
1437	0.007267	SRY (sex determining region Y)-box 9	NM 000346	Hs.2316	NP_000337
1437	0.007207		NIVI_000346	IUS.5310	INP_00033
	,	(campomelic dysplasia, autosomal sex-		ļ	(
	,	reversal) (SOX9), mRNA	•		
1	·	/cds=(373,1902) /gb=NM_000346	•		
4.440	0.040005	/gi=4557852 /ug=Hs.2316 /len=3936	,		
1443	0.040325	cDNA FLJ13106 fis, clone	AK023168	Hs.12707	ļ
		NT2RP3002455, highly similar to mRNA			
		for KIAA0678 protein. /gb=AK023168			
		/gi=10434970 /ug=Hs.12707 /len=3985			
			: 122	<u> </u>	
1444	0.036684	cDNA: FLJ23165 fis, clone LNG09846.	AK026818	Hs.279898	
	,	/gb=AK026818 /gi=10439763	•		1
		/ug=Hs.279898 /len=2117	_		
15	*				
1451	0.01302	polymerase (RNA) II (DNA directed)	NM_002696	Hs.14839	NP_002687
	)	polypeptide G (POLR2G), mRNA	. •		ì
		/cds=(107,625) /gb=NM_002696			
		/gi=4505946 /ug=Hs.14839 /len=828			
1453	0.036684	methyl-CpG binding domain protein 2	NM_015832	Hs.25674	NP_05664
-		(MBD2), transcript variant testis-			]
		specific, mRNA /cds=(230,1138)	2	÷	
		/gb=NM_015832 /gi=21464120	G ()		
		,	i (		

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gen	Unigene	Prot in
	-		Accession No.	Accession	Accession
				No.	No.
1488	0.022315	mannan-binding lectin serine protease 2	NM_006610	Hs.119983	NP_631947
		(MASP2), transcript variant 1, mRNA			
	- 34	/cds=(22,2082) /gb=NM_006610			l. ·
),		/gi=21264362 /ug=Hs.119983 /len=2460			. 4
		79. 2120 1002 749 113.110000 71611 2-100	Y.	÷	
1502	0.030215	putative dimethyladenosine transferase	NM 014473	Hs.125819	NP_055288
1002	0.0002.10	(HSA9761), mRNA /cds=(79,1020)	14101_014473	113.123013	141 _000200
	. *	/gb=NM_014473 /gi=7657197			ì
		/ug=Hs.125819 /len=1505	-		
1544	0.027356	hypothetical protein FLJ10357	NM_018071	Hs.22451	NP_060541
1344	0.027330		141VI_010071	IDS.22451	NF_000541
	[	(FLJ10357), mRNA /cds=(67,903)			
		/gb=NM_018071 /gi=8922375	;	*	
		/ug=Hs.22451 /len=1450	<u> </u>		
1555		KIAA1573 mRNA protein	AB046793		
1575	0.027356	WW domain-containing adapter with a	NM_100264	Hs.70333	NP_567823
		coiled-coil region (WAC), transcript			
		variant 2, mRNA /cds=(332,2140)		,	
		/gb=NM_100264 /gi=18379329		i .	
	L	/ug=Hs.70333 /len=3088			
1614	0.036684	hypothetical protein FLJ10579	NM 018145	Hs.8055	NP 060615
, , , , , ,		(FLJ10579), mRNA /cds=(186,1598)	10.0	1.10.0000	
		/gb=NM_018145 /gi=8922531			
•		, , <u> </u>		·	
1010	0.020245	/ug=Hs.8055 /len=2251	A D 0 4 4 4 4 2	Un 400040	
1618	0.030215	mRNA for KIAA0570 protein, partial	AB011142	Hs.180948	-
		cds. /cds=(480,10718) /gb=AB011142			
1		/gi=20521084 /ug=Hs.180948	- 10		
		/len=11269			ļ
1711	0.010368	KIAA0682 gene product (KIAA0682),	NM_014852	Hs.7482	NP_057280
		mRNA /cds=(80,2962) /gb=NM_014852	2.5		
		/gi=7662249 /ug=Hs.7482 /len=4422			
1741	0.036684	mRNA; cDNA DKFZp586F1822 (from	AL117461	Hs.82719	
		clone DKFZp586F1822) /gb=AL117461			
	(	/gi=5911922 /ug=Hs.82719 /len=3943			:
		g. oo tto za rag tto to to to to			* *
1749	0.033319	hypothetical protein MGC20781	NM 052935	Hs.237536	NP 443167
1740	0.000010	(MGC20781), mRNA /cds=(366,1139)	14141_002000	113.207000	_440107
		/gb=NM 052935 /gi=16418414		-	
•	3	,	*		
4770	0.040004	/ug=Hs.237536 /len=1476	DUIDOGGG	11 074050	
1778	0.018081	UI-CF-FN0-aet-p-19-0-UI s1 UI-CF-FN0	B0089895	Hs.374350	
	,an .	cDNA clone UI-CF-FN0-aet-p-19-0-UI	<b>,</b>	,	1
•		3', mRNA sequence /clone=UI-CF-FN0-	. *	1	
•	[	aet-p-19-0-UI /clone_end=3'		1	
		/gb=BU689895 /gi=23548080		1.	
		/ug=Hs.374350 /len=1121	. 6		
1830	0.024727	calmodulin-I (CALM1) mRNA, 3'UTR,	U16850	Hs.374441	7
		partial sequence. /gb=U16850	] - ; <del>-</del> - ;		

Snot	p-value	nding To Differ Intially Expressed Gene Description	Gene	Unigene	Protein
Shor	p-value	Description		_	
•			Accession No.	Accession No.	Accession No.
1847	0.01302	tropomyosin 3 (TPM3), mRNA	NM 153649	Hs.85844	NP_705935
, .		/cds=(52,798) /gb=NM 153649			
		/gi=24119202 /ug=Hs.85844 /len=2089	*	1.5	. •
1878	0.024727	capping protein (actin filament), gelsolin-	NM_001747	Hs.82422	NP_001738
		like (CAPG), mRNA /cds=(50,1096)			_
	. *	/gb=NM_001747 /gi=4502560			
		/ug=Hs.82422 /len=1221	*		
1879	0.036684	Rab9 effector p40 (RAB9P40), mRNA	NM_005833	Hs.19012	NP_005824
. "		/cds=(150,1268) /gb=NM_005833			
	1	/gi=5032014 /ug=Hs.19012 /len=1297	·		-
1927	0.010636	EST (tg16b07.x1 NCI_CGAP_CLL1	AI391567		NP_006488
		clone IMAGE:2108917 3' TR:Q14526			-
		Q14526 HIC-1 GENE FRAGMENT)			
1967	0.048502	CTL2 gene (CTL2), mRNA	NM_020428	Hs.105509	NP_065161
		/cds=(1,2121) /gb=NM_020428			
		/gi=9966908 /ug=Hs.105509 /len=2121			1
				6	
2006	0.040325	clathrin, light polypeptide (Lcb) (CLTB),	NM_007097	Hs.380749	NP_009028
		transcript variant brain, mRNA		*	
		/cds=(173,862) /gb=NM_007097			
		/gi=6005994 /ug=Hs.380749 /len=1134		٠.	4
2041	0.004406	ribosomal protein L32 (RPL32), mRNA	NM_000994	Hs.169793	NP_000985
•	,	/cds=(51,458) /gb=NM_000994		1	
		/gi=15812220 /ug=Hs.169793 /len=521		÷ .	
	0.007050	- "			ND 45000
2045	0.027356	T-cell activation protein (PGR1), mRNA	NM_033296	Hs.406590	NP_150638
-		/cds=(146,529) /gb=NM_033296			
		/gi=15193293 /ug=Hs.406590 /len=1534			*
2072	0.046224	Alamaniatian factor D4 miles handrial	NM 046000	U - 070000	ND 057404
2073	0.010234	transcription factor B1, mitochondrial	NM_016020	Hs.279908	NP_057104
2		(TFB1M), mRNA /cds=(73,1113)	-	·	İ
		/gb=NM_016020 /gi=7705784 /ug=Hs.279908 /len=1290	·		
2145	0.022210	polymerase (RNA) II (DNA directed)	NIM 002606	Hs.14839	NP 002687
2145	0.033319		NM_002696	ITS. 14039	INP_002667
	*	polypeptide G (POLR2G), mRNA			
		/cds=(107,625) /gb=NM_002696			
2158	0.027256	/gi=4505946 /ug=Hs.14839 /len=828 vesicle transport-related protein	NM_016106	Hs.27023	NP_057247
2100	0.027356	(RA410), mRNA /cds=(8,1930)	1 NINI_O 10 100	118.27023	NF_05/24/
		/gb=NM_016106 /gi=7706370			
•		/ug=Hs.27023 /len=2149			-
2236	0.033310	glia maturation factor, gamma (GMFG),	NM 004877	Hs.5210	NP_004868
2230	0.033319	mRNA /cds=(5,433) /gb=NM_004877	141VI_004677	113.32 10	111-004666
			-		
	*	/gi=4758439 /ug=Hs.5210 /len=561			
2304	0.007267	hypothetical gene supported by	XM_072157	-	
		COVERNIEM ALUEUE SUIDOHEH DV	INIVI U/ZIO/		i .

		nding To Differentially Expressed Gene			
Spot	p-yalu	Description	G ne	Unigene	Protein
		*	Accession No.	Accession	Accession
		J		No.	No.
2314	0.048502	specificity protein 3 (SP3) mRNA,	AY070137	Hs.154295	
		complete cds /cds=(385,2526)	• •		
		/gb=AY070137 /gi=18091786		0	-30
	]	/ug=Hs 154295 /len=3979		- 10	•
2338	0.048502	exostoses (multiple) 1 (EXT1), mRNA	NM 000127	Hs.184161	NP 000118
		/cds=(773,3013) /gb=NM 000127		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
		/gi=4557570 /ug=Hs.184161 /len=3304			1
		191 400101014g 113.104101 11ch 0004		,	Te t
2360	0.010368	hepatocyte growth factor-like protein	U28055		
2300	0.010300		020000	.:	
2004	0.005004	homolog (low match)	D00470		NID: 00070
2361		hypothetical protein (KIAA0142)	D63476		NP_66378
2391		heparin cofactor II (HCF2)	M58600		
2395	0.022315	Purkinje cell protein 4 (PCP4), mRNA	NM_006198	Hs.80296	NP_00618
		/cds=(59,247) /gb=NM_006198			
		/gi=5453857 /ug=Hs.80296 /len=540		7	
2553	0.048502	transmembrane protein vezatin	NM_017599	Hs.24135	NP_06006
-		(VEZATIN), mRNA /cds=(177,1886)	<i>t</i> . * »		
		/gb=NM_017599 /gi=19923537			
		/ug=Hs.24135 /len=3949			
2554	0.007267	chromodomain helicase DNA binding	NM_001270	Hs.22670	NP 00126
-90,.	0.,001.207	protein 1 (CHD1), mRNA	00		00120
		/cds=(164,5293) /gb=NM_001270		[	
		/gi=4557446 /ug=Hs.22670 /len=5947	.48		l
2561	0.040225	X-linked protein (DJ79P11.1), mRNA	NM_032621	Hs.283719	NP_11601
2001	0.040325		NIVI_032021	IDS.2037 19	NP_11001
		/cds=(101,487) /gb=NM_032621			
	*	/gi=14249131 /ug=Hs.283719 /len=744	*		
. = = =					
2580		KIAA0689	AB014589	1.	NP_05605
2595	0.010636	FLJ20288 protein (FLJ20288), mRNA	NM_020690	Hs.84045	NP_07894
		/cds=(142,2970) /gb=NM_020690			
		/gi=19923831 /ug=Hs.84045 /len=3418			ļ ·
				*	2
2629	0.018081	similar to S. pombe dim1 (DIM1),	NM_006701	Hs.433683	NP_00669
		mRNA /cds=(141,569) /gb=NM_006701	<del>-</del> ,	.,	-
		/gi=20070233 /ug=Hs.433683 /len=1415	, .		
2632	0.048502	hypothetical protein FLJ20432	NM 017819	Hs.57898	NP 06028
-002	0.010002	(FLJ20432), mRNA /cds=(603,1361)	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	113.07.000	1411_00020
		/gb=NM_017819 /gi=8923404	)		
	l - (	,			
2700	0.014000	/ug=Hs.57898 /len=1654	DO774604	115 425024	ļ
2702	0.011629	UI-H-EZ1-bbj-p-15-0-UI.s1	BQ771691	Hs.435931	, ,
-		NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-		ţ	
		bbj-p-15-0-UI 3', mRNA sequence			]
		/clone=UI-H-EZ1-bbj-p-15-0-UI		ļ.	ļ
		/clone_end=3' /gb=BQ771691			
	}	/gi=21980167 /ug=Hs 435931 /len=1072	•		ŀ
	1			I ',	ſ

Snot	p-value	Description	es in Figur 16 - G`n	Unigen	Protein
Shor	h-saine	Description			
		*	Accession No.	Accession	Accession
2892	0.024727	t-complex 1 (TCP1), mRNA	NM_030752	No. Hs.4112	<b>No.</b> NP 11037
2092	0.024727	/cds=(22,1692) /gb=NM 030752	NN _030752	П5.411Z <sub>/</sub> -	INF_11037
	vi				·
0000	0.04000	/gi=13540472 /ug=Hs.4112 /len=2019	NIM 004070	115 00040	ND 07005
2936	0.040325	hypothetical protein FLJ23441	NM_024678	Hs.90012	NP_07895
:		(FLJ23441), mRNA /cds=(877,1629)	•		:
		/gb=NM_024678 /gi=20070336			1
0000	0.044050	/ug=Hs.90012 /len=2119	11007100	11. 0774 40	· · · · · · · · · · · · · · · · · · ·
2963	0.044259	cDNA FLJ40109 fis, clone	AK097428	Hs.377146	
	į	TESTI2007685. /gb=AK097428			
		/gi=21757181 /ug=Hs.377146 /len=2007	* . "		
2968	0.048502	gycosyltransferase (LOC83468), mRNA	NM_031302	Hs.159993	NP_11259
		/cds=(408,1457) /gb=NM_031302		***	
	. X	/gi=21314737 /ug=Hs.159993 /len=1908	, in		.00- *
3004	0.011629	scavenger receptor class A, member 3	NM_016240	Hs.128856	NP_05732
		(SCARA3), mRNA /cds=(142,1962)		2	
1		/gb=NM_016240 /gi=7705335	*	3.0	-
		/ug=Hs.128856 /len=3636			
3160	0.027356	AF034176 mRNA (Tripodis and	AF034176	Hs.188882	
* .	χ	Ragoussis) cDNA clone ntcon5 contig			
		/gb=AF034176 /gi=2707738	1		
		/ug=Hs.188882 /len=7232			
3164	0.009227	adenylyl cyclase-associated protein 2	NM_006366	Hs.296341	NP_0063
		(CAP2), mRNA /cds=(84,1517)			
		/gb=NM_006366 /gi=5453592			
	-	/ug=Hs.296341 /len=1517			
3237	0.040325	mRNA for KIAA0725 protein, partial	AB018268	Hs.26450	
	1	cds. /cds=(1,1723) /gb=AB018268			1.4
		/gi=3882170 /ug=Hs.26450 /len=3911			
3268	0.016234	B protein (GRCB), mRNA	NM_014262	Hs.46458	NP 0550
		/cds=(89,1744) /gb=NM 014262	· .		
		/gi=7657207 /ug=Hs.46458 /len=2129			]
3298	0.040325	monocyte/neutrophil elastase inhibitor	AF053630	<del> </del>	
3479		expressed in T-cells and eosinophils in	NM. 014613	Hs.76591	NP_05542
	5.5.552	atopic dermatitis (ETEA), mRNA		1,10.7,000	000
		/cds=(32,1369) /gb=NM 014613			1
		/gi=24797105 /ug=Hs.76591 /len=4492		· ·	٠, .
		191 247 07 100 74g 113.7000 1 71611 4402			
3510	0.027356	adenylate kinase 3 like 1 (AK3L1),	NM_016282	Hs.43436	NP_05736
	0.52,000	mRNA /cds=(141,824) /gb=NM_016282	0 10202	1.10.10-100	100,00
		/gi=19923436 /ug=Hs.43436 /len=2642			
		/g =  2020700 /ug= 15.40400 /lef1=2042 			
3531	0.014551	mRNA for Sec24 protein (Sec24A	AJ131244	Hs.211612	
UUU I	0.0 1400   		/\J  \J  \Z44 	1175.21 1012	
		isoform), partial /cds=(1,3237)	0		
•		/gb=AJ131244 /gi=3947687		*	
	1	/ug=Hs.211612 /len=5967	I		I

		nding To Differentially Express d Gen				
Spot	p-valu	Description	Gen	Unigene	Protein	
			Accession No.	Accession	Accession	
	*			No.	No.	
3553	0.036684	scavenger receptor class B, member 2	NM_005506	Hs.323567	NP 005497	
		(SCARB2), mRNA /cds=(252,1688)	<del>-</del>		_	
		/gb=NM_005506 /gi=5031630	1	·	*	
					•	
ÓFE 4	0.000004	/ug=Hs.323567 /len=2329	NIM 000070	11- 57004	ND 000004	
3554	0.036684	mago-nashi proliferation-associated	NM_002370	Hs.57904	NP_002361	
		(Drosophila) (MAGOH), mRNA	7			
	, ,	/cds=(89,529) /gb=NM_002370				
		/gi=6006021 /ug=Hs.57904 /len=698	<u> </u>		·	
3617	0.033319	microtubule associated testis specific	NM 015112	Hs.101474	NP 055927	
•		serine/threonine protein kinase				
		(MAST205), mRNA /cds=(284,5488)				
•					• . •	
		/gb=NM_015112 /gi=14149670	*		[· ·	
000=	0.000	/ug=Hs.101474 /len=5737	1114 040000	11 00-0-0	NID COSES	
3687	0.020104	zinc finger protein 83 (HPF1) (ZNF83),	NM_018300	Hs.305953	NP_060770	
		mRNA /cds=(447,1997)		:	, ,	
2		/gb=NM_018300 /gi=21361788	*		1	
		/ug=Hs.305953 /len=2633		**	*	
3697	0.040325	elaC 2 (E. coli) (ELAC2), mRNA	NM_018127	Hs.12124	NP 060597	
5551	3.340020	/cds=(70,2550) /gb=NM_018127		]		
-			**	0		
		/gi=21359940 /ug=Hs:12124 /len=3006	* ;			
10.00	1 2 2 2 2 2 2 2 2			1. 1. 2. 2		
3747	0.048502	clathrin, heavy polypeptide (Hc) (CLTC),	NM_004859	Hs.178710	NP_004850	
		mRNA /cds=(173,5200)			1	
191		/gb=NM_004859 /gi=4758011	i .		Y 1	
-	, ,	/ug=Hs.178710 /len=6111				
3757	0.048502	tubulin, gamma complex associated	NM 006659	Hs.13386	NP 006650	
÷. V.		protein 2 (TUBGCP2), mRNA		1		
٠	<b>₹</b> : ` '					
	1	/cds=(64,2772) /gb=NM_006659				
1222	21222	/gi=5729839 /ug=Hs.13386 /len=2846	22.22			
3761	J 0.010368	peroxisomal acyl-coenzyme A oxidase	S69189		NP_009223	
		<u> </u>	<u> </u>		-	
3787	0.022315	secretory leukocyte protease inhibitor	NM_003064	Hs.251754	NP_003055	
		(antileukoproteinase) (SLPI), mRNA				
		/cds=(23,421) /gb=NM_003064		1		
		/gi=15834622 /ug=Hs.251754 /len=598				
		/gi-10004022 /ug=115.20 1/04 /left=090    -		· ·		
0700	0.007050		100040	<del> </del>	ND 00 450	
3799		collagenase type IV	J03210		NP_004521	
3809	0.044259	DiGeorge syndrome critical region gene	NM_033257	Hs.347285	NP_150282	
		6-like (DGCR6L), mRNA /cds=(98,760)		1.		
** ,	· .	/gb=NM_033257 /gi=15718677		1 7	1	
-()	* *	/ug=Hs.347285 /len=1182			1	
	, ,	1.29 1.010 1.225 1.011 1.02				
3835	0.036684	NEL-like 2 (chicken) (NELL2), mRNA	NM_006159	He 70290	NP 006150	
2025	0.030004		IAINI_000198	Hs.79389	ואר_טטס וטנ	
		/cds=(97,2547) /gb=NM_006159	}	1		
		/gi=5453765 /ug=Hs.79389 /len=3198				
3837	0.022315	CGI-48 protein (CGI-48), mRNA	NM_016001	Hs.6153 /	NP_057085	
		/cds=(108,1673) /gb=NM_016001				
	-	/gi=7705764 /ug=Hs.6153 /len=1873			1	

Genes	Corr spor	nding To Differentially Expressed Gen	es in Figure 16 -	LungDisease	
		Description	Gen	Unigene	Protein
			Acc ssion No.	Accession	Accession
				No.	No.
3839	0.048502	nudix (nucleoside diphosphate linked	NM 006703	Hs.4815	NP 006694
·		moiety X)-type motif 3 (NUDT3), mRNA			
		/cds=(154,672) /gb=NM_006703			ļ .
	,	/gi=5729803 /ug=Hs.4815 /len=1222			(.,
			·		÷
3844	0.033319	CGI-101 protein (F-LAN-1), mRNA	NM_016041	Hs.286131	NP 057125
		/cds=(7,636) /gb=NM_016041	,		
		/gi=7705603 /ug=Hs.286131 /len=1123		J	·
3883	0.008196	Meis1, myeloid ecotropic viral	NM_002398	Hs.170177	NP_002389
		integration site 1 (mouse) (MEIS1),			
		mRNA /cds=(66,1238) /gb=NM_002398			
*		/gi=4505150 /ug=Hs 170177 /len=2511		*	
3892	0.020104	small inducible cytokine subfamily E,	NM_004757	Hs.333513	NP_004748
		member 1 (endothelial monocyte-			
*	- 31	activating) (SCYE1), mRNA		ļ	l :
		/cds=(50,988) /gb=NM_004757		. 1	
		/gi=4758265 /ug=Hs.333513 /len=1057		,	·
3952	0.044259	interleukin 18 binding protein (IL18BP),	NM_005699	Hs.325978	NP_766632
-8-		transcript variant C, mRNA			
		/cds=(929,1522) /gb=NM_005699	.*?		:
	ľ	/gi=27502394 /ug=Hs.325978 /len=3630	••		]
2004	0.01000		101 000100	11 00000	ND 00 (507
3964	0.01302	transmembrane, prostate androgen	NM_020182	Hs.83883	NP_064567
		induced RNA (TMEPAI), mRNA			j j
,	{	/cds=(321,1184) /gb=NM_020182	İ	1 .	
		/gi=21361840 /ug=Hs.83883 /len=4839			
4000	0.007007	Using a sign because of the sign and base O (IVIDO)	NIA 004500	·	ND 004544
4002 4007		kinesin heavy chain member 2 (KIF2)	NM_004520	Hs.24485	NP_004511
4007	0.024121	chondroitin sulfate proteoglycan 6	NM_005445	115.2 <u>44</u> 00	NP_005436
	. '	(bamacan) (CSPG6), mRNA			}
		/cds=(92,3745) /gb=NM_005445	w.		Į į
	. ,	/gi=24475891 /ug=Hs.24485 /len=4096		1.0	
4029	0.024727	GAP-associated protein (p190)	M94721	<del></del>	
4036		IDN3 protein (IDN3), transcript variant	NM 133433	Hs.225767	NP_597677
.555	3.0 10204	A, mRNA /cds=(363,7160)	1	10.220101	
	·	/gb=NM_133433 /gi=19718748			
		/ug=Hs.225767 /len=8124			]
4062	0.044250	B-cell CLL/lymphoma 6 (zinc finger	NM_138931	Hs.155024	NP 620309
7002	0.044203	protein 51) (BCL6), transcript variant 2,	1.1.110000 1	1,10.100024	_020009
	,	mRNA /cds=(421,2541)		ĺ	
		/gb=NM_138931 /gi=21040335	1	,	1
		/ug=Hs.155024 /len=3630	ļ	**	[ [
	<u> </u>	1/49-113. 100024 /1611-0000	<u> </u>		

Genes	Correspon	nding To Differentially Expressed Gen	s in Figure 16 -	LungDisease	
	p-value	Description	Gene	Unigene	Protein
		,	Accession No.	Accession	Accession
	1			No.	No.
4115	0.011629	WNT1 inducible signaling pathway	NM_003880	Hs.194678	NP_569080
		protein 3 (WISP3), transcript variant 1,	- 7		
		mRNA /cds=(111,1175)			
	]	/gb=NM_003880 /gi=18491002		. *	]
	,	/ug=Hs.194678 /len=1307			{
4166	0.044259	ubiquitin hydrolyzing enzyme I (UBH1)	AF022789	Hs.42400	
ļ		mRNA, partial cds /cds=(153,1220)			
		/gb=AF022789 /gi=3220153		-	1.0
		/ug=Hs.42400 /len=4348			1
4167	0.048502	binder of Arl Two (BART1), mRNA	NM_012106	Hs.9552	NP 036238
		/cds=(115,606) /gb=NM_012106	- ; ;		-
		/gi=17978472 /ug=Hs.9552 /len=1973	*		
4204	0.027356	TBP-interacting protein (TIP120A),	NM_018448	Hs.184786	NP_060918
		mRNA /cds=(350,4042)			
180	1	/gb=NM_018448 /gi=21361793			
		/ug=Hs.184786 /len=5387			
4215	0.040325	prothymosin, alpha (gene sequence 28)	NM_002823	Hs.250655	NP_002814
. '	l	(PTMA), mRNA /cds=(182,514)			7 7
	-	/gb=NM_002823 /gi=21359859		1 2 0	-
		/ug=Hs.250655 /len=1233			
4250	0.010368	ras gene family, member A (ARHA),	NM_001664	Hs.77273	NP_001655
		mRNA /cds=(152,733) /gb=NM_001664			,
		/gi=10835048 /ug=Hs.77273 /len=1777	,		
					*
4266		cytovillin 2 (VIL2) (=X51521 ezrin)	J05021		NP_003370
4348	0.048502	stannin (SNN), mRNA /cds=(176,442)	NM_003498	Hs.76691	NP_003489
[	-	/gb=NM_003498 /gi=19923171			- 000
<u></u>		/ug=Hs.76691 /len=3295		*	
4399	0.011629	mitochondrial ribosomal protein L43	NM_032112	Hs.151945	NP_789764
		(MRPL43), mRNA /cds=(36,629)	1		
1		/gb=NM_032112 /gi=14149761		1	
		/ug=Hs.151945 /len=972	•		, ·
	0.036684		AB018285		NP_060903
4503	0.038037	ubiquitin-conjugating enzyme E2A	NM_003336	Hs.379466	NP_003327
		(RAD6 (UBE2A), mRNA /cds=(121,579)		1.	
		/gb=NM_003336 /gi=4507768		İ	
·		/ug=Hs.379466 /len=1743	ĺ	Ì.	
1555	0.045555				LID COOR
4556	J 0.010368	phosphorylase, glycogen; liver (Hers	NM_002863	Hs.771	NP_002854
1		disease, glycogen storage disease type			
		VI) (PYGL), mRNA /cds=(52,2595)	χ.		
	}	/gb=NM_002863 /gi=4506352			
1555	0.04000	/ug=Hs.771 /len=2643	111111111111111111111111111111111111111	11. 04000	
4583	0.016234	restin (Reed-Steinberg cell-expressed	NM_002956	Hs.31638	NP_002947
		intermediate filament-associated		-	
	· ·	protein) (RSN), mRNA /cds=(133,4416)	, 70		
<i>*</i>		/gb=NM_002956 /gi=4506750			
L	1	/ug=Hs.31638 /len=5857 ,		1	1

		nding To Differentially Expressed Gen			
Spot	p-value	D scription	Gene	Unigene	Protein
		*	Accession No.	Accession	Acc ssion
				No.	No.
4585	0.024727	vacuolar protein sorting 4B (yeast)	NM_004869	Hs.126550	NP_004860
		(VPS4B), mRNA /cds=(202,1536)		100	
		/gb=NM 004869 /gi=17865801	)		
		/ug=Hs.126550 /len=3337			
4587	0.007267	zinc finger protein 161 (mouse)	NM 003409	Hs.156000	NP 003400
		(ZFP161), mRNA /cds=(70,1419)	=		-
		/gb=NM_003409 /gi=19923241		-35-	
		/ug=Hs.156000 /len=2896			* *
4593	0.044259	Id2 protein (Id-2) mRNA, 3' end	M69293		NP 034626
4595		wc09c01.x1 NCI_CGAP_Pr28 cDNA	Al674177	Hs.200089	111 _00 1020
.000	0.0 10002	clone IMAGE:2314656 3' similar to	74107 4777	110.20000	
		gb:J05016 PROTEIN DISULFIDE	* +		
		ISOMERASE-RELATED PROTEIN	101		
	- 00	PRECURSOR mRNA sequence			
	, .	/clone=IMAGE:2314656 /clone_end=3'			
		/gb=Al674177 /gi=4874657			
					0 1
4000	0.040004	/ug=Hs 200089 /len=526	NINA 000545	11. 470705	ND 07705
4608	0.018081	MacGAP protein (MacGAP), mRNA	NM_033515	Hs.178705	NP_277050
		/cds=(23,1879) /gb=NM_033515	· · ·		
•	,	/gi=15723375 /ug=Hs.178705 /len=3305		}	
4612	0.022315	transporter 1, ATP-binding cassette,	NM_000593	Hs.352018	NP_000584
		sub-family B (MDR/TAP) (TAP1),			
		mRNA /cds=(165,2591)		120	
	· 7 ·	/gb=NM_000593 /gi=24797159			
		/ug=Hs.352018 /len=2960		1	<u> </u>
4628		OBPIIa gene	AJ251029	- X	
4665	0.048502	ribosomal protein L17 (RPL17), mRNA	NM_000985	Hs.82202	NP_000976
	Į.	/cds=(287,841) /gb=NM_000985			4 -
		/gi=14591906 /ug=Hs.82202 /len=898			
4747	0.016234	leucine zipper transcription factor-like 1	NM_020347	Hs.30824	NP_06508
-	·	(LZTFL1), mRNA /cds=(125,1024)			
		/gb=NM_020347 /gi=9966792			
	* ×.	/ug=Hs.30824 /len=3384			
4749	0.007267	N-myc downstream regulated gene 1	NM 006096	Hs.75789	NP_00608
.•		(NDRG1), mRNA /cds=(111,1295)	-		
	6	/gb=NM_006096 /gi=5174656			
		/ug=Hs.75789 /len=3020			
4989	0.030215	chloride intracellular channel 5 (CLIC5),	NM 016929	Hs.283021	NP_05862
	0.000210	mRNA /cds=(298,1053)	11111_010020	110.200021	-00002
		/gb=NM_016929 /gi=8393146			}
		/ug=Hs.283021 /len=2380		* 4	
5000	0.010369	diphtheria toxin receptor (heparin-	NM 001945	Hs.799	NP_00193
5000	0.010300		14141_00 1940	113.788	00 183
	1	binding epidermal growth factor-like		** *	}
	, .	growth factor) (DTR), mRNA			<u> </u>
of .		/cds=(262,888) /gb=NM_001945	•	· ·	0.0
		/gi=4503412 /ug=Hs.799 /len=2360		1	

Spot	p-value	nding To Differentially Express d Gen Description	Gene	Unig ne	Protein
Spot	p-value	Description	Accession No.	Accession	Acc ssion
			Accession No.	No.	No.
5058	0.018081	U6 snRNA-associated Sm-like protein	NM 012321	Hs.76719	NP 036453
0000	0.010001	(LSM4), mRNA /cds=(49,468)	14141_012021	113.70713	
		/gb=NM_012321 /gi=6912485	•		
7	*	/ug=Hs.76719 /len=1033			
5064	0.036684	nipsnap 1 (C. elegans) (NIPSNAP1),	NM_003634	Hs.173878	NP_003625
	0.000004	mRNA /cds=(255,1109)	11111_000004	1113.17.0070	_000020
`.		/gb=NM 003634 /gi=4505398	*		
	<u> </u>	/ug=Hs.173878 /len=2233		· ·	]
5103	0.009227	signal transducer and activator of	AF417842		:
0.00	0.000227	transcription 6, interleukin-4 induced	, ,	*	
		(STAT6) gene, complete cds		ľ	*
5124	0.016234	hematological and neurological	NM_016185	Hs.109706	NP_057269
0,-,	1 0.0.020	expressed 1 (HN1), mRNA	11111_010100	110.100700	
. : ' = '		/cds=(104,568) /gb=NM_016185		1	· ·
		/gi=7705876 /ug=Hs.109706 /len=704			
5127	0.036684	cDNA FLJ10627 fis, clone	AK001489	Hs.372616	
		NT2RP2005555. /gb=AK001489		1119.97.2910	
		/gi=7022777 /ug=Hs.372616 /len=1626			
	1.	19 10 22 17 7 7 dg			
5131	0.040325	cDNA FLJ30233 fis, clone	AK054795	Hs.351247	
	3,3,000	BRACE2001971. /gb=AK054795			
i.		/gi=16549404 /ug=Hs.351247 /len=1684	:	*	
5133	0.040325	glutathione S-transferase M1 (GSTM1),	NM 000561	Hs.301961	NP 666533
	. :	transcript variant 1, mRNA			- :, : -
		/cds=(55,711) /gb=NM_000561			
* ·		/gi=23065543 /ug=Hs.301961 /len=1161			× ,
5141	0.027356	ubiquitin carrier protein (E2-EPF),	NM_014501	Hs.174070	NP_055316
3 r.		mRNA /cds=(60,737) /gb=NM_014501			
		/gi=7657045 /ug=Hs 174070 /len=890		ļ ·	
5149		ribosomal RNA 18S	X03205		
5163	0.036684	KIAA0416 protein (KIAA0416), mRNA	NM_015564	Hs.114169	NP_056379
,	,	/cds=(410,1960) /gb=NM_015564			*
		/gi=7662101 /ug=Hs.114169 /len=5572			
					( *
5169	0.033319		X56160		NP_00215
5210	0.033319	RNA binding protein S1, serine-rich	NM_006711	Hs.75104	NP_542161
	-	domain (RNPS1), transcript variant 1,			
	-35-	mRNA /cds=(252,1169)			
	, ,	/gb=NM_006711 /gi=18379335			1 .
		/ug=Hs.75104 /len=2038			
5259	0.018081	nuclear matrix protein NMP200 related	NM_014502	Hs.173980	NP_05531
		to splicing factor PRP19 (NMP200),			
		mRNA /cds=(208,1722)	· · · · ·		
		/gb=NM_014502 /gi=7657380			1
	1	/ug=Hs.173980 /len=2167			*

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
•			Accession No.	Accession	Accession
	;	<u> </u>		No.	No.
5265	0.040325	ectonucleotide	NM_006208	Hs.11951	NP_006199
		pyrophosphatase/phosphodiesterase 1			
		(ENPP1), mRNA /cds=(173,2794)	·		
	]	/gb=NM_006208 /gi=13324676			
* .		/ug=Hs.11951 /len=3493			٠
5310	0.048502	cyclin D1 (PRAD1: parathyroid	NM_053056	Hs.82932	NP_444284
		adenomatosis 1) (CCND1), mRNA			_
~	1	/cds=(210,1097) /gb=NM_053056			
-		/gi=16950654 /ug=Hs.82932 /len=4306			
		1			
5318	0.033310	603021120F1 NIH_MGC_114 cDNA	BI488592	Hs.380956	
33 10	0.03331 <del>9</del>	clone IMAGE:5191733 5', mRNA	DI400392	IUS.200920	
	- 1				
		sequence /clone=IMAGE:5191733			
	- 100	/clone_end=5' /gb=BI488592			
	٠.	/gi=15327820 /ug=Hs.380956 /len=988			
5359	0.022315	RAP1A, member of RAS oncogene	NM_002884	Hs.865	NP_00287
	İ	family (RAP1A), mRNA /cds=(313,867)		= "	
		/gb=NM_002884 /gi=4506412	9	- ' .	
		/ug=Hs.865 /len=1579	:		
5363	0.048502	MAD, mothers against decapentaplegic	NM_004799	Hs.194716	NP_01556
		(Drosophila) interacting protein,	_	·	
		receptor activation anchor (MADHIP),			
		transcript variant 3, mRNA	•		
		/cds=(439,4410) /gb=NM_004799	· .		
/	-0	/gi=4759059 /ug=Hs.194716 /len=4839			
	1	3			
5393	0.044259	ubiquitination factor E4B (UFD2 yeast)	NM 006048	Hs.24594	NP_00603
		(UBE4B), mRNA /cds=(86,3994)		, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
	-	/gb=NM_006048 /gi=5174482			Ì
		/ug=Hs.24594 /len=5314			
5394	0.014551	hypothetical protein FLJ11294	NM_018383	Hs.107000	NP_06085
JJ94	0.014551		NIVI_010303	1115.107000	NF_00005
	1	(FLJ11294), mRNA /cds=(160,4170)			j.
	1	/gb=NM_018383 /gi=19923528			· ·
E 400	2010500	/ug=Hs 107000 /len=4602	1111 000101	11 1477 (00	115 00047
5493	0.048502	amyloid beta (A4) precursor protein	NM_000484	Hs.177486	NP_00047
		(protease nexin-II, Alzheimer disease)	]		1
		(APP), mRNA /cds=(148,2460)	6		. '
•		/gb=NM_000484 /gi=4502166			
		/ug=Hs.177486 /len=3579			
5502	0.005681	AGENCOURT_6626032	BM923381	Hs.437001	
		NIH_MGC_116 cDNA clone			
		IMAGE:5758987 5', mRNA sequence			- 00
	. 170	/clone=IMAGE:5758987 /clone_end=5'		•	
		/gb=BM923381 /gi=19373760	,		
	ļ	/ug=Hs.437001 /len=1729	*	. *	
5517	0.010368	Hypothetical protein (cDNA FLJ20702	AK000709		
	1 5.5 10500	fis, clone KAIA2174)			

Genes	Correspo	nding To Differentially Expressed Gen	s in Figure 16 -	LungDisease	
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	,			No.	No.
5528	0.033319	I(3)mbt-like 2 (Drosophila) (L3MBTL2),	NM_031488	Hs.265327	NP_113676
i.	· .	mRNA /cds=(53,2170) /gb=NM_031488	<del>-</del>		
٠.		/gi=20149697 /ug=Hs.265327 /len=3222			
					*
5530	0.040325	FLJ30953 fis, clone HCASM2000016	AK055515	Hs.288862	NP 005427
		/cds=UNKNOWN /gb=AK055515		• •	
		/gi=16550257 /ug=Hs.288862 /len=2620			
					* * * * * * * * * * * * * * * * * * * *
5583	0.01302	cardiotrophin 1 (CTF1), mRNA	NM_001330	Hs.25537	NP_001321
		/cds=(33,638) /gb=NM_001330	-		
		/gi=4503120 /ug=Hs.25537 /len=1539			
5589	0.022315	FLJ11040 (FLJ11040), mRNA	NM_018307	Hs. 14202	NP 060777
, 4000		/cds=(5,1459) /gb=NM_018307			
	•	/gi=8922837 /ug=Hs.14202 /len=2453			
5654	0.044259		U07802	- 1 18	7 7 7
5656		calcium channel, voltage-dependent,	NM 000723	Hs.635	NP_000714
0000	0.020.01	beta 1 subunit (CACNB1), mRNA	000.20	1.10.000	0007.11
	*	/cds=(150,1940) /gb=NM 000723			
		/gi=19923118 /ug=Hs.635 /len=3658	*		
5659	0.040325	RAD21 (S. pombe) (RAD21), mRNA	NM_006265	Hs.81848	NP 006256
3033	0.040323	/cds=(185,2080) /gb=NM_006265	14111_000200	113.010-10	_000200
4.		/gi=5453993 /ug=Hs.81848 /len=3647			
5672	0.040325	clone IMAGE:5265581, mRNA	BC035165	Hs.400548	
3072	0.040323	/gb=BC035165 /gi=23272508	DC039103	113,400040	
,		/ug=Hs.400548 /len=2237	* "		
5692	0.024727	mRNA for MEGF6 protein (KIAA0815),	AB011539	Hs.56186	
3032	0.024727	partial cds. /cds=(153,3893)	Apo 1 1555	113.50100	
		/gb=AB011539 /gi=20269128			1
- '		/ug=Hs.56186 /len=4501		] .	•
5726	0.033310	glutathione S-transferase M1 (GSTM1),	NM 000561	Hs.301961	NP_666533
3720	0.033313	transcript variant 1, mRNA	14141_000001	113.301301	_000000
1.		/cds=(55,711) /gb=NM_000561			
:		/gi=23065543 /ug=Hs.301961 /len=1161			
5781	0.040325	hect domain and RLD 3 (HERC3),	NM 014606	Hs.35804	NP_055421
3701	0.040323	mRNA /cds=(167,3319)	14101-014000	113.000,04	_000421
	*	//gb=NM_014606 /gi=7657151		1	1
		/ug=Hs.35804 /len=4894			
5842	0.006431	corin (PRSC), mRNA /cds=(94,3222)	NM 006587	Hs.340634	NP_006578
0072	0.000431	/gb=NM_006587 /gi=5729988	14141_000007	110.040004	
	·	/ug=Hs.340634 /len=4933	100	`}	
5869	0.048502	ATPase, Class I, type 8B, member 1	NM_005603	Hs.406187	NP_005594
1	0.040002	(ATP8B1), mRNA /cds=(1,3756)		1.13.133.131	
		/gb=NM_005603 /gi=5031696		1	1.
1		/ug=Hs.406187 /len=3756	•		
5871	0.022215	mRNA; cDNA DKFZp686H05116 (from	AL833453	Hs.254124	<del> </del>
] 3671	0.022313	clone DKFZp686H05116)	LC000400	110.207124	
[		/gb=AL833453 /gi=21734095			
		/ug=Hs 254124 /len=3731		]	
<u> </u>		1/49-113.20-124/1011-0/01	<u> </u>	<del> </del>	<del></del>

		nding To Differentially Expr ssed Gen			
Spot	p-value	Description	G ne Accession No.	Unig ne Accession No.	Protein Accession No.
5872	0.022315	TL132 protein (LOC220594), mRNA	NM 145809	Hs.234573	NP 665808
00.2	0.944.9	/cds=(1242,2306) /gb=NM 145809			
		/gi=21956646 /ug=Hs.234573 /len=4413		٠.	
5901	0.040325	lipin 1 (LPIN1), mRNA /cds=(68,2740)	NM_145693	Hs.81412	NP_663731
		/gb=NM_145693 /gi=22027647			
		/ug=Hs.81412 /len=5363			·
5923		retinol-binding protein (RBP)	M10934		0
5960	0.048502	zinc finger protein ANC_2H01	NM_016331	Hs.22879	NP_057415
		(LOC51193), mRNA /cds=(446,1903)	,		
•		/gb=NM_016331 /gi=7705934			
·	,	/ug=Hs.22879 /len=3013			
5964	0.007267	aspartylglucosaminidase (AGA), mRNA	NM_000027	Hs.207776	NP_000018
		/cds=(171,1211) /gb=NM_000027		*	
		/gi=4557272 /ug=Hs.207776 /len=2150			-
0055	,		1100755		42.
6055		Sprague-Dawley acidic calponin	U06755	11- 25004	ND 004204
6079	0.030215	extracellular matrix protein 2, female	NM_001393	Hs.35094	NP_001384
		organ and adipocyte specific (ECM2),			
		mRNA /cds=(74,2173) /gb=NM_001393			
•		/gi=4557542 /ug=Hs.35094 /len=3171			
6087	0.018081	microtubule-associated protein, RP/EB	NM_012325	Hs.234279	NP 036457
0007	0,010001	family, member 1 (MAPRE1), mRNA	11111_012020	113.204219	-000407
		/cds=(65,871) /gb=NM_012325		-3	
		/gi=6912493 /ug=Hs.234279 /len=2540	*		<b>1</b> .
•		, <b>3</b>	•		
6097	0.030215	tyrosine 3-monooxygenase/tryptophan 5	NM_012479	Hs.25001	NP_036611
		monooxygenase activation protein,		·	_
		gamma polypeptide (YWHAG), mRNA	**		
		/cds=(192,935) /gb=NM_012479		-	ļ
		/gi=21464100 /ug=Hs.25001 /len=3747			
			,	<u> </u>	1
6105	0.009227	retinoblastoma binding protein 6	NM_006910	Hs.91065	NP_008841
		(RBBP6), mRNA /cds=(92,2938)			
		/gb=NM_006910 /gi=5902043	• .	,	
	<u> </u>	/ug=Hs.91065 /len=2994			
6124	0.016234	prolyl endopeptidase (PREP), mRNA	NM_002726	Hs.86978	NP_002717
		/cds=(1,2133) /gb=NM_002726	-		
		/gi=20149544 /ug=Hs.86978 /len=2756			ļ
CADE	0.000005	Signification and a section of	NIM 002724"	Un 40500	ND 002700
6125	0.002905	Sjogren's syndrome nuclear	NM_003731	Hs.18528	NP_003722
		autoantigen 1 (SSNA1), mRNA			
•		/cds=(47,406) /gb=NM_003731	<b>\</b>	1	
121-21	0.044250	/gi=4505324 /ug=Hs.18528 /len=865 myosin, light polypeptide 3, alkali;	NM_000258	Hs.1815	NP_000249
6170	1.0.044239	proyosin, light polypeptide s, alkall,	HAINITOOOSOO	1115.1013	ייין _000248
6129	0.0	ventricular ekoletal clow (MVI 3)			l l
6129		ventricular, skeletal, slow (MYL3), mRNA /cds=(51,638) /gb=NM_000258			

C4	n volice		es in Figure 16 - Gen		
Spot	p-value	Description		Unigene	Protein
			Acc ssion No.	Acc ssion No.	Accession No.
6133	0.042188	core promoter element binding protein	NM 001300	Hs.285313	NP_001291
0.00	0.0 12.00	(COPEB), mRNA /cds=(118,969)		1.10,2000.0	
	,	/gb=NM_001300 /gi=9961346		,	•
	4	/ug=Hs.285313 /len=1470		* *	*
6167		karyopherin alpha 2 (RAG cohort 1,	NM 002266	Hs.159557	NP_002257
		importin alpha 1) (KPNA2), mRNA	· · · · · · · · · · · · · · · · · · ·		
		/cds=(133,1722) /gb=NM 002266	~	1	
		/gi=4504896 /ug=Hs.159557 /len=1976	· ·		7.
6189	0.003869	amylo-1, 6-glucosidase, 4-alpha-	NM_000028	Hs.904	NP 000637
. *		glucanotransferase (glycogen	· . ¬		- '
		debranching enzyme, glycogen storage		· ·	
	0.	disease type III) (AGL), transcript	* 0		
-		variant 4, mRNA /cds=(479,5077)			
	,-	/gb=NM_000028 /gi=4557274			
		/ug=Hs.904 /len=7445			
6226	0.027356	adenylate cyclase activating polypeptide	NM_001118	Hs.377783	NP '001109
		1 (pituitary) receptor type I	_		-
		(ADCYAP1R1), mRNA /cds=(74,1651)			
		/gb=NM_001118 /gi=4501922			
		/ug=Hs.377783 /len=1664			
6228	0.044259	prefoldin 2 (PFDN2), mRNA	NM_012394	Hs.298229	NP_036526
	_	/cds=(31,495) /gb=NM_012394			
: •		/gi=12408674 /ug=Hs.298229 /len=644			
			7.	:	
6251	0.014551	interferon-related developmental	NM_001550	Hs.7879	NP_001541
		regulator 1 (IFRD1), mRNA			
	,	/cds=(220,1581) /gb=NM_001550			* * 3
		/gi=4504606 /ug=Hs.7879 /len=1791			
6270	0.015503	mitochondrial ribosomal protein L50	NM_019051	Hs.288224	NP_061924
		(MRPL50), nuclear gene encoding		*. *	
		mitochondrial protein, mRNA		•	
• .	(3)	/cds=(23,499) /gb=NM_019051			
		/gi=21265095 /ug=Hs.288224 /len=1027			ļ
	7.77		**		<u> </u>
6306	0.036353	eukaryotic translation initiation factor 4E	NM_001968	Hs.79306	NP_001959
*		(EIF4E), mRNA /cds=(19,672)			
		/gb=NM_001968 /gi=4503534		<u>'</u>	`
		/ug=Hs.79306 /len=1842			
6307	0.032883	cDNA FLJ37296 fis, clone	AK094615	Hs.4983	
		BRAMY2015420. /gb=AK094615			
		/gi=21753707 /ug=Hs.4983 /len=3181			
6342	0.033319	oxidoreductase UCPA (LOC56898),	NM_020139	Hs.124696	NP_064524
		mRNA /cds=(70,807) /gb=NM_020139		1	
		/gi=10047131 /ug=Hs.124696 /len=1048			1

Spot	p-value	nding To Diff r ntially Expressed Gene Description	Gene	Unigene	Protein
	- 1		Accession No.	Accession No.	Accession No.
6370	0.036684	major histocompatibility locus class III	AF109905	IVO.	140.
		regions Hsc70t (smRNP, G7A, NG23,			,
		MutS homolog, CLCP, NG24, NG25,			
		and NG26)			
6394	0.027356	activin A receptor, type I (ACVR1),	NM_001105	Hs.150402	NP_001096
		mRNA /cds=(341,1870)	(X)		2
. •		/gb=NM_001105 /gi=10862690		. *	
	2.1.50.	/ug=Hs.150402 /len=2952		1	
6412	0.016234	KIAA0716 gene product (KIAA0716),	NM_014705	Hs.118140	NP_055520
*		mRNA /cds=(192,2489)			
,		/gb=NM_014705 /gi=7662263			**
6414	0.024727	/ug=Hs.118140 /len=4652 eukaryotic translation initiation factor 4	NM_001418	Un 102604	ND 001400
0414	0.024127	gamma, 2 (EIF4G2), mRNA	NIVI_UU 14 16	Hs.183684	NP_001409
		/cds=(307,3030) /gb=NM_001418	3.		*
1 1		/gi=4503538 /ug=Hs.183684 /len=3820	, ,	*	
	- C	/gi=4000000 /ug=115.			
6428	0.027356	serologically defined colon cancer	NM_004713	Hs.388584	NP_004704
	0.02,000	antigen 1 (SDCCAG1), mRNA			
,		/cds=(183,1271) /gb=NM_004713			
		/gi=4759077 /ug=Hs.388584 /len=2078		,	*
• • •					
6430	0.030215	retinoid binding protein 7 (CRBPIV),	NM_052960	Hs.422688	NP_443192
		mRNA /cds=(44,448) /gb=NM_052960			1
		/gi=16418454 /ug=Hs.422688 /len=661			
6470	0.029938	nucleolar GTPase (HUMAUANTIG),	NM_013285	Hs.75528	NP_037417
		mRNA /cds=(80,2275) /gb=NM_013285			
100		/gi=7019418 /ug=Hs.75528 /len=2331	. *	· ·	
6519	0.020245	automatic translation initiation factor	NIM O1ECOC	Un 160474	ND OFCAF
6518	0.030213	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa (EIF2B4),	NM_015636	Hs.169474	NP_05645
		transcript variant 1, mRNA			
		/cds=(20,1588) /gb=NM 015636			
		/gi=26986531 /ug=Hs.169474 /len=1643		* * . *	
				٠	
6537	0.010368	selenoprotein P, plasma, 1 (SEPP1),	NM_005410	Hs.275775	NP 00540
		mRNA /cds=(37,1182) /gb=NM_005410			
		/gi=4885590 /ug=Hs.275775 /len=2038			
			*		
6575	0.040325	epidermal growth factor receptor	NM_004447	Hs.2132	NP_00443
		pathway substrate 8 (EPS8), mRNA			
		/cds=(210,2678) /gb=NM_004447	,	***	
	- 11	/gi=4758295 /ug=Hs.2132 /len=3832			,
	1 0 040325	mRNA for KIAA0515 protein, partial	AB011087	Hs.405891	
6620	0.0	I	and the second second		
6620		cds. /cds=(1,2014) /gb=AB011087 /gi=3043553 /ug=Hs.405891 /len=6335	-		,

		nding To Differentially Expr ssed Gen			San Austria
Spot	p-value	Description	Gn	Unigene	Protein
			Accession No.	Accession	Accession
	0.01.2		1114 00400	No.	No.
6653	0.044259	ribosomal protein S27	NM_001030	Hs.195453	NP_00102
		(metallopanstimulin 1) (RPS27), mRNA		٠,٠	
		/cds=(36,290) /gb=NM_001030		*	[
		/gi=15011937 /ug=Hs.195453 /len=344			İ
)		1			
6662		integrin alpha 10 subunit (ITGA10)	AF112345		NP_00362
6732	0.027356		NM_130468	Hs.24947	NP_56973
		1), mRNA /cds=(1,1131)			·
		/gb=NM_130468 /gi=18497303			. '
		/ug=Hs.24947 /len=1960	·		
6855	0.014551	clone IMAGE:5264473, mRNA	BC045747	Hs.343411	
		/gb=BC045747 /gi=28279052			(9)
		/ug=Hs.343411 /len=2102			- T
6856	0.033319	calcium/calmodulin-dependent protein	NM_172127	Hs.111460	NP_74212
		kinase (CaM kinase) II delta (CAMK2D),	-		], –
		transcript variant 1, mRNA			<u> </u>
		/cds=(505,1941) /gb=NM_172127			
	*	/gi=26667185 /ug=Hs.111460 /len=4098			·
		3		*	
6866	0.036684	E1A binding protein p300 (EP300),	NM_001429	Hs.25272	NP_00142
		mRNA /cds=(1200,8444)			
	1	/gb=NM_001429 /gi=4557556	8		
		/ug=Hs.25272 /len=9046		de .	- 0
6867	0.048502	DNA (cytosine-5-)-methyltransferase 1	NM 001379	Hs.77462	NP 00137
0001	0.040002	(DNMT1), mRNA /cds=(238,5088)	11111_001010	110.77402	
	-	/gb=NM_001379 /gi=4503350		. :	
		/ug=Hs.77462 /len=5434			
6910	0.030215	Cip1-interacting zinc finger protein	NM 012127	Hs.23476	NP 03625
٥٩٨٥	0.030213	(CIZ1), mRNA /cds=(152,2692)	14141_012121	113.20470	111 _00020
	ţ.	/gb=NM_012127 /gi=6912307	,	-);-	
	47	/ug=Hs.23476 /len=2821			
7009	0.020104	crystallin, alpha B (CRYAB), mRNA	NM 001885	Hs.408767	NP_00187
7009	0.020104	/cds=(26,553) /gb=NM_001885	14141 00 1000	III 8.400707	NF_00 187
		_ , , , ,	1		j .
7049	0.044620	/gi=4503056 /ug=Hs.408767 /len=691 C3HC4-like zinc finger protein (ZFP26),	NM 016422	Hs.44685	NP 05750
7049	0.011629			ms.44000	NF_05/50
	1	mRNA /cds=(144,836) /gb=NM_016422			
		/gi=21361492 /ug=Hs.44685 /len=1108			-,
7050	0.046004	Station D. A. a. bis disc. seaters 4	NIA 040440	110 20704	NID 44424
7050	0.016234	cyclin D-type binding-protein 1	NM_012142	Hs.36794	NP_41124
	l .	(CCNDBP1), transcript variant 1, mRNA	<b>'</b>	<b>.</b>	
		/cds=(158,1240) /gb=NM_012142			
		/gi=16554565 /ug=Hs.36794 /len=1615		<b>.</b>	
<u> </u>			Su 4 2 2 2 2 2 2		ND 65
7069	0.004406	adenosine monophosphate deaminase	NM_000480	Hs.83918	NP_00047
	F .	(isoform E) (AMPD3), mRNA			. *-
.:	1	/cds=(345,2675) /gb=NM_000480	* *		
		/gi=4502078 /ug=Hs.83918 /len=3915			1

Snot	p-value	Description	es in Figur 16 - Gene	Unigene	Protein
Shor	in-Agine	peşeription	Accession No.	Accession	Accession
1				No.	No.
7072	0.044259	synovial sarcoma translocation gene on	NM_016305	Hs.9774	NP_057389
		chromosome 18-like 2 (SS18L2),		1 1	
•		mRNA /cds=(99,332) /gb=NM_016305			
		/gi=10047103 /ug=Hs.9774 /len=817	9.		
7084	0.022315	regulated in glioma (RIG), mRNA	NM_006394	Hs.278503	NP_006385
	İ	/cds=(26,358) /gb=NM_006394	,		-
	÷ .	/gi=5454007 /ug=Hs.278503 /len=2569			
					*
7120	0.033319		AB030001	X (177)	
7137	0.027356	DEAD (aspartate-glutamate-alanine-	NM_007841		
		aspartate) box polypeptide 6 (Ddx6)			
7148	0.014551	RAB13, member RAS oncogene family	NM_002870	Hs.151536	NP_002861
	. *	(RAB13), mRNA /cds=(140,751)			
		/gb=NM_002870 /gi=4506362			
		/ug=Hs.151536 /len=1238			
			10		
7151	0.018081	DNA (cytosine-5-)-methyltransferase 1	NM_001379	Hs.77462	NP_001370
		(DNMT1), mRNA /cds=(238,5088)	**	*	
		/gb=NM_001379 /gi=4503350	8		
		/ug=Hs.77462 /len=5434			*
7172	0.030215	damage-specific DNA binding protein 1,	NM_001923	Hs.108327	NP_001914
	y 10	127kDa (DDB1), mRNA			
		/cds=(110,3532) /gb=NM_001923		· .	
	i .	/gi=13435358 /ug=Hs.108327 /len=4221		* 4	
<u> </u>			<u></u>		
7185	0.027356	melanoma-associated antigen MG50	AF200348	Hs.118893	
		mRNA, partial cds /cds=(1,4491)			
. 9		/gb=AF200348 /gi=6273398			
		/ug=Hs:118893 /len=6847		1	
7206	0.011629	hypothetical protein FLJ13081	NM_024834	Hs.180638	NP_079110
		(FLJ13081), mRNA /cds=(171,2099)			
-	1 3	/gb=NM_024834 /gi=13376242			
		/ug=Hs.180638 /len=4113		<u> </u>	
7249	0.033319	chromosome 6 open reading frame 28	NM_021177	Hs.103106	NP_067000
		(C6orf28), mRNA /cds=(219,506)			-
		/gb=NM_021177 /gi=10863976	*	• •	
	,	/ug=Hs.103106 /len=864			
7265	0.046353	thioredoxin interacting protein (TXNIP),	NM_006472	Hs.179526	NP_006463
		mRNA /cds=(222,1397)			
		/gb=NM_006472 /gi=5454161		. "	100
		/ug=Hs.179526 /len=2704			
7278	0.027356	KIAA0648 protein (KIAA0648), mRNA	NM_015200	Hs.31921	NP_05601
		/cds=(232,4125) /gb=NM_015200			
		/gi=22094120 /ug=Hs.31921 /len=6744		*	l
			+		

Spot	p-value	Description	Gene	Unigene	Protein
- '	·	* * * * * * * * * * * * * * * * * * * *	Accession No.	Accession . No.	Accession No.
7304	0.020104	proteasome (prosome, macropain)	NM_002793	Hs.407981	NP_002784
100		subunit, beta type, 1 (PSMB1), mRNA		-	_
	1	/cds=(48,773) /gb=NM_002793			
• •		/gi=22538462 /ug=Hs.407981 /len=872	* *		٠,٠
7308	0.011629	thioredoxin related protein (MGC3178),	NM_030810	Hs.6101	NP_11043
•		mRNA /cds=(82,1056) /gb=NM_030810			
		/gi=13540603 /ug=Hs.6101 /len=2712			
7342	0.048502	KIAA0874 protein (KIAA0874), mRNA	NM_015208	Hs.27973	NP_05602
		/cds=(1,6189) /gb=NM_015208			
		/gi=14140237 /ug=Hs.27973 /len=6189			
	1				
7369	0.007267	cadherin 2, type 1, N-cadherin	NM_001792	Hs.161	NP_00178
		(neuronal) (CDH2), mRNA	**		
	* ",	/cds=(206,2926) /gb=NM_001792	*	•	. 4
7405	0.030315	/gi=14589888 /ug=Hs.161 /len=4122 MAGE-E1 protein (MAGE-E1), mRNA	NIM 020004	Up 7457	ND 0000
7400	0.030213	/cds=(146,1390) /gb=NM_030801	NM_030801	Hs.7457	NP_80388
٠.		/gi=13540587 /ug=Hs.7457 /len=2997		*	
7469	0.036684	GTPase regulator associated with focal	NM_015071	Hs.132942	NP 05588
, 100	U.000007	adhesion kinase pp125(FAK) (GRAF),	14141_013071	113.132342	-05500
*		mRNA /cds=(424,2868)		6 ,	
		/gb=NM_015071 /gi=7662207		*	
*		/ug=Hs.132942 /len=6906	*	*-	
7470	0.003391	Thy-1 co-transcribed (LOC94105),	NM_033209	Hs.345643	NP_149986
		mRNA /cds≂(1289,1717)			×
;	• .	/gb=NM_033209 /gi=24475732		*	
		/ug=Hs.345643 /len=1818		× 1	
7487	0.048502	protease, serine, 11 (IGF binding)	NM_002775	Hs.75111	NP_002766
		(PRSS11), mRNA /cds=(49,1491)			*
		/gb=NM_002775 /gi=21327712			,
7519	0.022210	/ug=Hs.75111 /len=2039 myotubularin related protein 3	NIM 024000	11- 62202	NID COACO
1313	0.033319	(MTMR3), transcript variant 3, mRNA	NM_021090	Hs.63302	NP_69469
	. \	/cds=(288,3884) /gb=NM_021090			
	• '	/gi=23510385 /ug=Hs.63302 /len=5963	*		*.
		/g250			,
7520	0.030215	hypothetical protein FLJ10350	NM_018067	Hs.177596	NP_06053
		(FLJ10350), mRNA /cds=(676,2340)			_,,,_,,,,,
		/gb=NM_018067 /gi=21361780	e y		٠.
		/ug=Hs.177596 /len=2811	*	<u> </u>	
7561	0.027356	FERM, RhoGEF (ARHGEF) and	NM_005766	Hs.183738	NP_00575
	1	pleckstrin domain protein 1	<b>179</b>		
		(chondrocyte-derived) (FARP1), mRNA			
. *		/cds=(49,3186) /gb=NM_005766	0		
		/gi=5031632 /ug=Hs.183738 /len=3442			

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7562	0.033319	snail zinc finger protein (SNAI1) gene, complete cds	AF155233		
7596	0.030215	zinc finger protein 26 (KOX 20) (ZNF26), mRNA /cds=(699,1298) /gb=NM_019591 /gi=11034838 /ug=Hs.26432 /len=2385	NM_019591	Hs.26432	NP_062537
7597	0.022315	nudix (nucleoside diphosphate linked moiety X)-type motif 1 (NUDT1), mRNA /cds=(100,639) /gb=NM_002452 /gi=21361345 /ug=Hs.388 /len=788	NM_002452	Hs.388	NP_002443
7627	0.020104	cylindromatosis (turban tumor syndrome) (CYLD), mRNA /cds=(392,3262) /gb=NM_015247 /gi=14165257 /ug=Hs.18827 /len=5371	NM_015247	Hs. 18827	NP_056062
7720		hypothetical protein MGC4604 (MGC4604), mRNA /cds=(591,926) /gb=NM_031487 /gi=24432023 /ug=Hs.375204 /len=5079	NM_031487	Hs.375204	NP_064517
7757	0.007267	B-cell CLL/lymphoma 9 (BCL9), mRNA /cds=(740,4924) /gb=NM_004326 /gi=4757845 /ug=Hs.122607 /len=6267	NM_004326	Hs.122607	NP_004317
7765	0.02571	hypothetical protein LOC51234 (LOC51234), mRNA /cds=(72,623) /gb=NM_016454 /gi=24475963 /ug=Hs.250905 /len=1013	NM_016454	Hs.250905	NP_057538
7845	0.018081	chemokine-like factor super family 4 isoform 1 (CKLFSF4) mRNA, complete cds /cds=(183,887) /gb=AF521889 /gi=25167082 /ug=Hs.325825 /len=3430	AF521889 (	Hs.325825	NP_848933
7851	0.016234	capillary morphogenesis protein 2 (CMG2), mRNA /cds=(46,783) /gb=NM_058172 /gi=17158002 /ug=Hs.5897 /len=2026	NM_058172	Hs.5897	NP_477520
7877	0.030215	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax Drosophila) (MLL5), mRNA /cds=(202,5778) /gb=NM_018682 /gi=23503326	NM_018682	Hs.333300	NP_061152
7878	0.036684	/ug=Hs.333300 /len=6543 EST(RC1-BT0721-050400-011-a06 BT0721)	BE090738		
7930	0.020104	EST (nz09e04.s1 NCI_CGAP_GCB1 IMAGE:1287294 3')	AA761167		
7943		EST (AV754618 TP cDNA clone TPGAAA04 5')	AV754618		
7951	0.048502	EST (am59f03.x1 Johnston frontal	AI124626	177	

	p-value	nding To Differentially Expressed Gen D scription	Gene	Unig ne	Protein
Spor	p-value	D scription	Acc ssion No.	Acc ssion	Accession
7965	0.036684	hypothetical protein FLJ12953 similar to Mus musculus D3Mm3e (FLJ12953), mRNA /cds=(89,1093) /gb=NM_032118 /gi=14149770 /ug=Hs.323537 /len=1146	_	No. Hs.323537	No. NP_115494
8018	0.024727	tubulin, gamma 1 (TUBG1), mRNA /cds=(25,1380) /gb=NM_001070 /gi=4507730 /ug=Hs.21635 /len=1568	NM_001070	Hs.21635	NP_001061
8078	0.030215	similar to claudin 12 (LOC115383), mRNA	XM_004591	, , ,	
8080	0.007267	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291	NM_002546	Hs.81791	NP_002537
8087	0.018081	cDNA FLJ36527 fis, clone TRACH2003941. /gb=AK093846 /gi=21752790 /ug=Hs.378776 /len=2526	AK093846	Hs.378776	
8115	0.036684	STRIN protein (STRIN), mRNA /cds=(100,837) /gb=NM_016271 /gi=21361538 /ug=Hs.180403 /len=3226	NM_016271	Hs.180403	NP_057355
8119		mRNA for KIAA1949 protein. /cds=(1149,3137) /gb=AB075829 /gi=18916754 /ug=Hs.101150 /len=4015	AB075829	Hs.101150	
8162	0.022315	hypothetical protein HSPC148 (HSPC148), mRNA /cds=(64,753) /gb=NM_016403 /gi=7705474 /ug=Hs.42743 /len=1046	NM_016403	Hs.42743	NP_057487
8163	0.048502	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa (NDUFB3), mRNA /cds=(253,549) /gb=NM_002491 /gi=4505360 /ug=Hs.109760 /len=693	NM_002491	Hs.109760	NP_002482
8198	0.007267	PHD zinc finger protein XAP135 (XAP135), transcript variant 2, mRNA /cds=(222,1448) /gb=NM_133325 /gi=19747275 /ug=Hs.7759 /len=1583	NM_133325	Hs.7759	NP_579866
8219	0.036684	hypothetical protein DKFZp564O1664 (DKFZP564O1664), mRNA /cds=(337,1893) /gb=NM_030800 /gi=13540585 /ug=Hs.6686 /len=2538	NM_030800	Hs.6686	NP_110427
8229	0.010368	hepatitis C virus core-binding protein 6 (HCBP6), mRNA /cds=(114,683) /gb=NM_023934 /gi=24371247 /ug=Hs.283674 /len=1157	NM_023934	Hs.283674	NP_076423

	p-value	nding To Differentially Expressed Gen Description	Gene	Unigene	Protein
Spot	p-value	Description			
	. "		Accession No.	Accession	Accession
00.44	0.000044	hthtilt-i- MOCO100	NIM 024004	No.	No.
8241	0.020841	hypothetical protein MGC3196	NM_024084	Hs.309161	
	0.	(MGC3196), mRNA /cds=(178,291)	*	2.7	
	. "	/gb=NM_024084 /gi=13129079	*		
	2 2 2 2 2 4 5	/ug=Hs.309161 /len=603			
8333	0.030215	EST (fb12g02.x1 zebrafish fin day0	Al384158	- × · · · ·	-
· · · · ·	1	regeneration)	, , , , , , , , , , , , , , , , , , , ,	4	
8339	0:018081	EST (Clontech human placenta polyA	D63238		NP_06763
		mRNA (#6572)GEN-511B02			
8376	0.01302	EST(zk54c05.r1	AA044356		NP_00176
	*	Soares_pregnant_uterus_NbHPU cDNA			_
		clone IMAGE:486632 5')			
8449	0.022315	hypothetical protein FLJ10619	NM_018156 ,	Hs.191436	NP_06062
		(FLJ10619), mRNA /cds=(65,1894)		7	
		/gb=NM_018156 /gi=8922552			
		/ug=Hs.191436 /len=3989	-		
8450	0.033319	skeletal muscle HSB84A051	Z28721		<del>- 2</del>
		STRATAGENE cDNA library, cat.	. *		* 000
		#936215. cDNA clone 84A05			*
8475	0.033319	sentrin/SUMO-specific protease	NM_020654	Hs.30443	NP 06570
- ,		(SENP7), mRNA /cds=(138,3092)			
		/gb=NM 020654 /gi=19923563			
٠.	90	/ug=Hs.30443 /len=4826			
8501	0.020104	hypothetical protein FLJ40137	NM 173478	Hs.412708	NP_77574
0001	10.020101	(FLJ40137), mRNA /cds=(149,1141)	110470	1110.412700	-
		/gb=NM_173478 /gi=27735056			
•	÷ ••	/ug=Hs.412708 /len=2241			1
8509	0.048502	pericentrin 1 (PCNT1), mRNA	NM 024844	Hs.184352	NP_07912
0505	0.040302	/cds=(81,2051) /gb=NM_024844		113.104372	NF_0/912
			+		
9		/gi=13376258 /ug=Hs.184352 /len=2147			
0550	0.000404	-DNIA EL 100E44 E1	A14000000	11- 404000	<del>-41</del>
8550	0.020104	cDNA FLJ36544 fis, clone	AK093863	Hs.101689	
		TRACH2006378. /gb=AK093863	3	*	
	· ·	/gi=21752807 /ug=Hs.101689 /len=2670			
050=	0.04000	11111 00 0 111	1111001500	11. 445000	
8587	0.040325	UI-H-BI2-agk-g-09-0-UI.s1	AW291592	Hs.445096	
		NCI_CGAP_Sub4 cDNA clone			
		IMAGE:2724688 3', mRNA sequence	·		
	0 3	/clone=IMAGE:2724688 /clone_end=3'			
		/gb=AW291592 /gi=6698228	8.00	1	
		/ug=Hs.445096 /len=680			9-1
8610	0.018081	EST, cDNA /gb=AW816379	AW816379	Hs.335018	
Dec 6		/gi=7909373 /ug=Hs.335018 /len=603		-	
8615	0.009227	cDNA clone IMAGE:3918063 5'	BE895919	1	NP_05515
		601432861F1 NIH_MGC_72		• 00	× -
8651	0.040325	clone IMAGE:4130494, mRNA	BC023543	Hs.112844	· · · · · · · · · · · · · · · · · · ·
	1.	/gb=BC023543 /gi=23270740			
	1 3	/ug=Hs.112844 /len=4567	*	1	

		nding To Differ ntially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
		*	Accession No.	Accession	Accession
•	. *			No.	No.
.8673	0.027356	jun1.P1.D7 conorm cDNA 3', mRNA	AI535800	Hs.369112	
		sequence /clone_end=3' /gb=AI535800	0 -		
	5	/gi=4449935 /ug=Hs.369112 /len=480	: .		9 '
				. *	
8680	0.006542	hypothetical protein FLJ32234	NM 152551	Hs.13366	NP_689764
0000	0.0000 12	(FLJ32234), mRNA /cds=(37,471)	102001	1119.10000	
		/gb=NM_152551 /gi=22749140			· ·
0000	0.044050	/ug=Hs.13366 /len=3051	010074400		
8692	0.044259	EST383274 MAGE resequences,	AW971186	Hs.442674	
		MAGL cDNA, mRNA sequence	)	->-	
		/gb=AW971186 /gi=8161031			
		/ug=Hs.442674 /len=603			
8724	0.033319	SMT3 suppressor of mif two 3 2 (yeast)	NM 006937	Hs.180139	NP 008868
		(SMT3H2), mRNA /cds=(137,424)			-
		/gb=NM_006937 /gi=21361387	74 1 8		
٠.		/ug=Hs.180139 /len=1478			÷.·*
	·	/ug=Hs. 160 139 /lett= 1476		•	
0700	0.044000	ECT DIVISION OF THE	41/740404		
8726	0.011629	ESTs, cDNA, 5' end /clone=GLCFNB12	AV/18434	Hs.282628	O)
		/clone_end=5' /gb=AV718434	-0		
		/gi=10815586 /ug=Hs.282628 /len=591			<b>\</b>
	196			*	
8756	0.020104	7m95c07.x1 NCI_CGAP_Brn23 cDNA	BF197659	Hs.289387	
		clone IMAGE:3562764 3' similar to			9 9
		contains Alu repetitive element; contains	*		*
	, ,	element MER33 repetitive element ,,			0)
				17	
		mRNA sequence			-
		/clone=IMAGE:3562764 /clone_end=3'	8.		
		/gb=BF197659 /gi=11086958	<u>.</u>		
-		/ug=Hs.289387 /len=516		,	
8798	0.024727	ESTs, cDNA, 3' end /clone=UI-E-EJ1-	BQ184236	Hs.373158	
		ajs-c-20-0-Uİ /clone_end=3'			8.8
		/gb=BQ184236 /gi=20359787	*		· ·
		/ug=Hs.373158 /len=734			
8799	0.010368	ubiquitin specific protease 7 (herpes	NM 003470	Hs.78683	NP 003461
0,00	0.910000	virus-associated) (USP7), mRNA	1.4141_000-470	1.13.70003	1.41 -00,540 1
			. **		1
1		/cds=(200,3508) /gb=NM_003470	* 0		
1 2 30	ļ	/gi=4507856 /ug=Hs.78683 /len=4022			1
8857	0.027356	UI-E-CK1-afh-f-18-0-ÚI.s1 UI-E-CK1	BU729774	Hs.238809	
		cDNA clone UI-E-CK1-afh-f-18-0-UI 3',			-
	i	mRNA sequence /clone=UI-E-CK1-afh-f	. ~		
	1	18-0-UI /clone_end=3' /gb=BU729774			
	1	/gi=23652993 /ug=Hs.238809 /len=1557	;		[
8863	0.044250	EST(cDNA clone IMAGE:290115 3'	N63269		
0003	0.044259	· ·	INUSZUS		*
	,	similar to contains Alu repetitive		*	
		element;contains element MSR1		1 .	•
	<u> </u>	repetitive element ; )			<u> </u>
8865	0.008196	cDNA FLJ12091 fis, clone	AK022153		
		HEMBB1002582		1	1

		nding T Differentially Expressed Gen			Desc
Spot	p-value	Description	Gene	Unig n	Protein
-			Accession No.	Accession	Accession
				No.	No.
8866	0.044259	DKFZp434B2122_r1 434 (synonym:	AL042731	Hs.292867	
		htes3) cDNA clone DKFZp434B2122 5',			
		mRNA sequence	· ·		
		/clone=DKFZp434B2122 /clone_end=5'			
	ţ.	/gb=AL042731 /gi=5935547		·	X-
		/ug=Hs.292867 /len=535			
8900	0.040325	hypothetical protein FLJ10252	NM_018040	Hs.53913	NP_060510
		(FLJ10252), mRNA /cds=(99,1685)			
		/gb=NM_018040 /gi=8922312	,		-
		/ug=Hs.53913 /len=2338			
8913	0.007267	EST xc94a04.x1 NCI_CGAP_Brn35	AW090604	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	<del>  </del>
	0.007207	cDNA clone IMAGE:2591886 3' similar	AVV030004		
				· · · · ·	·
		to contains element MSR1 repetitive			-
0045	0.040400	element;	A 10 400 7 4		
8915	0.013408	EST qh51c12.x1	Al242874	9 6	
)	- ;,	Soares_fetal_liver_spleen_1NFLS_S1			
	-00	H.sapiens cDNA clone IMAGE:1848214			
		3'		:	ĺ
8922	0.027356	EST RC3-CT0197-100999-021-F10	AW177654		
		CT0197 H.sapiens cDNA			
8946	0.018081	hypothetical protein FLJ33282	NM_152388	Hs.346509	
		(FLJ33282), mRNA /cds=(225,1523)	<del>-</del>		· -
	9 .	/gb=NM_152388 /gi=22748830	380		
		/ug=Hs.346509 /len=2078			
8950	0.016234	cDNA FLJ35790 fis, clone	AK093109	Hs.435026	
0000	0.0.020	TESTI2005720. /gb=AK093109	,	110.400020	
0.0		/gi=21751874 /ug=Hs.435026 /len=2405			·
·		/gi-21/310/4/ug-113.435020/ieii-2403 	*0		
8959	0.022315	xp63c01.x1 NCI_CGAP_Ov39 cDNA	AW277126	Hs.254883	<u> </u>
0909	0.022313	clone IMAGE:2745024 3', mRNA	AVV277120	ITIS.204003	
			,		
		sequence /clone=IMAGE:2745024	*		· ·
		/clone_end=3' /gb=AW277126			,
		/gi=6664156 /ug=Hs.254883 /len=427			
9012	0.030215	EST(AV707271 ADB cDNA clone	AV707271		NP_003109
		ADBCNC11 5')			
9071	0.040325	clone MGC:43690 IMAGE:5271254,	BC040606	Hs.366735	
		mRNA, complete cds /cds=(111,911)		*	
	-	/gb=BC040606 /gi=26252017			
		/ug=Hs.366735 /len=3191			
9092	0.024727	EST(cDNA clone IMAGE:4430342 5')	BG179708		NP_005819
9096		C1q and tumor necrosis factor related	NM_031911	Hs.153714	NP 114117
		protein 7 (C1QTNF7), mRNA	55 15 11		[ -
		/cds=(234,1103) /gb=NM_031911	· · · · · · · · · · · · · · · · · · ·		
4.7		· · · · ·			
		/gi=21314748 /ug=Hs.153714 /len=3959	* *		
0400	0.044554	alama INAA OF, 40 45000	D0047004	11-40000	
9160	0.014551	clone IMAGE:4245930, mRNA	BC017984	Hs.10683	
		/gb=BC017984 /gi=17389952		-	
	0.0	/ug=Hs.10683 /len=1190	l .		Ī

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigen	Protein
	: **		Accession No.	Accession	Accession
9235	0.033310	cDNA FLJ13558 fis, clone	AK023620	<b>No.</b> Hs.86043	No.
3233	0.055515	PLACE1007743. /gb=AK023620	AR023020	1113.00043	
			- 8		
		/gi=10435601 /ug=Hs.86043 /len=2271	•		
9263	0.036684	mRNA; cDNA DKFZp564G112 (from	AL049990	Hs.51515	
		clone DKFZp564G112) /gb=AL049990			
		/gi=4884242 /ug=Hs.51515 /len=1719			7
9269	0.020104	EST(cDNA clone IMAGE:2368136 3'	Al742789		NP 001959
		similar to gb:M15353 EUKARYOTIC			
		INITIATION FACTOR 4E (HUMAN); )	and the second		•
9303	0.044259	No significant match	SEQ.ID.No.29		-
9317		No significant match,	OLG.ID.I10.20 .		1 1 2 2 2
9317	0.030213	ORF+1(37~252,298~399)	SEQ.ID.No.95		
9318	0.01202	No significant match	SEQ.ID.No.102		
9330	0.046353	EST(CM4-CT0310-170300-114-f06	AW861413		
00.4=	0.044554	CT0310 cDNA, MRNA sequence)	050 15 11 70		<u>.</u>
9347		No significant match	SEQ.ID.No.76		
9368	0.024727	fms-related tyrosine kinase 1 (vascular	NM_002019	Hs.381093	NP_00201
		endothelial growth factor/vascular			
		permeability factor receptor) (FLT1),		,	
	:	mRNA /cds=(250,4266)		· · · · · · · · · · · ·	
		/gb=NM_002019 /gi=4503748		·	
	,	/ug=Hs.381093 /len=7680			*
9389	0.036684	proteolipid protein 1 (Pelizaeus-	NM_000533	Hs.1787	NP_00052
• 5		Merzbacher disease, spastic paraplegia	· · ·		
		2, uncomplicated) (PLP1), mRNA		200	
		/cds=(122,955) /gb=NM_000533			
		/gi=19923103 /ug=Hs.1787 /len=2938			
		, in the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second		10	
9391	0.022315	mitochondrial ribosomal protein S31	NM_005830	Hs.154655	NP_00582
, - , .		(MRPS31), nuclear gene encoding	3		
		mitochondrial protein, mRNA			
		/cds=(22,1209) /gb=NM_005830		000	
-		/gi=16950599 /ug=Hs.154655 /len=1284	0		
•	*	/g = 10930399 /ug=113: 134033 /ieii= 1204 	0.0	,	8 8
9415	0.027356	UPF3 regulator of nonsense transcripts	NM_023011	Hs.399740	NP_54241
		A (yeast) (UPF3A), transcript variant 1,			
		mRNA /cds=(38,1468) /gb=NM_023011	•		
		/gi=18375523 /ug=Hs.399740 /len=2381	., .	'	
				*	
	,				
9463	0.020104	tropomyosin 3 (TPM3), mRNA	NM_153649	Hs.85844	NP_70593
		/cds=(52,798) /gb=NM 153649	_ = = = = = = = = = = = = = = = = = = =		
		/gi=24119202 /ug=Hs.85844 /len=2089			
	1	1.3 1110202./dg .110.00044 /1011-2000	0)	-	1

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Acc ssion
9512	0.027356	mitochondrial ribosomal protein L32	NM_031903	No. Hs.50252	<b>No.</b> NP_114109
00.2	0.027000	(MRPL32), nuclear gene encoding	1111,_001000	1.0.00202	1 -11
		mitochondrial protein, mRNA			
		/cds=(47,613) /gb=NM 031903			
. •		· · · · · · · · · · · · · · · · · · ·			· ·
9543	0.014551	/gi=13994260 /ug=Hs.50252 /len=903 NADH dehydrogenase (ubiquinone) Fe-	NM_004551	Hs.429506	NP 004542
9040	0.014551	S protein 3, 30kDa (NADH-coenzyme Q		IUS.45300	INF_004542
,			) ·		
		reductase) (NDUFS3), mRNA			
		/cds=(13,807) /gb=NM_004551		· .	
05.40	0.000004	/gi=4758787 /ug=Hs.429506 /len=899	1114 000000	11. 05000	NID COOKS
9548	0.036684	ubiquitin specific protease 1 (USP1),	NM_003368	Hs:35086	NP_003359
		mRNA /cds=(246,2603)		18 8	
		/gb=NM_003368 /gi=21361109		• 0	· ·
		/ug=Hs.35086 /len=3379		1	
9583	0.048502	nuclear receptor subfamily 4, group A,	NM_006186	Hs.82120	NP_775265
	10.	member 2 (NR4A2), transcript variant 1,			
		mRNA /cds=(336,2132)	0		
	ļ	/gb=NM_006186 /gi=27894347			1
		/ug=Hs.82120 /len=3447			
9614	0.01302	ligand of numb-protein X (LNX), mRNA	NM_032622	Hs.66295	NP_116011
		/cds=(236,2134) /gb=NM_032622			
		/gi=14249127 /ug=Hs.66295 /len=3737			
9632	0.024727	clone MGC:9947 IMAGE:3876105,	BC013590	Hs!2437	
,		mRNA, complete cds /cds=(51,2216)			
7	oc-	/gb=BC013590 /gi=15488925	*		
		/ug=Hs.2437 /len=2651			
9635	0.022315	hypothetical protein FLJ11838	NM_024664	Hs.72531	NP 078940
		(FLJ11838), mRNA /cds=(8,862)			
	1	/gb=NM_024664 /gi=13375918	*	*	
		/ug=Hs.72531 /len=1430			
9666	0.048502	EST(za56e09.r1 Soares fetal liver	W01022		<del></del>
3000	0.040002	spleen 1NFLS cDNA clone 296584 5')	7401022	·	8-
9681	0.030215	EST(EST185852 Colon carcinoma	AA313967	· · · · · · · · · · · · · · · · · · ·	<del> </del>
3001	0.030213	(HCC) cell line II 5')	70.010001	Į.	
9700	0.048502	AUT-like 1, cysteine endopeptidase (S.	NM_032852	Hs.7353	NP_835739
3100	0.040302	cerevisiae) (AUTL1), mRNA	NIVI_032032	113.7333	1410007.08
			- 1	*	
		/cds=(208,1548) /gb=NM_032852	•		
0740	0.044050	/gi=14249577 /ug=Hs.7353 /len=2576	A A 7005 40	1 · · ·	
9710	0.044259	EST(nw52g07.s1 NCI_CGAP_Ew1	AA736548	·	
		clone IMAGE:1250268)			
9743	0.033319	hypothetical protein FLJ20507	NM_017849	Hs.202955	NP_060319
		(FLJ20507), mRNA /cds=(258,974)			
		/gb=NM_017849 /gi=8923465	<u>.</u> *	-	**.
		/ug=Hs.202955 /len=4223			
9757	0.020104	RAB18, member RAS oncogene family	NM_021252	Hs.21094	NP_067075
		(RAB18), mRNA /cds=(63,683)			
	~	/gb=NM_021252 /gi=19923574			
	1	/ug=Hs.21094 /len=2821	100		1

		nding To Diff r ntially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Acc ssion	Accession
				No.	No.
9767	0.036684	EST(wx72f07.x1 NCI_CGAP_Brn53	Al952357		NP_116128
		clone IMAGE:2549221 3' contains		y .	
		PTR7 repeat)	·		·
9782	0.018081	EST(RC0-CT0204-240999-031-e02	AW752488		NP 003332
0.02		CT0204)			
9805	0.033319	EST (qh12h02.x1	AI240516		
0000	0.000010	Soares_NFL_T_GBC_S1	,		
		IMAGE:1844499 3')			
9854	0.020104	SH3-domain GRB2-like 1 (SH3GL1),	NM_003025	Hs.97616	NP_003016
9004	0.020104	mRNA /cds=(16,1122) /gb=NM_003025	14141_000020	113.37010	1111 _0000 10
:		/gi=4506928 /ug=Hs.97616 /len=2349	•		
	,	/gi=4506926 /ug=Hs.976 to /ieti=2549			
0004	0.000040	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	NINA 004000	11- 200462	ND 004000
9934	0.033319	aconitase 2, mitochondrial (ACO2),	NM_001098	Hs.300463	NP_001089
1 54		nuclear gene encoding mitochondrial	,		
		protein, mRNA /cds=(21,2363)			
		/gb=NM_001098 /gi=4501866			**
		/ug=Hs.300463 /len=2467	8		
9972	0.044259	caldesmon 1 (CALD1), transcript variant	NM_033138	Hs.325474	NP_149347
•		1, mRNA /cds=(230,2611)	-0.0		
		/gb=NM_033138 /gi=15149460		1	
	·	/ug=Hs.325474 /len=3610			
10188	0.01302	chromosome 20 open reading frame 77	NM_021215	Hs.27192	NP_067038
		(C20orf77), mRNA /cds=(298,1278)			
- (		/gb=NM_021215 /gi=22507393			•
		/ug=Hs.27192 /len=4219			
10346	0.030215	UI-E-EO1-aiv-e-19-0-UI.s1 UI-E-EO1	BU742864	Hs.356716	N
		cDNA clone UI-E-EO1-aiv-e-19-0-UI 3',	*		
		mRNA sequence /clone=UI-E-EO1-aiv-	- * -		
		e-19-0-UI /clone_end=3' /gb=BU742864			
	•	/gi=23689787 /ug=Hs.356716 /len=1044			
		79. 20000 01 7dg 110.000 10 700 10 10 10 10 10 10 10 10 10 10 10 10 1	*	*	
10357	0.027356	ribosomal protein L23 (RPL23), mRNA	NM 000978	Hs.234518	NP 000969
1.0007	0.027330	/cds=(27,449) /gb=NM_000978	11111_000010	110.20-10 10	
•		/gi=14591907 /ug=Hs.234518 /len=493		1.	
		1/gi=14391907/dg=118.234310/lefi=493		C.	
10375	0.000104	DEAD/H (Asp-Glu-Ala-Asp/His) box	NM 018180	Hs.171835	NP 060650
10375	0.020104		NIVI_0 10 100	1115.17 1033	NF_000030
•		polypeptide 32 (DDX32), mRNA	-3:-		
		/cds=(492,2723) /gb=NM_018180			
		/gi=20336299 /ug=Hs.171835 /len=3070	'		
466=	0.000015	   FOT ( 00 - 00 - 1	A A 077 407		
10377	0.033319	EST (on60a02.s1	AA977467	-	
	,	Soares_NFL_T_GBC_S1	(2)		
· · · ·	·	IMAGE:1561034 3')	1	1	·
10433	0.044259	clone IMAGE:5275753, mRNA	BC044623	Hs.418416	
,		/gb=BC044623 /gi=27882398			
	<u> </u>	/ug=Hs.418416 /len=1997		<u> </u>	
10462	0.013822	EST (zs87f05.s1 NCI_CGAP_GCB1	AA279790		187
	8	cDNA clone IMAGE:704481 3')			

		nding To Differentially Expressed G n			
Spot	p-value	Description	Gen	Unigene	Protein
		1	Accession No.	Accession	Accession
				No.	No.
10480	0.040325	cDNA, 3' end /clone=IMAGE:1573685	AI733318	Hs.128357	NP_849172
		/clone_end=3' /gb=AI733318	.:		
		/gi=5054431 /ug=Hs.128357 /len=555			
10486	0.018081	zw70c12.s1 Soares_testis_NHT cDNA	AA431310	Hs.98724	
*	,	clone IMAGE:781558 3', mRNA		0.	
	-	sequence /clone=IMAGE:781558	·		
	. 6	/clone_end=3' /gb=AA431310		1.	
		/gi=2115018 /ug=Hs.98724 /len=365			
10505	0.007267	mRNA; cDNA DKFZp451B134 (from	AL832009	Hs.102796	1.
		clone DKFZp451B134) /gb=AL832009			
	*	/gi=21732549 /ug=Hs.102796 /len=4843			
	2 0.000		***		1
10510	0.020841	3'-5' RNA exonuclease (OLD35), mRNA	NM_033109	Hs.392004	NP_149100
		/cds=(19,2370) /gb=NM_033109		20	*.
		/gi=24308347 /ug=Hs.392004 /len=2616			
		EST(cDNA clone IMAGE:4151045 5')	BF343757		NP_078836
10589	0.018081	BX104984 Soares placenta Nb2HP	BX104984	Hs.287980	* * .
	. 0	cDNA clone IMAGp998G22188, mRNA			
4.		sequence		100	
		/clone=IMAGp998G22188_;_IMAGE:13			
• •	;	3677 /gb=BX104984 /gi=27833283			
		/ug=Hs.287980 /len=752			
10612	0.044259	cDNA FLJ39382 fis, clone	AK096701	Hs.293799	
		PERIC2000473. /gb=AK096701			
	· · · :	/gi=21756253 /ug=Hs.293799 /len=2425	a)(s		
40040	0.044050	FOT ( D) ( )	A1 50700 /		110 000100
10618	0.044259	EST(cDNA clone CS0DF024YE20 3	AL567394		NP_003109
40004	0.040400	prime )	A14/000040		
10631	0.042188	EST380924 cDNA	AW968848	Hs.268326	
		/gb=AW968848/gi=8158689			
40004	0.040004	/ug=Hs 268326 /len=746	0.222520	445770	
10661	0.018081	ip18c02.y1 HR85 islet cDNA clone	CA777576	Hs.115779	
		IMAGE:6217706 5', mRNA sequence			
		/clone=IMAGE:6217706 /clone_end=5			
		/gb=CA777576 /gi=26015451			·
10005	0 0 1 10 50	/ug=Hs.115779 /len=700			
10685	0.044259	UI-CF-EN1-acq-g-14-0-UI.s1 UI-CF-	BM982571	Hs.429805	
		EN1 cDNA clone UI-CF-EN1-acq-g-14-		7 .	
	3	0-UI 3', mRNA sequence /clone=UI-CF-		·	
	, =	EN1-acq-g-14-0-UI /clone_end=3'			
•	[	/gb=BM982571 /gi=19606203	*		· ·
		/ug=Hs.429805 /len=693			
10701	0.018081	cDNA FLJ90504 fis, clone	AK074985	Hs.171802	NP_775918
		NT2RP3004090, weakly similar to			ļ ·
	-	GOLIATH PROTEIN. /cds=(103,1305)			
		/gb=AK074985 /gi=22760786	1 Post 1		
		/ug=Hs.171802 /len=2452	. 0	1	ŀ

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
10737	0.016234	cDNA FLJ11997 fis, clone	AK022059	Hs.432755	
		HEMBB1001458. /gb=AK022059			
		/gi=10433379 /ug=Hs.432755 /len=2393			
10809	0.033319	estrogen receptor gene, 5' partial (422	AJ002562		
		(dp)			
10821	0.048502	601584240F1 NIH_MGC_7 cDNA clone	BE798289	Hs.446578	100
		IMAGE:3938912 5', mRNA sequence			
	<u>                                     </u>	/clone=IMAGE:3938912 /clone 'end=5'			1.
•••		/gb=BE798289 /gi=10219487			4
		/ug=Hs.446578 /len=793			· ·
		rag Tie. Troops hen yes	0		
10842	0.030215	EST (nc45b12.s1 NCI CGAP Pr3	AA229160		× .
		cDNA clone IMAGE:1011071 similar to			
		contains Alu repetitive element)	*		* .
10847	0.048502	hypothetical protein MGC3200	NM_032305	Hs.9088	NP_115681
	0.0,000	(MGC3200), mRNA /cds=(108,764)		110.0.00	- 1000 .
		/gb=NM_032305 /gi=14150063			9
		/ug=Hs:9088 /len=1191	*	]	8
10860	0.048502	mitochondrion, complete genome	NC 001807	1	
10863		EST(TCBAP1E0695 Pediatric pre-B cell			NP 006241
10003	0.033319	acute lymphoblastic leukemia Baylor-	DE243037		INP_000241
		HGSC project=TCBA clone	a t		
10000	0.000404	TCBAP0695)	NIA 450000	11. 054470	NE COCCO
10893	0.020104	hypothetical protein FLJ33167	NM_152683	Hs.351470	NP_689896
		(FLJ33167), mRNA /cds=(217,1899)			
	1 -	/gb=NM_152683 /gi=22749372			1
		/ug=Hs.351470 /len=2078			
10927	0.036684	cDNA FLJ30816 fis, clone	AK055378	Hs.350229	*
		FEBRA2001571. /gb=AK055378	:	25	
		/gi=16550091 /ug=Hs.350229 /len=2296			
					<u>.</u>
10966	0.040325	mRNA; cDNA DKFZp586C1723 (from	AL050192	Hs.80285	
		clone DKFZp586C1723) /gb=AL050192	8 0		
		/gi=4884408 /ug=Hs.80285 /len=1797	. 8/		
10997	0.048502	mRNA; cDNA DKFZp313C0432 (from	AL833123	Hs.134366	
	*	clone DKFZp313C0432) /gb=AL833123			
-		/gi=21733744 /ug=Hs.134366 /len=2626			
	, e		* -		
11004	0.024727	Similar to UDP-N-acetyl-alpha-D-	BC037341	Hs.351204	-
	1,	galactosamine:polypeptide N-			· ·
	1,0	acetylgalactosaminyltransferase 9	* :		,
	:	(GalNAc-T9), clone MGC:43305	÷,		
		IMAGE:5265475, mRNA, complete cds			
		/cds=(416,2239) /gb=BC037341	*.	ì	1
		/gi=22713621 /ug=Hs.351204 /len=2525	8		*
	<del></del>	I	<u> </u>	<del></del>	1 ,

Snot	p-value	nding To Differentially Expressed Gene Description	Gen	Unigene	Protein
Spor	p-value	Description			
9			Accession No.	Accession No.	Acc ssion No.
11082	0.022315	UI-1-BB1p-avc-e-03-0-UI.s1	BU754312	Hs.355575	NO.
11002	0.022313	NCI_CGAP_Pl6 cDNA clone UI-1-BB1p-	•	15.555575	
. •		avc-e-03-0-UI 3', mRNA sequence	- V	*	.*
		/clone=UI-1-BB1p-avc-e-03-0-UI			
		/clone_end=3' /gb=BU754312		ι,	
		/gi=23713100 /ug=Hs.355575 /len=1086	89.		
11160	0.033310	Similar to LOC168246, clone	BC027989	Hs.180059	
11100	0.055519	MGC:40162 IMAGE:4995539, mRNA,	DC021909	115.160009	÷
	•	complete cds /cds=(214,402)	- 00		
			• • •		
•-		/gb=BC027989 /gi=20380198		- * *	
11167	0.022240	/ug=Hs.180059 /len=1748	AK055625		
11107	0.033319	cDNA FLJ31063 fis, clone	AKUSS625		
14400	0.040400	HSYRA2001105	A 1/07/10F0	U- 254507	
11198	0.042188	cDNA FLJ23679 fis, clone HEP09084.	AK074259	Hs.351597	
		/gb=AK074259 /gi=18676812	0.		
44007	0.040500	/ug=Hs.351597 /len=2006	1114 000000	11 0470	N.B. 00000
11287	0.048502	fucosyltransferase 4 (alpha (1,3)	NM_002033	Hs.2173	NP_00202
	- (X)	fucosyltransferase, myeloid-specific)			
		(FUT4), mRNA /cds=(174,1766)			· .
		/gb=NM_002033 /gi=4503810	* = -		. * *
		/ug=Hs.2173 /len=2861			
11328	0.033319	solute carrier family 16 (monocarboxylic	NM_006517	Hs.75317	NP_006508
		acid transporters), member 2 (putative ,	) ,		
	20 2	transporter) (SLC16A2), mRNA		-8-	` .
\$ ·	*	/cds=(167,2008) /gb=NM_006517			
-		/gi=5730044 /ug=Hs.75317 /len=4371			()
4				*	
11330	0.01302	mitochondrial ribosomal protein L9	NM_031420	Hs.288936	NP_113608
		(MRPL9), nuclear gene encoding	111		
4.		mitochondrial protein, mRNA	-	.e:	0.0
		/cds=(86,889) /gb=NM_031420		-	
		/gi=22035596 /ug=Hs.288936 /len=1314			
		X			
11339	0.040325	hypothetical protein FLJ20986	NM_024524	Hs.324507	NP_07880
		(FLJ20986), mRNA /cds=(1758,3863)		1	
		/gb=NM_024524 /gi=21362055			
		/ug=Hs.324507 /len=5226			* *
11391	0.011629	putative S1 RNA binding domain protein	NM_016505	Hs.54971	NP_057589
		(PS1D), mRNA /cds=(137,862)			
		/gb=NM_016505 /gi=21361575			
		/ug=Hs.54971 /len=1602			
11397	0.033319	Niemann-Pick disease, type C2 (NPC2),	NM 006432	Hs.433222	NP_00642
		mRNA /cds=(116,571) /gb=NM_006432			
		1	9	1	
		/gi=20149580 /ug=Hs.433222 /len=929	ŀ		

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
	,		Accession No.	Accession	Accession
		*		No.	No.
11410	0.007267	ring finger protein 38 (RNF38), mRNA	NM_022781	Hs.77823	NP_073618
•		/cds=(563,1861) /gb=NM_022781			·
-		/gi=21918874 /ug=Hs.77823 /len=4694		,	
1					
11439	0.006431	hypothetical protein FLJ10292	NM_018048	Hs.104650	NP 060518
*		(FLJ10292), mRNA /cds=(53,499)	<del>-</del>		
		/gb=NM_018048 /gi=21361685	- 2 -	. 1	•
	*, *	/ug=Hs.104650 /len=2579			•
11459	0.016234	chromodomain helicase DNA binding	NM 024568	Hs:14570	NP_078844
, , , , ,	0.0.0	protein 1-like (CHD1L), mRNA			
		/cds=(332,1897) /gb=NM_024568		*	
		/gi=24308292 /ug=Hs.14570 /len=2936			
	• • • • • • • • • • • • • • • • • • •	7g1 24000202 7dg 113.14070 7611 2000			
11507	0.048502	ATPase, H transporting, lysosomal	NM_004888	Hs.90336	NP 004879
11301	0.040302	13kDa, V1 subunit G isoform 1	NIVI_004000	115.90550	141 _004079
	i '	(ATP6V1G1), mRNA /cds=(94,450)	0.10	1	
				• 5 8 .	
		/gb=NM_004888 /gi=20357534		-	
44544	0.040500	/ug=Hs.90336 /len=1110	NIN 004040	11. 400.400	115 004040
11514	0.048502	chromosome 21 open reading frame 33	NM_004649	Hs.182423	NP_004640
	4	(C21orf33), mRNA /cds=(85,891)		20	
		/gb=NM_004649 /gi=5031690			
		/ug=Hs.182423 /len=1652			
11546	0.020104	EST(PM3-NT0011-120400-001-b03	AW888715		
		NT0011)			
		EST(yv89b04.s1 clone 249871 3')	H96982		NP_775876
11572	0.044259	ir85f07.x1 HR85 islet cDNA clone	CA943825	Hs.347857	*
		IMAGE:6609350 3', mRNA sequence			- )( -
		/clone=IMAGE:6609350 /clone_end=3'	* 0	:	- 00
		/gb=CA943825 /gi=27432305	-	• .	*
		/ug=Hs.347857 /len=591		3.0	
11573	0.010368	EST(STS WI-10817)	G11888		
11591	0.048502	EST(zx08b10.s1 Soares total fetus	AA449121		
		Nb2HF8 9w clone 785851 3')		*	
11595	0.020104	hypothetical protein FLJ22104	NM_022918	Hs.183887	NP_075069
		(FLJ22104), mRNA /cds=(63,1127)			
e* .		/gb=NM_022918 /gi=12597666			
		/ug=Hs.183887 /len=2952	* *	-	
11637	0.020104	EST(at70b02.x1 Barstead colon	A1832565		
		HPLRB7 clone IMAGE:2377323 3'			
		contains L1.t3 L1 repeat)			
11680	0.048502	EST ys96h09.r1 Soares retina N2b5HR	H84275		
1 100,0	0.040002	cDNA clone IMAGE:222689 5'	110-270		
•		CONTROL MINOL. 222009.0			(a)
11682	0.010369	EST(zt35h04.r1 Soares ovary tumor	AA411101		NP_751896
11002	0.0 (0300	NbHOT cDNA clone IMAGE:724375 5')	1/V7411101		111 -73 1030
		INDITIO F CONA CIONE NVIAGE. 124375 5)			
	<u> </u>	L	L	L	<del>L.,,</del>

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Spot	p-value	Description	Gene	Unigene	Protein
		2	Accession No.	Accession	Accession
11000	0.040500	humath atical partain MCC5206	NIM COAAAC	No.	No.
11699	0.048502	hypothetical protein MGC5306	NM_024116	Hs.301732	NP_07702
		(MGC5306), mRNA /cds=(207,1043)			
		/gb=NM_024116 /gi=13129135			
T. 22 .		/ug=Hs.301732 /len=2336			
11784	0.036684	sperm associated antigen 9 (SPAG9),	NM_003971	Hs.129872	NP_75885
		transcript variant 1, mRNA			
		/cds=(79,4002) /gb=NM_003971	•		•
		/gi=27436919 /ug=Hs.129872 /len=4663	·		w
11812	0.033319	wl84f02.x1 NCI_CGAP_Brn25 cDNA	AI884779	Hs 380770	
,		clone IMAGE:2431611 3', mRNA		,	" =
		sequence /clone=IMAGE:2431611			
•	,	/clone_end=3' /gb=Al884779	•	*	
		/gi=5589943 /ug=Hs.380770 /len=527			
11841	0.033319	lin-7 C (C. elegans) (LIN7C), mRNA	NM_018362	Hs.91393	NP_06083
	0.000	/cds=(22,615) /gb=NM_018362			
	)	/gi=8922943 /ug=Hs.91393 /len=2372			
11888	0.005008	FLJ00071 protein, partial cds	AK024478	Hs.7049	NP 06085
	0.00000	/cds=UNKNOWN /gb=AK024478		11.0.7010	
		/gi=10440469 /ug=Hs.7049 /len=4194			
11916	0.022315	Probe hTg737 (polycystic kidney	NM 175605	Hs.2291	NP_78319
	0.022010	disease, autosomal recessive) (TG737),	111111_170000	113.2201	_, 00, 10,
•		transcript variant 1, mRNA	*		-8-
		/cds=(358,2832) /gb=NM_175605	0		1
		/gi=28329441 /ug=Hs.2291 /len=3035	·		
11923	0.044250	unidentified mRNA, partial sequence.	U43604	Hs.159901	
11923	0.044239	/gb=U43604 /gi=1171236	043004	115.159901	
		/ug=Hs.159901 /len=1677	4.		
11959	0.026694		VM 010524		1-7
11909	0.030004	similar to cortistatin (H. sapiens)	XM_010524		-
11064	0.007256	(LOC126684), mRNA	NM 015530	Lie COOO	ND OFCOAL
11964	0.027356	golgi reassembly stacking protein 2,	NIVI_U 1553U	Hs.6880	NP_05634
	*	55kDa (GORASP2), mRNA	- X-		4
		/cds=(52,1524) /gb=NM_015530			
11072	0.000004	/gi=20127538 /ug=Hs.6880 /len=2424	NC 004007		
11973		mitochondrion, complete genome	NC_001807		<del> </del>
12005	0.005681	EST(no44e03.s1 NCI_CGAP_Pr23	AA622352		
40040	0.00000	cDNA clone IMAGE:1103548)	4.4054.40		
12019	0.00000	EST(zv83c02.s1 Soares total fetus	AA425140		
		Nb2HF8 9w clone 760226 3' contains			
40040	0.000004	MER14.t2 MER14 repeat)	1111070 100		
12043	0.036684	EST385456 MAGE resequences,	AW973463	-	
4040=	0.007007	MAGM	DE4.40.4		·
12165	0.007267	EST CM3-HT0185-061099-021-c03	BE144941		
10155		HT0185 cDNA			N.D. 0===
12183	0.020104	cDNA sequence (cDNA FLJ14256 fis,	AK024318		NP_07374
	,	clone PLACE1000007, weakly similar to		1	
		PROBABLE UBIQUITIN CARBOXYL-	· .		
		TERMINAL HYDROLASE R10E11.3)			
	15	Length = 3176		1	

C	m val··-	Decarintian	Como	I Indiana	D4-
spot	p-value	Description	Gene	Unigene	Protein
	)		Accession No.	Accession No.	Accession No.
12189	0.044259	EST AV750486 NPC H sapiens cDNA	AV750486	140.	140.
	5,5	clone NPCDCF06 5'	*	1	
12191	0.01302	kruppel-like zinc finger protein	NM_052860	Hs.288928	NP 443092
7		(ZNF300), mRNA /cds=(268,2082)			- 10002
:		/gb=NM_052860 /gi=16604251		0	*
	•	/ug=Hs.288928 /len=3104			
12193	0.048502	EST (yd68e02.s1 Soares fetal liver	T78464		NP_000436
		spleen 1NFLS IMAGE:113402 3')		•	*
12210	0.048502	cDNA FLJ38039 fis, clone	AK095358	Hs.46506	- N 1
	j	CTONG2013934. /gb=AK095358	-		•
	÷	/gi=21754600 /ug=Hs.46506 /len=2956	* <b>'</b>	0	* *
12220	0.027356	wb40b11.x1 NCI_CGAP_GC6 cDNA	Al652865	Hs.374238	
	-	clone IMAGE:2308125 3, mRNA			
		sequence /clone=IMAGE:2308125			
		/clone_end=3' /gb=Al652865		: 2	
•		/gi=4736844 /ug=Hs.374238 /len=598	*		· · ·
12242	0.030215	EST372182 MAGE resequences,	AW960111		
	,	MAGF	•	· .	
12244	0.040325	EST(601812732F1 NIH_MGC_54	BF211120	1	NP 071942
		cDNA clone IMAGE:4047222 5')	* *		
12245	0.016234	EST380358 MAGE resequences,	AW968163	Hs.432535	
		MAGJ cDNA, mRNA sequence			
		/gb=AW968163 /gi=8158123		'	
		/ug=Hs.432535 /len=557			ix
12287	0.040325	EST(HS_2057_B2_G07_MR CIT	AQ901098		
		Approved Genomic Sperm Library D			
191 -	:	genomic clone Plate=2057 Col=14			. `
		Row=N)			
12316	0.048502	oc55d08.s1 NCI_CGAP_GCB1 cDNA	AA830598	Hs.266825	
		clone IMAGE:1353615 3', mRNA			1
		sequence /clone=IMAGE:1353615	*		
		/clone_end=3' /gb=AA830598			1
	•	/gi=2903697 /ug=Hs.266825 /len=512			
12326	0.009227	EST(UI-H-BI3-akh-f-06-0-UI.s1	AW449287	18	
		NCI_CGAP_Sub5 cDNA clone			
		IMAGE:2734235 3')			
12355	0.01302	cDNA FLJ36238 fis, clone	AK093557	Hs.345588	
		THYMU2001422. /gb=AK093557			
	-30	/gi=21752458 /ug=Hs.345588 /len=2269		* 5 °	
7 8 11 7 8		*		1	
12507	0.024727	UI-E-CQ1-acq-b-08-0-UI.r1 UI-E-CQ1	BM688644	Hs.253634	100 CH 9 COLL
	-	cDNA clone UI-E-CQ1-acq-b-08-0-UI 5',			1
:		mRNA sequence /clone=UI-E-CQ1-acq-	• (0		:
	-)(-	b-08-0-UI /clone_end=5' /gb=BM688644		*	
		/gi=19001902 /ug=Hs.253634 /len=1017			
				1	

		nding To Differentially Expr ssed Gen			
	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	-			No.	No.
12509	0.038336	EST(NISC_It08e07.y1 COGENE 8.5	CA335266		
	- ·	EPT Homo sapiens cDNA clone			
		IMAGE:5606125 5')			*
12515	0.048502	stress 70 protein chaperone,	NM_006948	Hs.352341	NP_008879
		microsome-associated, 60kDa (STCH),	<del></del>	1	
!		mRNA /cds=(37,1452) /gb=NM_006948	0.		
	*	/gi=24431965 /ug=Hs.352341 /len=3998			*
		3			*
2517	0.040325	UI-H-DP0-avt-a-17-0-UI.s1	BQ000272	Hs.371473	
= 7	7.	NCI_CGAP_Fs1 cDNA clone			
		IMAGE:5883928 3', mRNA sequence	*	,	
	- 00	/clone=IMAGE:5883928 /clone_end=3'	*		
		/gb=BQ000272 /gi=19725172	*	N.	
. * *		/ug=Hs.371473 /len=1051	0	. ·	-
12530	0.048502	AGENCOURT_7566238 NIH_MGC_92	BQ226831	Hs.21887	
_000	0.0-0002	cDNA clone IMAGE:6043519 5', mRNA	D G Z Z C C C	113.21007	
· .		sequence /clone=IMAGE:6043519			
	*	/clone_end=5' /gb=BQ226831	.*	-	
	\$ °	/gi=20408231 /ug=Hs.21887 /len=1223		- ·	
		/gi=20406231/ug=HS.21667/lefi=1223			
2572	0.020104	EST, clone IMAGE:4151959, mRNA	BC011194	Hs.367863	
2312	0.020104	/cds=UNKNOWN /gb=BC011194	0011194	115.507605	
		/gi=15277441 /ug=Hs.367863 /len=1842	(¥)	* *	
		/gi= 132774417ug=11s.3070037leti=1042 		:	
2608	0.044259	mRNA; cDNA DKFZp586L081 (from	AL080234	Hs.432862	
2,000	0.044203	clone DKFZp586L081) /gb=AL080234	AL000204	113.402002	
		/gi=5262727 /ug=Hs.432862 /len=2159			
*		0202121 /ug=113.402002 /1611=2109	40		
2669	0.044250	hypothetical protein FLJ31438	NM 152385	Hs.24423	NP 689598
-000	3.5-7253	(FLJ31438), mRNA /cds=(347,2107)	102000	113.27720	
•		/gb=NM_152385 /gi=22748824		2 1	
		/ug=Hs.24423 /len=2266	*		
2671	0.007267	cDNA FLJ40904 fis, clone	AK098223	Hs.375905	
2011	0.001201	UTERU2004564. /gb=AK098223	MINDOZZO	11 18.07 0800	
		/gi=21758192 /ug=Hs.375905 /len=2224			
		/g -2   / 30   32 /ug-  15.3 / 3303 /le 1=2224 			
2686	0.040335	mucosa associated lymphoid tissue	NM_006785	Hs:180566	NP_776216
2000	0.040325	lymphoma translocation gene 1	14i4i_0007.00	113.100000	NE _ / / OZ 10
		(MALT1), transcript variant 1, mRNA	*	l ·	
-	y.	/cds=(259,2733) /gb=NM_006785	9		
	2 111			*	*
		/gi=27886564 /ug=Hs.180566 /len=5029		3	
12697	0.049502	mitochandrian complete conome	NC 001907		·
2706		mitochondrion, complete genome hypothetical protein MGC14801	NC_001807	He 122016	NP_116094
2100	0.011029		NM_032705	Hs.132816	110094
		(MGC14801), mRNA /cds=(132,416)			
		/gb=NM_032705 /gi=14249301	J J		
		/ug=Hs.132816 /len=762		1	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Acc ssion	Accession
				No.	No.
12707	0.009227	mRNA for KIAA1902 protein, partial	AB067489	Hs.7149	
•	1.	cds. /cds=(79,3417) /gb=AB067489			-
	-	/gi=15620862 /ug=Hs.7149 /len=5344	*		
12714		mRNA for KIAA0789 protein, partial	AB018332	Hs.158319	
		cds. /cds=(580,2442) /gb=AB018332	,, ,, ,		
		/gi=14133216 /ug=Hs.158319 /len=4217			
		/gi=14133210/ug=113. 130319/leti=421/			
40704	0.040200	BX099644 NCI CGAP Kid3 cDNA	BX099644	Hs.125353	1000
12731	0.010368		DXU99044	INS. 120000	
		clone IMAGp998A103336, mRNA	(Pro		
		sequence		*	
		/clone=IMAGp998A103336_;_IMAGE:1			
		323153 /gb=BX099644 /gi=27830124			
*		/ug=Hs.125353 /len=472			<u> </u>
12734	0.016234	mRNA for FLJ00201 protein.	AK074129	Hs.353001	
		/cds=(1,2119) /gb=AK074129			
•	-	/gi=18676605 /ug=Hs.353001 /len=4443	· · · · · · · · · · · · · · · · · · ·		
		/gi=100/0000 /ug 110.00000 / /icij 4-1-10	*>		
12764	0.048502	UI-H-EU1-bac-h-16-0-UI.s1	BQ447010	Hs.437398	<del></del>
12/04	0.046302		DQ447010	IDS.437390	0 200
		NCI_CGAP_Ct1 cDNA clone UI-H-EU1-	**		
		bac-h-16-0-UI 3', mRNA sequence	,	0	
	1,	/clone=UI-H-EU1-bac-h-16-0-UI			
		/clone_end=3' /gb=BQ447010			*
	}	/gi=21250122 /ug=Hs.437398 /len=1089			
				-	* *
12775	0.027356	acidic (leucine-rich) nuclear	NM 006401	Hs.84264	NP 006392
		phosphoprotein 32 family, member B			
		(ANP32B), mRNA /cds=(211,966)			
	*	/gb=NM_006401 /gi=5454087	. 7		
		/ug=Hs.84264 /len=1475		1 " "	
40004	0.044050		AL571019	Hs.397285	
12831	0.044259	AL571019 LTI_NFL006_PL2 cDNA	AL5/1019	HS.397200	
*		clone CS0DI028YD01 3 prime, mRNA			
	-	sequence /clone=CS0DI028YD01			· .
		/clone_end=3' /gb=AL571019	÷		
		/gi=12927901 /ug=Hs.397285 /len=345	<u> </u>	(1)	100
	122	Y	:		<u>.</u>
12837	0.048502	cDNA, 5' end /clone=IMAGE:5214599	BI911779	Hs.13370	NP_05476:
	1-	/clone_end=5' /gb=Bl911779			_
	- 10	/gi=16175651 /ug=Hs.121740 /len=818			
		13 / 1 0 0 0 1 / ag   1   0 . 12   1 40 /   0     0		` '	
12871	0.024727	WG07c03 V1 NCL CCAR Kid11 aDNA	AI762342	Hs.304298	
120/7	0.024727		M1102342	175.304290	1
. •		clone IMAGE:2379172 3' similar to	10	. ,	
		contains L1.b1 L1 repetitive element ;,		1	
		mRNA sequence		1 .	
		/clone=IMAGE:2379172 /clone_end=3'			
:		/gb=Al762342 /gi=5178009	7.		

Spot	p-value	Description	Gene	Unig n	Prot in
			Accession No.	Accession	Acc ssion
				No.	No.
12878	0.040325	cDNA PSEC0152 fis, clone	AK075459	Hs.350475	
		PLACE1007885. /cds=(20,1144)			: .
		/gb=AK075459 /gi=22761560			
		/ug=Hs.350475 /len=2130			
12882	0.014551	DKFZp564A2463 (from clone	AL137573	Hs.43143	
•		DKFZp564A2463) /cds=UNKNOWN			
		/gb=AL137573 /gi=6808283			
		/ug=Hs.43143 /len=1320			:
12902	0.044259	ESTs, FLJ25251 fis, clone STM03603	AK057980	Hs.256801	
		/cds=UNKNOWN /gb=AK057980			1.0
		/gi=16553972 /ug=Hs.256801 /len=1727			•
12974	0.027356	BX101970 Soares fetal liver spleen	BX101970	Hs.12950	i
		1NFLS cDNA clone IMAGp998A1818,			*
-		mRNA sequence			
		/clone=IMAGp998A1818_;_IMAGE:663			
	1 1 1	29 /gb=BX101970 /gi=27831534			
<u> </u>		/ug=Hs.12950 /len=677			
12981	0.044259	selenoprotein H (SELH), mRNA	NM_170746	Hs.290874	NP_73446
		/cds=(243,611) /gb=NM_170746			
		/gi=25014108 /ug=Hs.290874 /len=834		,	
•-	- 0				, ,
13016	0.033319	AGENCOURT_6613737 NIH_MGC_41	BM912985	Hs:351869	5.
		cDNA clone IMAGE:5474977 5', mRNA		- In T	
	. 8	sequence /clone=IMAGE:5474977	*		
		/clone_end=5' /gb=BM912985			
	+	/gi=19363364 /ug=Hs.351869 /len=1565			
	·				
	0.044259			4.01	
		No significant match	SEQ.ID.No.31		
13166	0.030215	hypothetical protein FLJ22029	NM_024949	Hs.285243	NP_07922
		(FLJ22029), mRNA /cds=(40,1473)			
	1	/gb=NM_024949 /gi=21361978			1
	. 1	/ug=Hs.285243 /len=4189		*	
13190	0.022315	membrane-spanning 4-domains,	NM_152852	Hs.17914	NP_69059
•		subfamily A, member 6A (MS4A6A),			
		transcript variant 1, mRNA			
		/cds=(239,985) /gb=NM_152852	2. 8		
		/gi=23238237 /ug=Hs.17914 /len=1564			
13289	0.036684	cDNA: FLJ23538 fis, clone LNG08010,	AK027191	Hs.240443	*.
		highly similar to BETA2 MEN1 region		-	
	,	clone epsilon/beta mRNA.	*		
		/gb=AK027191 /gi=10440260			<b>.</b> *
	1	/ug=Hs.240443 /len=1746	I .	1. '	

		nding To Differentially Express d Gen			B
Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
				No.	No.
3299	0.044259	likely ortholog of mouse acyl-Coenzyme	NM 012332	Hs.18625	NP_03646
		A thioesterase 2, mitochondrial			
		(ACATE2), mRNA /cds=(148,1368)	74	6 4.	
	٠	/gb=NM_012332 /gi=6912517		4	
			* _		
10050	0.000040	/ug=Hs.18625 /len=1954	NIA 000405	11- 000000	ND 00000
13356	0.033319		NM_000405	Hs.289082	NP_00039
		(GM2A), mRNA /cds=(96,677)			
		/gb=NM_000405 /gi=16507969		i i	1 1 1
		/ug=Hs.289082 /len=2478			
13380	0.048502	similar to HYPOTHETICAL 34.0 KDA	NM_033416	Hs.91579	NP_21948
ļ	.*	PROTEIN ZK795.3 IN CHROMOSOME	er :		1
:		IV (MGC19606), mRNA /cds=(18,893)			* .
		/gb=NM_033416 /gi=15529981	, ,		.70
		/ug=Hs.91579 /len=1074	*		-
	,	749 110.0 1010 Non-1014		Ŷ	
1220F	0.027256	mombrano bound transprintion factor	NIM 002701	Hs.75890	NP 00378
13385	0.027356	membrane-bound transcription factor	NM_003791	F15.7509U	in=_003/8
		protease, site 1 (MBTPS1), mRNA		*	
		/cds=(497,3655) /gb=NM_003791			
		/gi=4506774 /ug=Hs.75890 /len=4338			
13392	0.034779	hypothetical protein FLJ30162	NM_152731	Hs.311163	NP_68994
-		(FLJ30162), mRNA /cds=(272,841)	7		•
		/gb=NM_152731 /gi=22749448		1.	-
		/ug=Hs.311163 /len=2278		. 0	
13407	0.01302	EST(zi68c01.s1 Soares fetal liver	AA701957		
13407	0.01302	spleen 1NFLS S1 cDNA clone 435936	7,04701307		0
	-	In the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of th			*
10.10.1	0.000040	50T/ - 60-04-4 Ob-to-to	A 4 4 5 0 7 5 0		-
13421	0.033319	EST(zo63g01.s1 Stratagene panCReas	AA 158759	*	
		(#937208) clone IMAGE:591600 3'	1		.:
	: .	contains Alu repeat)	-1		
13445	0.009227	PEST-containing nuclear protein	NM_020357	Hs.71618	NP_06509
		(PCNP), mRNA /cds=(19,555)		•	
		/gb=NM_020357 /gi=9966826			
		/ug=Hs.71618 /len=2250			
13470	0.036684	putative intramembrane cleaving	NM 032802	Hs.28980	NP 11619
. 5 . 7 5	5.555007	protease (SPPL2A), mRNA		[	
		/cds=(144,1706) /gb=NM_032802			
	-	/gi=21314754 /ug=Hs.28980 /len=2012			
			1000000		110 4450
13513	0.022315	EST(PM3-SN0020-270300-001-h08	AW865025	1. 1.	NP_11566
		SN0020)			
13556	0.014551	EST (RC4-BT0311-251199-012-c08	BE064435		
	* *	BT0311)			
13571	0.025072	EST (7d70f02.x1 NCI_CGAP_Lu24	BE673855		
		IMAGE:3278331 3')		·	
	0.016234	PTK7 protein tyrosine kinase 7 (PTK7),	NM_002821	Hs.90572	NP 69062
13584		In item biorous ratoonio mingoost (1 1161)!	155252,	1	1 -00002
13584	0.010254	transcript variant DTK7_1 mDNA			1
13584	0.010204	transcript variant PTK7-1, mRNA			
13584	0.010204	transcript variant PTK7-1, mRNA /cds=(199,3411) /gb=NM_002821 /gi=27886610 /ug=Hs.90572 /len=4249		.y	

		nding To Differ ntially Expressed Gen			
Spot	p-value	Description	Gen	Unigene	Protein
		4	Accession No.	Accession	Accession
				No.	No.
13620	0.022315	cDNA FLJ36860 fis, clone	AK094179	Hs.352406	NP 612398
	9.1	ASTRO2015295. /gb=AK094179			
	1	/gi=21753186 /ug=Hs.352406 /len=2882		, ,	<b>l</b> .
•	j	791 211 00 100 749 110.002 400 71011 2002	3 _		
13633	0.040325	guanine nucleotide binding protein (G	NM_005273	Hs.91299	NP_005264
		protein), beta polypeptide 2 (GNB2),	0001/0	110.01.200	
		mRNA /cds=(259,1281)	,	}	-
		/gb=NM_005273 /gi=20357528	*		
		/ug=Hs.91299 /len=1666			
13746	0.044250	mRNA; cDNA DKFZp451N2217 (from	AL832616	Hs.335812	<del>:</del> .
157.40	0.044259		AL032010	IUS:332015	
		clone DKFZp451N2217) /gb=AL832616	*		
	i	/gi=21733191 /ug=Hs.335812 /len=4940		- 8-	Ì
10771	0.000404		1114 004 50		115 00 1150
13774	0.020104	fetal Alzheimer antigen (FALZ), mRNA	NM_004459	Hs.99872	NP_004450
4.		/cds=(37,2469) /gb=NM_004459	d.		
		/gi=6552329 /ug=Hs.99872 /len=2616	,		
13782	0.022315	citrate synthase (CS), nuclear gene	NM_004077	Hs.239760	NP_004068
		encoding mitochondrial protein, mRNA			1
		/cds=(1,1401) /gb=NM_004077			
		/gi=4758075 /ug=Hs.239760 /len=1401			
2	*				•
13798	0.048502	SET binding protein 1 (SETBP1),	NM_015559	Hs.151717	NP_056374
		mRNA /cds=(6,4634) /gb=NM_015559	_		_
		/gi=7662121 /ug=Hs.151717 /len=5744	÷		
13836	0.048502	non-SMC (structural maintenance of	NM_145080	Hs.284295	NP_659547
•	-	chromosomes) element 1 protein			
	,	(NSE1), mRNA /cds=(24,794)	• • •	- 1	
		/gb=NM 145080 /gi=21489972			
· ·		/ug=Hs.284295 /len=992			
13878	0.048502	EST(yr18g03.r1 cDNA clone 205684 5')	Hesone		<del> </del>
10070	0.040002	Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont	1100000		
13885	0.016234	EST DKFZp434H1418 r1 434	AL048856	<u> </u>	NP_006531
10000	0.010204	(synonym:htes3) cDNA clone			
	i	DKFZp434H1418			-
13889	0.016234	protein phosphatase 1, regulatory	NM 005398	Hs.303090	NP 005389
13009	0.010234		NNI_002396	IU8.303080	NP_005369
		(inhibitor) subunit 3C (PPP1R3C),	ŕ	,	
i		mRNA /cds=(58,1011) /gb=NM_005398	*		
		/gi=21314622 /ug=Hs.303090 /len=2524			
12052	0.044050	hungth stiggt protein EL 120007	NINA 047746	Un 26260	ND 000040
13953	0.044259	hypothetical protein FLJ20287	NM_017746	Hs.26369	NP_060216
		(FLJ20287), mRNA /cds=(132,2921)			
-		/gb=NM_017746 /gi=8923268			÷ ,
		/ug=Hs.26369 /len=3043		<u></u>	
13955	0.023168	cDNA FLJ32123 fis, clone	AK056685	Hs.349397	
	,	PEBLM1000174. /gb=AK056685			
		/gi=16552158 /ug=Hs.349397 /len=2326			
		· ·			1

Snot	p-value	Description	Gene	Unig ne	Protein
Opot	p-value	Description	Accession No.	Accession	Accession
			Accession No.	No.	No.
13974	0.036684	mRNA for KIAA1013 protein, partial	AB023230	Hs.96427	NO.
		cds. /cds=(1,3189) /gb=AB023230			* .
		/gi=4589675 /ug=Hs.96427 /len=4783			~.
14029	0.036684	EST (zk36c07.r	AA037529		<del>                                     </del>
14023	0.000004	Soares pregnant uterus NbHPU	70-037-323		
	. '	IMAGE:484908 5')		-1	
14032	0.016234	cDNA sequence (cDNA sequence	AK021798		
14032	0.010234	FLJ11736 fis, clone HEMBA1005468)	AR021790	8	*
14051	0.044250	EST(yh44h12.r1 Soares placenta	R26018		****
14051	0.044259		1 1 2 2 0 1 0		
		Nb2HP cDNA clone IMAGE:132647-5')		0.5	
14050	0.046004	FOT (-DNA -lane IMACE: 2400076 21)	A10700E4		NID 000000
		EST (cDNA clone IMAGE:2490676 3')	AI972954	11- 000004	NP_000996
14097	0.018081	MR0-HT0559-290500-027-d10 HT0559	BE708268	Hs 209224	
		cDNA, mRNA sequence /gb=BE708268	*		
	*	/gi=10096533 /ug=Hs.209224 /len=619			• ** *
	*				
14098	0.027356	clone IMAGE:5261776, mRNA	BC035093	Hs.288339	
		/gb=BC035093 /gi=23272456	*		
		/ug=Hs.288339 /len=1880			
14130	0.044259	EST (yx14d09.r1 Soares melanocyte	N23550		
		2NbHM IMAGE:261713 5')		•	
14135		mitochondrion, complete genome	NC_001807		
14171	0.036684	nz80g08.s1 NCI_CGAP_GCB1 cDNA	AA767226	Hs.368058	
		clone IMAGE:1301822 3', mRNA	1		
		sequence /clone=IMAGE:1301822			
		/clone_end=3' /gb=AA767226			
		/gi=2818241 /ug=Hs.368058 /len=542			
14192	0.024727	EST(PM0-HT0452-140100-002-a07	AW607067	7 - 0	NP_000198
		HT0452)	· ·	<u>(1)</u>	
14240	0.030215	EST(cDNA clone IMAGE:1076536 3'	AA592920	•	
	•	similar to TR:G56589 G56589 LONG	101		
		INTERSPERSED REPETITIVE DNA		1	-
		CONTAINING 7 ORF'S.; contains L1.t3	20 F.	٠. د	• .
		L1 repetitive element ; )			, ,
14244	0.033319	cDNA FLJ11946 fis, clone	AK022008	Hs.323231	
		HEMBB1000709. /gb=AK022008		. 19.04	
		/gi=10433321 /ug=Hs.323231 /len=3241	1,000		
		10 10 10 10 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 11 10 10		•	7 31
14265	0.028482	UI-H-EZ1-bbj-p-15-0-UI.s1	BQ771691	Hs.435931	· · · · ·
1-12-00	0.020102	NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-		113.400001	
		bbj-p-15-0-UI 3', mRNA sequence	1		
		/clone=UI-H-EZ1-bbj-p-15-0-UI			- 33 -
		/clone_end=3' /gb=BQ771691		.[	.[
	,	//gi=21980167 /ug=Hs.435931 /len=1072	-		
		/g -2  900  07  /ug-  15.45595   /le  -  072 		-	1
1/276	0.027250	EL 111084 fig. clone UEMPD1001249	VK033046	He 202022	1
14276	0.02/356	FLJ11984 fis, clone HEMBB1001348	AK022046	Hs.293922	] ·
	l ·	/cds=UNKNOWN /gb=AK022046			
	I	/gi=10433365 /ug=Hs.293922 /len=3161			

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene	Unigene	Protein
	Y P E	* * *	Accession No.	Accession	Accession
	0.040000		512 / 12 22	No.	No.
14280	0.048502	cDNA clone IMAGE:5243592 57	BI914006		
		603179205F1 NIH_MGC_121			
14292	0.044259	EST(WashU MPIMG EST Danio rerio	AI965287	7.1	7
		cDNA clone IMAGE:3728540 3')			••
14305	0.033319	hh32h11.x1 NCI_CGAP_Lu24 cDNA	AW615336	Hs.281215	• - *
		clone IMAGE:2956869 3', mRNA			
		sequence /clone=IMAGE:2956869			[. · · · · ·
,	- ()	/clone_end=3' /gb=AW615336	•	, %	
*		/gi=7320522 /ug=Hs.281215 /len=391			
14322	0.018081	clone IMAGE:4297077, mRNA	BC017920	Hs.375771	
	*	/gb=BC017920 /gi=17389820			٠.
		/ug=Hs.375771 /len=1247		0	
14332	0.040325	EST(cDNA clone IMAGE:1860591 3'	Al199593		TALE OF THE SALES
1		similar to contains MER30.b2 MER30			
		repetitive element;)	-000		
14365	0.010368	EST (UI-H-BI2-agu-d-09-0-UI s1 3' end)	Δ\Λ/202213	Hs.255048	
14000	0.010000	/clone=IMAGE:2725672 /clone_end=3	AVVZ3ZZ 13	113.200040	
		/gb=AW292213 /gi=6698849			· · · ·
44074	0.04202	/ug=Hs.255048 /len=318	DE454400	11- 450000	*
14374	0.01302	RC4-HT0277-160200-013-d07 HT0277	BE151126	Hs 158600	
٠. د		cDNA, mRNA sequence /gb=BE151126		,	
		/gi=8613847 /ug=Hs.158600 /len=571			P
1 1 2 2 2					· ·
14390	0.020104	BX097880 NCI_CGAP_Thy1 cDNA	BX097880	Hs.208961	
		clone IMAGp998F242841, mRNA	19.00		
		sequence			
:		/clone=IMAGp998F242841_;_IMAGE:1	1		
	•	133207 /gb=BX097880 /gi=27829041			
*		/ug=Hs.208961 /len=354			
14406	0.02571	EST, cDNA, 5' end /clone=UI-E-CL1-afd	BM692499	Hs.354146	
		d-06-0-UI /clone_end=5' /gb=BM692499			
		/gi=19005757 /ug=Hs.354146 /len=577		* * * * * * * * * * * * * * * * * * * *	
•	* .			¥ .	
14431	0.015011	cDNA clone e443-f /He443-f Adult	T82627	1 20	<u> </u>
		heart, Clontech		- 3370	
14444	0.027356	mitochondrion, complete genome	NC 001807	· · · · · · · · · · · · · · · · · · ·	<del> </del>
14445		BX117007 NCI CGAP Lu5 cDNA clone		Hs.240728	
	0.010001	IMAGp998F154684, mRNA sequence	, DX117,007	113.240720	
		/clone=IMAGp998F154684_;_IMAGE:1	*	•	
		910414 /gb=BX117007 /gi=27840344	-		
		/ug=Hs.240728 /len=496			
		/ug=ns.2407267len=496 	- OC	* ÷ %	
14440	0.010004	plana 25022 mDNA comica co	AE404047	11- 00050	
14449	0.018081	clone 25023 mRNA sequence	ÅF131817	Hs.90858	
	,	/gb=AF131817 /gi=4406652			
4747466	10.000 : 5	/ug=Hs 90858 /len=1466			
14486	0.020104	No significant match,			
		ORF+1(121~228),+3(240~353)	SEQ.ID.No.10		-
14514	0.027356	EST xv68d08.x1 NCI_CGAP_Lu28	AW273612		NP_06837
		cDNA clone IMAGE:2818287 3'		1	1

Spot p-value	n-value	orresponding To Differentially Expressed General Value Description	G ne	Unigene	Protein	
opor	p-vaide	Description	Accession No.	Accession	Accession	
		*		No.	No.	
14528	0.022315	EST (EST34421 Embryo, 6 week I	AA330691			
	**	cDNA 5' end similar to EST containing	•	-90		
		L1 repeat)				
14535	0.008374	EST (oh07d11.s1 NCI_CGAP_Kid3	AA862627	*		
		cDNA clone IMAGE:1457109 3')	*. i * i *			
14546	0.048502	EST (601819273F1 NIH MGC 58	BF130672	1	NP_003655	
		cDNA clone IMAGE:4051098 5')		ļ.	_	
14567	0.020104	UI-H-FH1-bfp-m-06-0-UI.s1	BU619573	Hs.312629		
	0.020.0.	NCI_CGAP_FH1 cDNA clone UI-H-FH1-		7.0.0 120,20		
		bfp-m-06-0-UI 3', mRNA sequence			•	
	, ,	/clone=UI-H-FH1-bfp-m-06-0-UI				
		/clone_end=3' /gb=BU619573	e- 1	ū		
	20	/gi=23285788 /ug=Hs.312629 /len=1168				
:		/gi-232637667ug-Hs.3126297ie1i-1166				
14502	0.046776	EST (0)/00/00 v4	AI051247	20.00	177 12 1	
14593	0.016776	EST (oy90d09.x1	AIU5 1247	-		
		Soares_fetal_liver_spleen_1NFLS_S1	1			
8		cDNA clone IMAGE:1673105 3')		*.		
*	1 2 3 3 2 3 3 3					
14624	0.018715	cDNA FLJ37264 fis, clone	AK094583	Hs.185018	1.	
		BRAMY2011105. /gb=AK094583		,	· .	
		/gi=21753670 /ug=Hs.185018 /len=2047	· ·	=		
14715	0.048502	ADP-ribosylation factor-like 6 interacting	NM_015161	Hs.75249	NP_055976	
	}	protein (ARL6IP), mRNA /cds=(70,681)	,			
(%)		/gb=NM_015161 /gi=24308006				
	*	/ug=Hs.75249 /len=2280				
14718	0.048502	cDNA PSEC0070 fis, clone	AK075380	Hs.183454	NP_849193	
		NT2RP2001508, moderately similar to		. 3		
		OLIGOSACCHARYL TRANSFERASE	7			
		STT3 SUBUNIT. /cds=(94,954)	6,			
		/gb=AK075380 /gi=22761428	9 -	·	٠.	
		/ug=Hs.183454 /len=2510	· ·	·		
14719	0.033319	EST(cDNA clone IMAGE:2387836 3'	AI760555	*	NP 658913	
]		similar to contains Alu repetitive			-	
	-	element;contains element MER22				
		repetitive element;)		,		
14720	0.024727	cDNA FLJ32224 fis, clone	AK056786	Hs.406907	7.00	
, ,, ,,	0.027121	PLACE6004336. /gb=AK056786	, ,,,,,,,,,	1.10.100007		
Į.		/gi=16552290 /ug=Hs.406907 /len=3076		1	Į	
		ngi-10002200 /ug-115.400007 /ie11-5070		1 .		
14724	0.042400	HNC17-1-F3.R HNC Normal Cartilage)	BG927109	Hs.145637		
14724	0.013408			JI 15. 140037		
		cDNA, mRNA sequence /gb=BG927109	1			
		/gi=14321632 /ug=Hs.145637 /len=614	l .	1	71	
	<u> </u>			<u></u>	1	
14748	0.022315	EST(K0830A11-3 NIA Mouse 8.5-dpc	BM249217		NP_082518	
		Whole Embryo cDNA Library (Long)	1	·	Y	
:	l ·	Mus musculus cDNA clone K0830A11 -	*	1 .		
5	1	21M13 Forward)		1	1 .	

		nding To Differentially Expressed Gen			
Spot	p-value	Description	Gene Accession No.	Unigene Accession	Protein Accession
		* y	Accession No.	No.	No.
14753	0.028482	FLJ14068 fis, clone HEMBB1001500	AK024130	Hs.287620	INO.
17700	0.020402	/cds=UNKNOWN /gb=AK024130	711024100	113.207020	
		/gi=10436435 /ug=Hs.287620 /len=3901		* * *	•
				0.	
14790	0.038336	cDNA FLJ40926 fis, clone	AK098245	Hs.303205	
		UTERU2006524. /gb=AK098245			
•		/gi=21758221 /ug=Hs.303205 /len=2110			
14806	0.033319	cDNA FLJ14279 fis, clone	AK024341	Hs.250383	
		PLACE1005574. /gb=AK024341			9
		/gi=10436703 /ug=Hs 250383 /len=2005		4.	
				4	
14807	0.016234	clone IMAGE:5186761, mRNA	BC044843	Hs.125346	
		/gb=BC044843 /gi=27924105			
		/ug=Hs.125346 /len=1589		20.000	
14825	0.023168	clone IMAGE:3847423, mRNA	BC020562	Hs 352245	
		/gb=BC020562 /gi=18088249	*		
4 4 0 0 0	0.000004	/ug=Hs.352245 /len=2742			
14833	0.036684	EST380251 MAGE resequences,	AW968281	Hs.319460	L
•	-	MAGJ cDNA, mRNA sequence			*
	· ·	/gb=AW968281 /gi=8158016			,
44054	0.044050	/ug=Hs.319460 /len=689	DE540700	11 440004	8
14851	0.044259	UI-H-BW1-amm-h-09-0-UI.s1	BF512783	Hs 443691	, 1
		NCI_CGAP_Sub7 cDNA clone			• .
		IMAGE:3070696 3', mRNA sequence	2.0%	···	
•		/clone=IMAGE:3070696 /clone_end=3'			
. (	•	/gb=BF512783 /gi=11597962		Y	*
14859	0.046224	/ug=Hs.443691 /len=568 cDNA FLJ13364 fis, clone	AK023426	Hs.28959	·
14009	0.010234	PLACE1000292 /cds=UNKNOWN	MKU23420	IDS.20909	
		/gb=AK023426 /gi=10435358	*		
	9	/ug=Hs.28959 /len=2775	*		
14870	0.018081	602035495F1 NCI CGAP Brn64 cDNA	BE340626	Hs.405924	
14070	0.010001	clone IMAGE:4183511 5', mRNA	DI 040020	113.400524	
		sequence /clone=IMAGE:4183511		- 1	. *
.8		/clone_end=5' /gb=BF340626			
		/gi=11287186 /ug=Hs.405924 /len=1036			
14872	0.027356	UI-H-EU0-azs-i-07-0-UI.s1	BQ183049	Hs.442214	# Y .
		NCI_CGAP_Car1 cDNA clone IMAGE:			
		5853006 3', mRNA sequence			
		/clone=IMAGE:_5853006 /clone_end=3'			
		/gb=BQ183049 /gi=20358599	*		•
	1	/ug=Hs.442214 /len=913		* .	e Y e
14875	0.040325	RC1-NN0073-090500-012-f02 NN0073	AW898615	Hs.130729	
		cDNA, mRNA sequence	*		
•		/gb=AW898615 /gi=8062820			
	i	/ug=Hs.130729 /len=660	J ·		1

Spot	p-value	Description	Gene	Unigene	Protein
			Accession No.	Accession	Accession
	•			No.	No.
14906	0.01302	EST, cDNA: FLJ21479 fis, clone	AK025132	Hs.397727	NP_004710
		COL05032 /cds=UNKNOWN			- T
•	_	/gb=AK025132 /gi=10437589			
	, '	/ug=Hs.139315 /len=1920			10 P 8
14911	0.044259	UI-1-BB1p-akk-b-05-0-UI.s1	BU753775	Hs.279870	
		NCI_CGAP_PI6 cDNA clone UI-1-BB1p-			*
		akk-b-05-0-UI 3', mRNA sequence	• •		
		/clone=UI-1-BB1p-akk-b-05-0-UI			
. *		/clone_end=3' /gb=BU753775	*		
		/gi=23712051 /ug=Hs.279870 /len=1533	4		
14912	0.048502	cDNA FLJ25001 fis, clone CBL00443	AK057730		NP 203524
14947	0.028482	EST(cDNA clone IMAGE:3267894 3')	BF435209		
14952	0.016232	RC1-DT0029-120100-011-h01 DT0029	AW579207	Hs.414692	1
		cDNA, mRNA sequence	341		
		/gb=AW579207 /gi=7254256			*
		/ug=Hs 414692 /len=697			* * 7
14955	0.040325	No significant match	SEQ.ID.No.32	7 1 1 1 1	

t gay their		TABLE 3J			
Genes Correspoi	nding To D	ifferentially Expressed Genes in F	igure 17 - Bla	dder Cancer	
Gene Identifier	p-value	Description	G ne	Unigen	Protein
		<u>`</u>	Accession	Accession	Accession
- W			No.	No.	No.
1053_at	0.003368	replication factor C (activator 1) 2,	NM_002914		NP_002905
• •		40kDa		Hs.139226	
121_at	0.033381	EST, Highly similar to	X69699		NP_054698
		PAX8_HUMAN Paired box protein		* • • • •	
*		Pax-8 [H.sapiens]		Hs.400990	
1294_at	0.002418	ubiquitin-activating enzyme E1-like	NM_003335		NP_003326
				Hs.16695	
1316_at	0.041055	thyroid hormone receptor, alpha	NM_003250		NP_003241
,		(erythroblastic leukemia viral (v-erb-		000	
		a) oncogene homolog, avian)	1	Hs.724	
160020_at	0.010205	matrix metalloproteinase 14	NM_004995		NP_004986
		(membrane-inserted)		Hs.2399	
1729_at	5.03E-04	TNFRSF1A-associated via death	L41690		NP_700474
		domain		Hs.89862	
179_at	0.003928	postmeiotic segregation increased	U38980		
	·	2-like 2		Hs.177548	
200002_at	0.041055	gb:NM_007209.1 /DEF=Homo	NM_007209		NP_009140
		sapiens ribosomal protein L35	) '		
• (		(RPL35), mRNA. /FEA=mRNA	*		-
***		/GEN=RPL35 /PROD=ribosomal			
* 1		protein L35			
8		/DB_XREF=gi:6005859			
		/UG=Hs.182825 ribosomal protein	, ,		
		L35 /FL=gb:BC000348.1			
		gb:U12465.1 gb:NM_007209.1			
200006_at	0.004341	gb:NM_007262.1 /DEF=Homo	NM_007262		NP_009193
		sapiens RNA-binding protein			
		regulatory subunit (DJ-1), mRNA.	±		
. 5		/FEA=mRNA /GEN=DJ-1		9	
		/PROD=RNA-binding protein	*	a 131	
		regulatory subunit		-	
		/DB_XREF=gi:6005748			
*		/UG=Hs.10958 RNA-binding	4		
*		protein regulatory subunit		Į.	l
* 1 *	,	/FL=gb:AF021819.1			
		gb:NM_007262.1 gb:D61380.1	1	1	1

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
200007_at	0.001116	gb:NM_003134.1 /DEF=Homo	NM_003134		NP_003125
		sapiens signal recognition particle	-		_
	1	14kD (homologous Alu RNA-		·	
,		binding protein) (SRP14), mRNA.		1.00	
*		/FEA=mRNA /GEN=SRP14			
		/PROD=signal recognition particle	`. ;		
1		14kD (homologous AluRNA-			
		binding protein)	8		1
		/DB_XREF=gi:4507210	4	· .	·
		/UG=Hs.180394 signal recognition			i.e
	· .	particle 14kD (homologous Alu			9
		RNA-binding protein)	· ·		
· ()		/FL=gb:NM 003134.1			
		gb:U07857.1			
200009_at	0.003171	gb:NM_001494.2 /DEF=Homo	NM_001494		NP_001485
		sapiens GDP dissociation	7		
		inhibitor 2 (GDI2), mRNA.			
**	1	/FEA=mRNA /GEN=GDI2	P (*)		
}	}	/PROD=GDP dissociation inhibitor			
		2 /DB XREF=gi:6598322			
		/UG=Hs.56845 GDP dissociation			,
-		inhibitor 2 /FL=gb:BC005145.1	11		
		gb:D13988.1 gb:NM_001494.2			
		_	*		
* *					
200011_s_at	1.26E-04	gb:NM_001659.1 /DEF=Homo	NM 001659		NP 001650
		sapiens ADP-ribosylation factor 3	, –		_
		(ARF3), mRNA. /FEA=mRNA			
	İ	/GEN=ARF3 /PROD=ADP-			
		ribosylation factor 3			
		/DB_XREF=gi:4502202			
		/UG=Hs.119177 ADP-ribosylation	· ·		
		factor 3 /FL=gb:M74491.1			
.,	1.	gb:NM_001659.1			
200015_s_at	0.026891	gb:NM_004404.1 /DEF=Homo	NM_004404		NP_004395
r		sapiens neural precursor cell		*	
	·	expressed, developmentally down-		<u> </u> -	
		regulated 5 (NEDD5), mRNA.			*
	1	/FEA=mRNA /GEN=NEDD5	- 1	*. :	e •
		/PROD=neural precursor cell			
		expressed, developmentallydown-			
		regulated 5		·	
		/DB_XREF=gi:4758157			-
		/UG=Hs.155595 neural precursor		l '	
		cell expressed, developmentally	. 1		
		down-regulated 5			
	1	/FL=gb:D28540.1			α.
	-	gb:NM_004404.1 gb:D63878.1			

Gene Identifier	p-value	D scription	Gene	Unigene	Prot in
		9	Accession	Acc ssion	Accession
			No.	No.	No.
200020_at	0.026891	gb:NM_007375.1 /DEF=Homo	NM_007375		NP_031401
<del>-</del>		sapiens TAR DNA binding	_		
* ,		protein (TARDBP), mRNA.	-		
	6	/FEA=mRNA /GEN=TARDBP		ľ	
		/PROD=TAR DNA binding protein			3
*		/DB_XREF=gi:6678270			
· ·		/UG=Hs.193989 TAR DNA			
		binding protein	<u>.</u>	·	
0		/FL=gb:AL050265.1			
*		gb:NM_007375.1 gb:U23731.1			1
200022 at	0.010205	gb:NM_000979.1 /DEF=Homo	NM 000979	4 · (E) - 4 · - 4 ·	NP_000970
		sapiens ribosomal protein L18			
		(RPL18), mRNA. /FEA=mRNA		;	1,
		/GEN=RPL18 /PROD=ribosomal		-	
(		protein L18			
:		/DB_XREF=gi:4506606			
e *		/UG=Hs.75458 ribosomal protein			
		L18 /FL=gb:BC000374.1			
		gb:L11566.1 gb:NM_000979.1			
200024_at	0.026801	gb:NM_001009.1 /DEF=Homo	NM 001009		NP 001000
200024_at	0.020091	sapiens ribosomal protein S5	14141_001009		NI001000
		(RPS5), mRNA. /FEA=mRNA		-	
		/GEN=RPS5 /PROD=ribosomal			
•		protein S5 /DB_XREF=gi:4506728	y	. '	0
		/UG=Hs.76194 ribosomal protein			
	1 "	S5 /FL=gb:NM_001009.1			
	= 7	· · · · · · - ·			,
		gb:U14970.1			
200020 0 04	0.010205	abiNM 003635 1 (DEE-Home	NIM COOCSE		ND OCEOZO
200030_s_at	0.010203	gb:NM_002635.1 /DEF=Homo sapiens solute carrier family 25	NM_002635	,	NP_005879
		1 '	i i	3-	
	1	(mitochondrial carrier; phosphate			•
		carrier), member 3 (SLC25A3),	•		
		nuclear gene encoding			A Table
	].	mitochondrial protein, transcript	•		
		variant 1b, mRNA /FEA=mRNA		-	
i i	1	/GEN=SLC25A3			
3	1	/PROD=phosphate carrier			
* * * * *		precursor isoform 1b			1
	*	/DB_XREF=gi:4505774			
<u>'</u> .	1	/UG=Hs.78713 solute carrier	1		3
	1 .	family 25 (mitochondrial carrier;	* 41		
		phosphate carrier), member 3	) 8		
	1 .	/FL=gb:BC000998.1			1
		gb:BC001328.1 gb:BC003504.1	. *	] ' '	
		gb:BC004345.1 gb:NM_002635.1			1

Gen Identifier	p-value	Description	Gene	Unigen	Protein
			Accession No.	Accession No.	Accession No.
200031_s_at	0.016934	gb:NM_001015.1 /DEF=Homo sapiens ribosomal protein S11 (RPS11), mRNA /FEA=mRNA /GEN=RPS11 /PROD=ribosomal	NM_001015		NP_001006
		protein S11 /DB_XREF=gi:4506680 /UG=Hs.182740 ribosomal protein S11 /FL=gb:NM_001015.1	*	* .*	
200035_at	0.00161	gb:NM_015343.1 /DEF=Homo sapiens hypothetical protein (HSA011916), mRNA	NM_015343		NP_056158
		/FEA=mRNA /GEN=HSA011916 /PROD=hypothetical protein /DB_XREF=gi:7661721 /UG=Hs.84359 hypothetical	*	*	
200037_s_at		protein /FL=gb:NM_015343.1 gb:NM_016587.1 /DEF=Homo sapiens heterochromatin-like protein 1 (HECH), mRNA. /FEA=mRNA /GEN=HECH /PROD=heterochromatin-like protein 1 /DB_XREF=gi:7705406 /UG=Hs.278554 heterochromatin-like protein 1 /FL=gb:AF136630.1 gb:NM_016587.1	NM_016587		NP_057671
200039_s_at	7.58E-04	gb:NM_002794.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA. /FEA=mRNA /GEN=PSMB2 /PROD=proteasome (prosome, macropain) subunit, betatype, 2 /DB_XREF=gi:4506194 /UG=Hs.1390 proteasome (prosome, macropain) subunit, beta type, 2 /FL=gb:BC000268.1 gb:NM_002794.1 gb:D26599.1	NM_002794		NP_002785

Gene Identifier	p-value	Description	Gene	Unig ne	Protein
			Accession	Acc ssion	Accession
000010		1	No.	No.	No.
200040_at	0.00228	gb:NM_006559.1 /DEF=Homo	NM_006559		NP_006550
**		sapiens GAP-associated tyrosine		100	
*		phosphoprotein p62 (Sam68)			
		(SAM68), mRNA. /FEA=mRNA	* ()		*
	)	/GEN=SAM68 /PROD=GAP-			•
		associated tyrosine	1 *		
		phosphoprotein p62(Sam68)			
	, ,	/DB_XREF=gi:5730026			
.:		/UG=Hs 119537 GAP-associated			*
*	· .	tyrosine phosphoprotein p62			*
1		(Sam68) /FL=gb:BC000717.1			
*	** 1/4	gb:M88108.1 gb:NM_006559.1	×		
200043_at	0.001116	gb:NM_004450.1 /DEF=Homo	NM_004450		NP_004441
		sapiens enhancer of rudimentary			
		(Drosophila) homolog (ERH),	·		
		mRNA. /FEA=mRNA /GEN=ERH	-		
	- 1	/PROD=enhancer of rudimentary			
		(Drosophila) homolog	fee s		
	:	/DB_XREF=gi:4758301			
		/UG=Hs.118757 enhancer of			
	1	rudimentary (Drosophila) homolog		• =	
		/FL=gb:D85758.1 gb:U66871.1			
		gb:NM_004450.1	8.07		
200044 at	1.26E-04	gb:NM_003769.1 /DEF=Homo	NM 003769	4- X C	NP_003760
		sapiens splicing factor,	_		7
30,3		arginineserine-rich 9 (SFRS9),			
		mRNA /FEA=mRNA			
•		/GEN=SFRS9 /PROD=splicing			· ·
* "		factor, arginineserine-rich 9			
*	9	/DB_XREF=gi:4506902			
	- *	/UG=Hs.77608 splicing factor,			
		arginineserine-rich 9			
		/FL=gb:U30825.1			*
		gb:NM_003769.1	,		
200046_at	0.001116	gb:NM_001344.1 /DEF=Homo	NM_001344	1 2 201 1 2	NP_001335
		sapiens defender against cell	_		_
*		death 1 (DAD1), mRNA.			
		/FEA=mRNA /GEN=DAD1			* ' .
		/PROD=defender against cell	ľ	gi e	
		death 1 /DB_XREF=gi:4503252			
	6	/UG=Hs.82890 defender against			
		cell death 1 /FL=gb:NM_001344.1	• • •		
* * * *		gb:D15057.1			
		ľ		1	7
<del></del>	<del></del>	L	1000	<del> </del>	L

Gene Identifier	p-value	D scription	Gene	Unigene	Protein
			Accession No.	Accession No.	Accession No.
200047 s_at	0.02145	gb:NM: 003403.2 /DEF=Homo	NM 003403	110.	NP 003394
		sapiens YY1 transcription factor			
		(YY1), mRNA. /FEA=mRNA		l	
	*	/GEN=YY1 /PROD=YY1	*	,	3.
		transcription factor		· ·	
		/DB_XREF=gi:6042207	*		
	]	/UG=Hs.97496 YY1 transcription			2 0
		factor /FL=gb:M77698.1			
		gb:M76541.1 gb:NM_003403.2			
200048_s_at	0.026891	gb:NM_006694.1 /DEF=Homo	NM_006694		NP_006685
		sapiens jumping translocation	8 8		Э
	1	breakpoint (JTB), mRNA.			+ 0
		/FEA=mRNA /GEN=JTB			
		/PROD=jumping translocation breakpoint /DB_XREF=gi:5729888			
		/UG=Hs.6396 jumping			
		translocation breakpoint			
		/FL=qb:BC000499.1	-8-1		
		gb:BC001363.1 gb:BC000996.2			* 9
		gb:BC001667.1 gb:AB016488.1		* *	
		gb:AF131797.1 gb:NM_006694.1			
		gb:AF115850.2			
200049_at	0.02145	gb:NM_007067.1 /DEF=Homo	NM_007067		NP_008998
		sapiens histone acetyltransferase			, · · · · .
		(HBOA), mRNA. /FEA=mRNA			
	44.00	/GEN=HBOA /PROD=histone			
		acetyltransferase	30 E 40		
	,	/DB_XREF=gi:5901961	4.	·	
		/UG=Hs.21907 histone			
		acetyltransferase /FL=gb:AF074606.1		-)(-	
	* *	gb:AF140360.1 gb:NM_007067.1		٠	
		gb./4 140000.1			3
200053_at	0.005852	gb:NM_004890.1 /DEF=Homo	NM_004890		NP 004881
		sapiens sperm associated			· · · -
		antigen 7 (SPAG7), mRNA.			
		/FEA=mRNA /GEN=SPAG7	1.	( ·	
		/PROD=sperm associated antigen			<b>B</b>
		7 /DB_XREF=gi:4757715	1.0		
		/UG=Hs.90436 sperm associated			1
* * * * * *	,	antigen 7 /FL=gb:AF047437.1		1	} :
		gb:NM_004890.1			
			<u> </u>		

Gene ld ntifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
200055_at	0.00161	gb:NM_006284.1 /DEF=Homo	NM_006284		NP_006275
		sapiens TATA box binding			· ·
	1	protein (TBP)-associated factor,		\	
		RNA polymerase II, H, 30kD			
		(TAF2H), mRNA. /FEA=mRNA			
		/GEN=TAF2H /PROD=TATA box	***	:	
		binding protein (TBP)-			
		associatedfactor, RNA			, .
		polymerase II, H, 30kD			
		/DB_XREF=gi:5454105	-		
i		/UG=Hs.89657 TATA box binding	*		
		protein (TBP)-associated factor,			* (
		RNA polymerase II, H, 30kD			
-		/FL=gb:NM_006284.1	-	* *	
		gb:U13991.1			
200056_s_at	0.004341	gb:NM_006333.1 /DEF=Homo	NM_006333		NP_775269
		sapiens nuclear DNA-binding			*
		protein (C1D), mRNA.			
		/FEA=mRNA /GEN=C1D			6
	1	/PROD=nuclear DNA-binding		ad "Topa	
- 1	1.	protein /DB_XREF=gi:5453582			
		/UG=Hs.15164 nuclear DNA-			
	;	binding protein		· · · · · · · · · · · · · · · · · · ·	
		/FL=gb:NM_006333.1			
200059_s_at	0.001116	gb:BC001360.1 /DEF=Homo	BC001360	}	NP_001655
,		sapiens, ras homolog gene		0	
	,	family, member A, clone			
		MGC:2330, mRNA, complete cds.			
*		/FEA=mRNA /PROD=ras homolog		1	
		gene family, member A			
		/DB_XREF=gi:12655024	*		
* 4	1	/UG=Hs.77273 ras homolog gene	4 3	Į.	
		family, member A			
*		/FL=gb:NM_001664.1			·
		gb:BC001360.1 gb:L25080.1		<u></u>	

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Acc ssion	Accession
			No.	No.	No.
200063_s_at	2.05E-04	gb:BC002398.1 /DEF=Homo	BC002398		NP_002511
		sapiens, nucleophosmin			
	Ď.	(nucleolar phosphoprotein B23,		,	\
		numatrin), clone MGC:8463,			
4		mRNA, complete cds.			. 28
		/FEA=mRNA	, :		
,		/PROD=nucleophosmin (nucleolar			
	n.	phosphoprotein B23,numatrin)	,		
		/DB_XREF=gi:12803184			
	-	/UG=Hs.9614 nucleophosmin			-
		(nucleolar phosphoprotein B23,		. 0	
		numatrin) /FL=gb:NM 002520.1		•	
		gb:BC002398.1 gb:BC003670.1			1
		gb:M23613.1 gb:M26697.1	(	(	
0 .		gb:M28699.1		. ·	
		3-:	-30		1
200065 s at	0.041055	gb:AF052179.1 /DEF=Homo	AF052179	· · · · · · · · · · · · · · · · · · ·	NP_001649
200000_3_at	3.071033	sapiens clone 24537 ADP-	002173		_001049
*		ribosylation factor 1 mRNA,			
		complete cds. /FEA=mRNA			-00
				• .	}
		/PROD=ADP-ribosylation factor 1			* *
		/DB_XREF=gi:3360490	1		
	:	/UG=Hs.74571 ADP-ribosylation		ļ	
		factor 1 /FL=gb:M84326.1			* -
*	1	gb:M36340.1 gb:AF055002.1	47		
2222	1.005.01	gb:AF052179.1 gb:NM_001658.2	-		ļ
200067_x_at	1.26E-04	Consensus includes gb:AL078596	AL0/8596	•	
		/DEF=Human DNA sequence	1		
*		from clone RP3-429G5 on		· ,	:
10 T		chromosome 6q21-22.1. Contains	1		1
		the NR2E1 gene for nuclear			
		receptor 2E1 (tailless, TLL, TLX,	1		21. 1
	• .	XTLL), the 3 end of the SNX3			
		gene for sorting nexin 3, ESTs,			
,		STSs, GSSs and four predicted	1		
		CpG islands /FEA=mRNA_2	l .	1	
		/DB_XREF=gi:6010168	9	**	
*	1	/UG=Hs.12102 sorting nexin 3			1
		/FL=gb:AF062483.1			,
<u>'</u>		gb:AF034546.1 gb:NM_003795.1		Ì .	}
-		·			
200068_s_at	2.05E-04	gb:M94859.1 /DEF=Human	M94859		NP_001737
<b>-</b> -		calnexin mRNA, complete cds.			_
		/FEA=mRNA /PROD=calnexin	. (>-		1
		/DB_XREF=gi:179831	J		1
		/UG=Hs.155560 calnexin	}	ļ	9
		/FL=gb:NM_001746.1	1		
. 1		gb:BC003552.1 gb:M94859.1	9 * *	1	1
1		gb:M98452.1 gb:L10284.1			
		lgb:L18887.1	1	9	
<u> </u>	1	Ign.r 10001.1	بسينسب	نـــــــــــــــــــــــــــــــــــــ	L

Gene Identifier	p-valu	Description	Gene	Unigene	Prot in
			Accession	Accession	Accession
			No.	No.	No.
200070_at	7.58E-04	gb:BC001393.1 /DEF=Homo	BC001393		NP_056495
	•	sapiens, hypothetical protein,			
· · · · · · · · · · · · · · · · · · ·		clone MGC:782, mRNA, complete	8	00	
		cds. /FEA=mRNA			1
		/PROD=hypothetical protein			
		/DB_XREF=gi:12655084			
1		/UG=Hs.4973 hypothetical protein			
		/FL=gb:BC001393.1			
200071_at	0.00228	splicing factor 30, survival of motor	BF224259		NP_005862
	1	neuron-related		Hs.79968	
200072_s_at	3.26E-04	gb:AF061832.1 /DEF=Homo	AF061832		NP_112480
		sapiens M4 protein deletion			
* * * * * * * * * * * * * * * * * * * *		mutant mRNA, complete cds.			
5.		/FEA=mRNA /PROD=M4 protein	\ <u>.</u>		
		deletion mutant			
		/DB_XREF=gi:3126877			000
		/UG=Hs.79024 heterogeneous			
		nuclear ribonucleoprotein M	*	ļ.,	
		/FL=gb:AF061832.1			٠
200073_s_at	0.026891	gb:M94630.1 /DEF=Homo sapiens	M94630		NP_112738
		hnRNP-C like protein mRNA,			
		complete cds. /FEA=mRNA		1	
		/PROD=DNA-binding protein			
	, , ,	/DB_XREF=gi:181913			
		/UG=Hs.303627 heterogeneous	,	(	1
	· .	nuclear ribonucleoprotein D (AU-			
.v. 0		rich element RNA-binding protein	· .	9	y
		1, 37kD) /FL=gb:M94630.1			
			•	' '.	
200078_s_at	0.033381	gb:BC005876.1 /DEF=Homo	BC005876	]	NP_004038
		sapiens, ATPase, H+			
		transporting, lysosomal (vacuolar			1
		proton pump) 21kD, clone			
		MGC:4498, mRNA, complete cds.			
1		/FEA=mRNA /PROD=ATPase, H+	}	<b>\</b>	}.
		transporting, lysosomal		1 .	1
		(vacuolarproton pump) 21kD			
	1	/DB_XREF=gi:13543437		1	
* *		/FL=gb:BC005876.1		· ·	1
20000			 		<u> </u>
200083_at	0.003171	ubiquitin specific protease 22	AA621731	Hs.12064	L

Gene Identifi r	p-value	Description	Gene	Unigene	Protein
		* * * * * * * * * * * * * * * * * * * *	Accession	Accession	Acc ssion
	. •		No.	No.	No.
200085 s at	0.00228	Consensus includes	NM_007108		NP 009039
· · · · · · · · · · · · · · · ·		gb:NM_007108.1 /DEF=Homo		;	
* * *		sapiens transcription elongation			
*		factor B (SIII), polypeptide 2			
		(18kD, elongin B) (TCEB2),		li li	
		mRNA. /FEA=CDS /GEN=TCEB2		,	*
		/PROD=elongin B	9 9 9		
		/DB XREF=gi:6005889		1	
		/UG=Hs.172772 transcription			
		elongation factor B (SIII),			
iii s		polypeptide 2 (18kD, elongin B)			
*		/FL=gb:NM_007108.1 gb:L42856.1			
	1 1	J 3.,			
200086 s_at	0.033381	cytochrome c oxidase subunit IV	AA854966		NP 001852
		isoform 1		Hs.347969	<u> </u>
200087_s_at	0.001116	Consensus includes	AK024976 '		NP 006806
		gb:AK024976.1 /DEF=Homo			
* * *	2° 1	sapiens cDNA: FLJ21323 fis,			
9	3	clone COL02374. /FEA=mRNA	<del>-</del>		W 10
		/DB_XREF=gi:10437405		-	
		/UG=Hs.75914 Homo sapiens			
	,	cDNA: FLJ21323 fis, clone			
* * *		COL02374		· · · · · ·	T
200095 x at	0.010205	ribosomal protein S10	AA320764	Hs.76230	NP 001005
200096 s at		ATPase, H+ transporting,	AI862255		NP 003936
		lysosomal 9kDa, V0 subunit e		Hs.24322	
200594 x at	0.00161	gb:NM_004501.1 /DEF=Homo	NM 004501		NP 114032
<del>1,0</del> 1,000 m		sapiens heterogeneous nuclear		[	
3		ribonucleoprotein U (scaffold	4		60 ays
		attachment factor A) (HNRPU),	*		
*:		mRNA. /FEA=mRNA		*.	
		/GEN=HNRPU	] .		
		/PROD=heterogeneous nuclear			-
	1,8	ribonucleoprotein U(scaffold	-8-		
		attachment factor A)			
		/DB_XREF=gi:4758545			
	e i	/UG=Hs.103804 heterogeneous	*		
	,	nuclear ribonucleoprotein U			
		(scaffold attachment factor A)			, · .
		/FL=gb:BC003367.1			
	•	gb:BC003621.1 gb:NM_004501.1			
		100.00.00002   C 00.14W 00400			
200596 s at	0.007779		BE614908		NP 003741
200596_s_at	0.007779	eukaryotic translation initiation factor 3, subunit 10 theta,	BE614908		NP_003741

G ne Identifi r	p-valu	Description	Gene	Unigen	Prot in
			Accession No.	Accession No.	Accession
200600_at	0.02145	gb:NM 002444.1 /DEF=Homo	NM_002444	NO.	No. NP 002435
200000_at	0.02,140	sapiens moesin (MSN), mRNA.	14101_002-44-4		141 _002455
		/FEA=mRNA /GEN=MSN			
g. * . / . *		/PROD=moesin			
		/DB_XREF=gi:4505256			
		/UG=Hs.170328 moesin			
		/FL=gb:M69066:1			
-	4 005 04	gb:NM_002444.1	1111 000101		
200602_at	1.26E-04	gb:NM_000484.1 /DEF=Homo	NM_000484		NP_000475
21		sapiens amyloid beta (A4)			*
		precursor protein (protease nexin-			
		II, Alzheimer disease) (APP),			
		mRNA /FEA=mRNA /GEN=APP	<u>.</u> .		
* //		/PROD=amyloid beta (A4)	-50-		
		precursor protein (proteasenexin-			
		II, Alzheimer disease)			
*		/DB_XREF=gi:4502166	*		
		/UG=Hs.177486 amyloid beta			
	1	(A4) precursor protein (protease			1,0
		nexin-II, Alzheimer disease)			
		/FL=gb:NM_000484.1			
200603_at	3 26F-04	Consensus includes	AL050038		NP 002725.
	0.202 0	gb:AL050038.1 /DEF=Homo	, .200000	\ \ \	-002720
	114	sapiens mRNA; cDNA			
		DKFZp566J0124 (from clone			
		DKFZp566J0124). /FEA=mRNA	,		
1	,	/DB_XREF=gi:4884279			
				• •);•	
		/UG=Hs.183037 protein kinase,		0.00	
	-	cAMP-dependent, regulatory, type	1		
* *		I, alpha (tissue specific	,		
		extinguisher 1) /FL=gb;M18468.1	* * 1		
		gb:M33336.1 gb:NM_002734.1			
					·
200605_s_at	0.003171		NM_002734		NP_002725
, .		sapiens protein kinase, cAMP-			1
		dependent, regulatory, type I,			
		alpha (tissue specific extinguisher			
0		1) (PRKAR1A), mRNA.			
•		/FEA=mRNA /GEN=PRKAR1A			
		/PROD=protein kinase, cAMP-		,	
		dependent, regulatory, typel,			1
	3	alpha /DB_XREF=gi:4506062			
· .		/UG=Hs.183037 protein kinase,		4	'
		cAMP-dependent, regulatory, type	1.		
·		I, alpha (tissue specific	1		
		extinguisher 1) /FL=gb:M18468.1	· ·	1	1
		gb:M33336.1 gb:NM_002734.1			
		gb.M33330.1 gb.MM_002734.1			1
	0 -				ŀ
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Gene Identifier	p-valu	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
200606_at	0.015516	gb:NM_004415.1 /DEF=Homo	NM_004415		NP_004406
		sapiens desmoplakin (DPI, DPII)	-		
		(DSP), mRNA. /FEA=mRNA			
		/GEN=DSP /PROD=desmoplakin		· · · · · · · · · · · · · · · · · · ·	
	1	(DPI, DPII)	· ·	* 4	- 10-
		/DB_XREF=gi:4758199			,
		/UG=Hs.74316 desmoplakin (DPI,		0.0	
* )		DPII) /FL=gb:M77830.3			
X	1	gb:NM 004415.1			
200609_s_at	1.26F-04	gb:NM_017491.1 /DEF=Homo	NM 017491		NP 059830
		sapiens WD repeat domain 1		, , , , ,	
		(WDR1), transcript variant 1,			
	*	mRNA. /FEA=mRNA			
*		/GEN=WDR1 /PROD=WD repeat-			
		containing protein 1, isoform 1			
		/DB_XREF=gi:9257256	. 0		* .
		/UG=Hs.85100 WD repeat			
		domain 1 /FL=gb:BC000201.1			
	2.				
		gb:BC002489.1 gb:AF020056.1	·· :		
000044	0.040004	gb:AB010427.2 gb:NM_017491.1	40040407		NE OSCOCO
200611_s_at	0.016934	gb:AB010427.2 /DEF=Homo	AB010427		NP_059830
0.5		sapiens mRNA for NORI-1,			
	6	complete cds. /FEA=mRNA			
W.		/PROD=NORI-1			×
		/DB_XREF=gi:5103672			
		/UG=Hs.85100 WD repeat			
		domain 1 /FL=gb:BC000201.1			
		gb:BC002489.1 gb:AF020056:1	* 3		
	1. 1.	gb:AB010427.2 gb:NM_017491.1			
200614_at	3.26E-04		NM_004859		NP_004850
		sapiens clathrin, heavy			
		polypeptide (Hc) (CLTC), mRNA.			
9.4		/FEA=mRNA /GEN=CLTC	1		
		/PROD=clathrin heavy chain			
		/DB_XREF=gi:4758011			]
		/UG=Hs.178710 clathrin, heavy			
		polypeptide (Hc) /FL=gb:D21260.1	*		
		gb:NM_004859.1			
			8		
200615_s_at	0.009907	adaptor-related protein complex 2,	AL567295	.,,-	NP 001273
		beta 1 subunit		Hs.74626	_
200618 at	1.26E-04	gb:NM_006148.1 /DEF=Homo	NM 006148		NP_006139
		sapiens LIM and SH3 protein 1			
		(LASP1), mRNA: /FEA=mRNA			
		/GEN=LASP1 /PROD=LIM and		35	
*		SH3 protein 1	*		,
	1	/DB_XREF=gi:5453709		a	
		/UG=Hs.75080 LIM and SH3			1
		protein 1 /FL=gb:NM_006148.1		PA .	
	1	Thioteni i /i L-gu.ivivi 000 (40.1	L	L ,	

Gene Identifier	p-value	Description	Gen	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
200619_at	5.03E-04	gb:NM_006842.1 /DEF=Homo	NM_006842	, , ,	
		sapiens splicing factor 3b,			
		subunit 2, 145kD (SF3B2),		- 11	
		mRNA. /FEA=mRNA		,	191
1		/GEN=SF3B2 /PROD=splicing			
	(C)	factor 3b, subunit 2, 145kD		* 0.	
		/DB_XREF=gi:5803154			·
		/UG=Hs.75916 splicing factor 3b,			
		subunit 2, 145kD			
0		/FL=gb:U41371.1			
		gb:NM_006842.1		1 V	
200020	0.001116	gb:NM_004872.1 /DEF=Homo	NM 004872		ND 004963
200620_at	0.001116		NIVI_004672	~ .	NP_004863
	} '	sapiens chromosome 1 open			
	1	reading frame 8 (C1ORF8),			
	- 1 -	mRNA. /FEA=mRNA			
0		/GEN=C1ORF8			
		/PROD=chromosome 1 open			
		reading frame 8			]
		/DB_XREF=gi:4758571			
		/UG=Hs.11441 chromosome 1			
		open reading frame 8			
		/FL=gb:BC003106.1			
		gb:AF290615.1 gb:AF047439.1			
,		gb:NM_004872.1			
200621 at	5.03E-04		NM 004078		NP 004069
		sapiens cysteine and glycine-rich			_
		protein 1 (CSRP1), mRNA.		1	
		/FEA=mRNA /GEN=CSRP1			
*	i	/PROD=cysteine and glycine-rich			
0	}	protein 1 /DB_XREF=gi:4758085			1 1 1 1 1 1 1 1 1
		//UG≈Hs.108080 cysteine and			
0.0	† , .·				
		glycine-rich protein 1			
		/FL=gb:M33146.1			*
	, ,	gb:NM_004078.1			
	 	<u> </u>			VIS 5551-5
200622_x_at	1.26E-04	calmodulin 3 (phosphorylase	AV685208		NP_005175
	1	kinase, delta)		Hs.334330	
200623_s_at	0.001116	gb:NM_005184.1 /DEF=Homo	NM_005184		NP_005175
	1	sapiens calmodulin 3		j	
	1	(phosphorylase kinase, delta)			•
	1	(CALM3), mRNA. /FEA=mRNA	1)(-		
	1.	/GEN=CALM3 /PROD=calmodulin	1		1
		3 (phosphorylase kinase, delta)			-
l		/DB_XREF=gi:4885108			
	1	/UG=Hs.141011 calmodulin 3	i		
. *	ł	(phosphorylase kinase, delta)	1		
,	1	/FL=gb:BC005137.1 gb:J04046.1	1	1	
ŀ.		gb:NM_005184.1		1 =	
	1	95.14141_000104.1			
L	1		<u></u>		ــــــــــــــــــــــــــــــــــــــ

Gene Identifier	p-value	Description	Gen	Unigene	Protein
***	<b>"</b> •		Accession	Accession	Accession
•			No.	No.	No.
200625_s_at	3.26E-04	gb:NM 006367.2 /DEF=Homo	NM 006367		NP_006358
		sapiens adenylyl cyclase-			_
	j	associated protein (CAP), mRNA.		*	9
	. ,	/FEA=mRNA /GEN=CAP			
	1 . :	/PROD=adenylyl cyclase-			*)
	1 .	associated protein			
		/DB_XREF=gi:10938021		-	100
		/UG=Hs.104125 adenylyl cyclase-		· .	4
		associated protein		,	
	1	/FL=gb:NM_006367.2 gb:L12168.1			
		gb:M98474.1			p)
200627_at	0.005852	gb:BC003005.1 /DEF=Homo	BC003005		NP_006592
2000,21_at.	0.000002	1~	BC003003		INF_000392
1	{	sapiens, unactive progesterone			\\\ - \\\ - \\\
		receptor, 23 kD, clone		340	
		MGC:4004, mRNA, complete cds.			(1) 41
9		/FEA=mRNA /PROD=unactive			
		progesterone receptor, 23 kD		\ \	
		/DB_XREF=gi:12804292			* *
		/UG=Hs.278270 unactive			
- 30	] .	progesterone receptor, 23 kD			
	1	/FL=gb:BC003005.1 gb:L24804.1			
		gb.NM_006601.1		*(**	
<u>.</u>			19	1	
200630_x_at	0.001116	SET translocation (myeloid	AV702810		NP_003002
	=	leukemia-associated)		Hs.145279	
200632_s_at	1.26E-04	gb:NM_006096.1 /DEF=Homo	NM_006096		NP_006087
		sapiens N-myc downstream			_
	1.*	regulated (NDRG1), mRNA.			
		/FEA=mRNA /GEN=NDRG1		W.C.	
	A .	/PROD=N-myc downstream	· :	-1	
		regulated /DB_XREF=gi:5174656	. 41		:
		/UG=Hs.75789 N-myc	1		· ·
		downstream regulated			
	1	/FL=gb:BC003175.1 gb:D87953.1	<b>†</b>	]	}
	-	gb:AF004162.1 gb:NM_006096.1			
200633_at	0.013223	gb:NM_018955.1 /DEF=Homo	NM_018955		NP_061828
		sapiens ubiquitin B (UBB),			_
		mRNA. /FEA=mRNA /GEN=UBB		} •	
		/PROD=ubiquitin B			1
. "-	. 1	/DB_XREF=gi:11024713	, y		-
-		/UG=Hs.183842 ubiquitin B	,		ľ
1	1	/FL≈gb:NM 018955.1		:	ł
	.]	gb:BC000379.1		•}	
1 22	<u> </u>	Tan: no no no no no no no no no no no no no	J	<u> </u>	L

G n Identifier	p-value	Description	Gene	Unigene	Prot in
7. A.			Accession	Accession	Acc ssion
		***	No.	No.	No.
200634_at	3.26E-04	gb:NM_005022.1 /DEF=Homo	NM_005022		NP_005013
-		sapiens profilin 1 (PFN1), mRNA.			
		/FEA=mRNA /GEN=PFN1			j
		/PROD=profilin 1			
		/DB XREF=gi:4826897			
	*	/UG=Hs.75721 profilin 1		* .	
		/FL=gb:BC002475.1 gb:J03191.1			
		gb:NM 005022.1			*
200638_s_at	0.026891	gb:BC003623.1 /DEF=Homo	BC003623		NP_663723
		sapiens, tyrosine 3-			
		monooxygenasetryptophan 5-			
		monooxygenase activation		*.	
		protein, zeta polypeptide, clone		* * * * * * * * * * * * * * * * * * * *	
	4. 4	MGC:2153, mRNA, complete cds.			
0.		/FEA=mRNA /PROD=tyrosine 3-			
		monooxygenasetryptophan5-			
	- 4	monooxygenase.ryptophano-	111		
	1	protein, zeta polypeptide		* * * * * * * * * * * * * * * * * * * *	
3		/DB_XREF=gi:13177678			
* ' g	10				
	0	/UG=Hs.75103 tyrosine 3-			
		monooxygenasetryptophan 5-			i
		monooxygenase activation	,		
		protein, zeta polypeptide	* *	*	
	*	/FL=gb:BC003623.1 gb:M86400.1	ļ		*
	× ×	gb:NM_003406.1 gb:U28964.1			
			0, 0	* *	
200639_s_at	1.26E-04	gb:NM_003406.1 /DEF=Homo	NM_003406	Ì	NP_663723
		sapiens tyrosine 3-	* .		
	*	monooxygenasetryptophan 5-			
		monooxygenase activation			
		protein, zeta polypeptide		!	* *
*		(YWHAZ), mRNA. /FEA=mRNA		ì	×-
		/GEN=YWHAZ /PROD=tyrosine 3-	*		
	*	monooxygenasetryptophan5-			1
		monooxygenase activation			
	. ()	protein, zeta polypeptide		1000	•
(-		/DB_XREF=gi:4507952			1
		/UG=Hs.75103 tyrosine 3-	-		
	·	monooxygenasetryptophan 5-	* * .	ļ	, •
		monooxygenase activation	•		
		protein, zeta polypeptide		,	
,	0 .	/FL=gb:BC003623.1 gb:M86400.1		1	
	,	gb:NM_003406.1 gb:U28964.1	į.		:

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
200640 at	3.26E-04	gb:NM_003406.1 /DEF=Homo	NM 003406		NP 663723
		sapiens tyrosine 3-	· .		
2		monooxygenasetryptophan 5-			
		monooxygenase activation			]
** * *		protein, zeta polypeptide			
		(YWHAZ), mRNA. /FEA=mRNA			
		/GEN=YWHAZ /PROD=tyrosine 3-			
		monooxygenasetryptophan5-			
* .	1	monooxygenase activation	2		
. *		protein, zeta polypeptide			
		/DB_XREF=gi:4507952			\.
			* * * * * * * * * * * * * * * * * * * *		
	{	/UG=Hs.75103 tyrosine 3-			
	į ·	monooxygenasetryptophan 5-			
. 1		monooxygenase activation	1		
		protein, zeta polypeptide			
	100	/FL=gb:BC003623.1 gb:M86400.1			, ,
v s		gb:NM_003406.1 gb:U28964.1			( )
	<u> </u>				
200644_at	1.26E-04	gb:NM_023009.1 /DEF=Homo	NM_023009		NP_075385
		sapiens macrophage			
,	1 .	myristoylated alanine-rich C			
	:	kinase substrate (MACMARCKS),	×		
		mRNA. /FEA=mRNA			
	10.	/GEN=MACMARCKS		1	
		/PROD=macrophage myristoylated			
* 171		alanine-rich C kinasesubstrate		***	
		/DB_XREF=gi:13491173		no.	
		/UG=Hs.75061 macrophage		8	000
• • •		myristoylated alanine-rich C			
		kinase substrate			4.1
*		/FL=gb:NM_023009.1			
0	1	// L=gb./4W_023003.1		f	· '
		,			
200650 c at	1.26E 04	ab:NM 005566 1 /DEE-Home	NIM OOFFCC		ND OCEET
200650_s_at	1.20E-04	gb:NM_005566.1 /DEF=Homo sapiens lactate dehydrogenase A	NM_005566		NP_005557
		(LDHA), mRNA. /FEA=mRNA		p e	
		/GEN=LDHA /PROD=LDHA			
*		/DB_XREF=gi:5031856			
: .	- 9	/UG=Hs.2795 lactate	·. 🖺	e y	
		dehydrogenase A	(0.00)		
		/FL=gb:BC001829.1	* * 1	*	
*		gb:NM_005566.1		4	<u> </u>

Gene Identifier	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
200653_s_at	0.005852	gb:M27319.1 /DEF=Human	M27319		NP_008819
		calmodulin mRNA, complete cds.			
<b>.</b>		/FEA=mRNA /PROD=calmodulin			
*		/DB_XREF=gi:179809	* *		
•	,	/UG=Hs.177656 calmodulin 1			
,		(phosphorylase kinase, delta)			
		/FL=gb:M27319.1	·		
		gb:NM_006888.1		i .	
200654 at	0:041055	gb:J02783.1 /DEF=Human thyroid	J02783	10	NP_000909
		hormone binding protein (p55)			
		mRNA, complete cds.		1	9 6
		/FEA=mRNA /GEN=P4HB			
		/DB_XREF=gi:339646			
		/UG=Hs.75655 procollagen-			
		proline, 2-oxoglutarate 4-			
	. *	dioxygenase (proline 4-			
	7 -2	hydroxylase), beta polypeptide			
1.7	30	(protein disulfide isomerase;	* * *	* * *	**
		thyroid hormone binding protein			
		p55) /FL=gb:J02783.1			
		gb:NM 000918.1			
200655 s_at	0.02145	gb:NM: 006888.1 /DEF=Homo	NM_006888	********	NP_008819
		sapiens calmodulin 1	}		-
		(phosphorylase kinase, delta)			
		(CALM1), mRNA. /FEA=mRNA			
		/GEN=CALM1 /PROD=calmodulin	.,		* /
		1 (phosphorylase kinase, delta)		*	
		/DB XREF=gi:5901911	· .		1
	}	/UG=Hs.177656 calmodulin 1			
		(phosphorylase kinase, delta)		***	
	{	/FL=gb:M27319.1		. 0	
		gb:NM_006888.1	1		
	1	T	*-	*	

p-value		Gene		Protein
		Acc ssion .	Accession	Accession
			No.	No.
0.00228	gb:NM 001152 1 /DEE=Homo			NP 001143
		1411,_001.102		
		. ".		
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				- 1
	member 5 /FL=gb:J02683.1		* * *	1
	gb:NM_001152.1			
0:018973	gb:NM_002634:2 /DEF=Homo	NM_002634		NP_002625
10 - 1	sapiens prohibitin (PHB), mRNA.			
	/FEA=mRNA /GEN=PHB			*
	/PROD=prohibitin			
			, i	
0.001116		NM 005620		NP 005611
0.00		000020_		
<u>.</u>				*
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, * !		<u>'</u>		
1	[gb:D38583.1			
0.000004	L NIM 000000 4 (DEE 1)	NIA 000000		ND 00000
0.026891		MW_000308		NP_000299
		.*		
*		h .		]
		1 ** ;		
•				
: -	galactosidase	1		
,				
	/UG=Hs.118126 protective protein			
	for beta-galactosidase	1		
**	(galactosialidosis)		1	1
	/FL=gb:BC000597.1 gb:M22960.1	2.00		1
	gb:NM_000308.1	1	1	1
	0:018973	0:018973 gb:NM_002634.2 /DEF=Homo sapiens prohibitin (PHB), mRNA. /FEA=mRNA /GEN=PHB /PROD=prohibitin /DB_XREF=gi:6031190 /UG=Hs.75323 prohibitin /FL=gb:NM_002634.2   0.001116 gb:NM_005620.1 /DEF=Homo sapiens S100 calcium-binding protein A11 (calgizzarin) (S100A11), mRNA. /FEA=mRNA /GEN=S100A11 /PROD=S100 calcium-binding protein A11 (DB_XREF=gi:5032056 /UG=Hs.256290 S100 calcium-binding protein A11 (calgizzarin) /FL=gb:D49355.1 gb:BC001410.1 gb:D50374.1 gb:NM_005620.1 gb:D38583.1   0.026891 gb:NM_000308.1 /DEF=Homo sapiens protective protein for beta-galactosidase (galactosidase /DB_XREF=gi:4505988 /UG=Hs.118126 protective protein for beta-galactosidase (galactosialidosis)	9b:NM_001152.1 /DEF=Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=SLC25A5 /PROD=solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 /DB_XREF=gi:4502098 /UG=Hs.79172 solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 /FL=gb:J02683.1 gb:NM_001152.1  0:018973 gb:NM_002634:2 /DEF=Homo sapiens prohibitin (PHB), mRNA. /FEA=mRNA /GEN=PHB /PROD=prohibitin /DB_XREF=gi:6031190 /UG=Hs.75323 prohibitin /FL=gb;NM_002634.2  0.001116 gb:NM_005620.1 /DEF=Homo sapiens S100 calcium-binding protein A11 (calgizzarin) (S100A11), mRNA. /FEA=mRNA /GEN=\$100A11. /PROD=\$100 calcium-binding protein A11 (calgizzarin) /FL=gb:D49355.1 gb:BC001410.1 gb:D50374.1 gb:NM_005620.1 ,gb:D38583.1  0.026891 gb:NM_000308.1 /DEF=Homo sapiens protective protein for beta-galactosidase (galactosialidosis) (PPGB), mRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase (galactosialidosis) (PPGB), mRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase (galactosialidosis) (PPGB), mRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase (galactosialidosis)	0.00228 gb:NM_001152.1 /DEF=Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=SLC25A5 /PROD=solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 /DB_XREF=gi:4502098 /UG=Hs.79172 solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 /FL=gb:J02683.1 gb:NM_001152.1 0.018973 gb:NM_002634.2 /DEF=Homo sapiens prohibitin (PHB), mRNA. /FEA=mRNA /GEN=PHB /PROD=prohibitin /JDB_XREF=gi:6031190 /UG=Hs.75323 prohibitin /FL=gb:NM_002634.2 0.001116 gb:NM_005620.1 /DEF=Homo sapiens S100 calcium-binding protein A11 (calgizzarin) (S100A11), mRNA. /FEA=mRNA /GEN=\$100A11. /PROD=\$100 calcium-binding protein A11 (calgizzarin) (JDB_XREF=gi:5032056 /UG=Hs.256290 S100 calcium-binding protein A11 (calgizzarin) /FL=gb:D49355.1 gb:RC001410.1 gb:D50374.1 gb:NM_005620.1 gb:D33583.1 0.026891 gb:NM_000308.1 /DEF=Homo sapiens protective protein for beta-galactosidase (galactosialidosis) (PPGB), mRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase /JDB_XREF=gi:4505988 /UG=Hs.118126 protective protein for beta-galactosidase (galactosialidosis) (PGB), mRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase (galactosialidosis) (PGB), mRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase /JDB_XREF=gi:4505988 /UG=Hs.118126 protective protein for beta-galactosidase (galactosialidosis) (PGB)

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
200663_at	1.26E-04	gb:NM_001780.1 /DEF=Homo	NM_001780		NP 001771
<b>-</b>		sapiens CD63 antigen			
	1	(melanoma 1 antigen) (CD63),	}		ŀ
	*	mRNA. /FEA=mRNA /GEN=CD63			, i.
4 1		/PROD=CD63 antigen (melanoma			
		1 antigen) /DB_XREF=gi:4502678		1 2	
		/UG=Hs.76294 CD63 antigen		: :	
		(melanoma 1 antigen)			}
* .		/FL=gb:BC002349.1 gb:M59907.1			
0		gb:NM 001780.1			
		J			: .
200667 at	0.00228	ubiquitin-conjugating enzyme E2D	BF448062		NP_003331
	3.332.0	3 (UBC4/5 homolog, yeast)		Hs.118797	
200668_s_at	7.58F-04	gb:BC003395.1 /DEF=Homo	BC003395		NP: 003331
1 <del>2.</del> 77.	7.002 0	sapiens, ubiquitin-conjugating	J-0000000		
	1	enzyme E2D 3 (homologous to			
		yeast UBC45), clone MGC:5416,	,		
	4	mRNA, complete cds.	100	3	
	*. (	/FEA=mRNA /PROD=ubiquitin-			7.7
* (		conjugating enzyme E2D 3	}		
	{ · .*	(homologousto yeast UBC45)			
		/DB_XREF=gi:13097281	<u>.</u>		
		/UG=Hs.118797 ubiquitin-			
	4				
4		conjugating enzyme E2D 3	*		
	( , i , a)	(homologous to yeast UBC45)			
		/FL=gb:U39318.1 gb:BC003395.1		,	
		gb:NM_003340.1	*		
200000	5 005 04	1 111 2000 10 1 1055 11	1111 0000		
200669_s_at	5.03E-04	gb:NM_003340.1 /DEF=Homo	NM_003340		NP_003331
		sapiens ubiquitin-conjugating			}
8 7 8		enzyme E2D 3 (homologous to		100	
	1	yeast UBC45) (UBE2D3), mRNA.			)
7		/FEA=mRNA /GEN=UBE2D3			* 1
	{ · · · · ·	/PROD=ubiquitin-conjugating	7		
		enzyme E2D 3 (homologousto			
* *		yeast UBC45)		₹	}
		/DB_XREF=gi:4507776			
		/UG=Hs.118797 ubiquitin-			1
	: .	conjugating enzyme E2D 3			
	•	(homologous to yeast UBC45)			*
	1	/FL≈gb:U39318.1 gb:BC003395.1	,		}
		gb:NM_003340.1			

Gene Identifier	p-valu	Description	Gen	Unigene	Protein
		· ·	Acc ssion	Accession	Acc ssion
			No.	No.	No.
200673_at	1.26E-04	gb:NM_014713.2 /DEF=Homo	NM_014713		NP_055528
4		sapiens lysosomal-associated			
• ,		protein transmembrane 4 alpha	· 6		
		(MBNT), mRNA. /FEA=mRNA			
		/GEN=MBNT /PROD=lysosomal-			~
	1	associated protein			
		transmembrane 4alpha		*	
	- 2	/DB_XREF=gi:13518239	•		<u> </u>
		/UG=Hs 111894 lysosomal-			·
*		associated protein	. "	)	
		transmembrane 4 alpha			
		/FL=gb:BC000421.1			
		gb:BC003158.1 gb:NM_014713.2			
		gb:D14696.1			
200674_s_at	0.026891	gb:NM_000994.1 /DEF=Homo	NM_000994		NP_000985
		sapiens ribosomal protein L32			
	]	(RPL32), mRNA. /FEA=mRNA	× -	40	
*	0	/GEN=RPL32 /PROD=ribosomal			
"	8	protein L32	1		
		/DB_XREF=gi:4506634			
	•	/UG=Hs.169793 ribosomal protein			
		L32 /FL=gb:NM_000994.1			
			*		
200676 s at	0.012818	gb:NM 003347.1 /DEF=Homo	NM 003347		NP 003338
		sapiens ubiquitin-conjugating		]	ļ. <del>-</del> .
• •		enzyme E2L 3 (UBE2L3), mRNA.			
	4 3	/FEA=mRNA /GEN=UBE2L3		1	<b>]</b>
		/PROD=ubiquitin-conjugating			•
		enzyme E2L 3			
	1	/DB_XREF=gi:4507788			
. ()		/UG=Hs.108104 ubiquitin-			'
		conjugating enzyme E2L 3			
	1	/FL=gb:NM_003347.1			
200677_at	1.26E-04	gb:NM_004339.2 /DEF=Homo	NM_004339	7	NP_004330
		sapiens pituitary tumor-	_	*	_
		transforming 1 interacting protein			
		(PTTG1IP), mRNA. /FEA=mRNA			-[
	-	/GEN=PTTG1IP /PROD=pituitary	į		1
,	1	tumor-transforming protein1-			1
		interacting protein precursor		¥	1
1	}	/DB_XREF=gi:11038670	* *		1
1		/UG=Hs.111126 pituitary tumor-			1.
· .		transforming 1 interacting protein		{	1
		/FL=gb:NM 004339.2			
r -	1 .	gb:BC000415.1 gb:AF149785.1		1	
		100:DC0004 [3.1 00:A): 143/103.1			

Gene ld ntifier	p-value	Description	Gene	Unigene	Protein
* * *			Accession	Accession	Accession
	181		No.	No.	No.
200678_x_at	0.041055	gb:NM_002087.1 /DEF=Homo	NM_002087		NP_002078
	*	sapiens granulin (GRN), mRNA.			
		/FEA=mRNA /GEN=GRN			
		/PROD=granulin			
	1	/DB_XREF=gi:4504150		1	1
		/UG=Hs.180577 granulin			
		/FL=gb:M75161.1 gb:AF055008.1			· -
	1 :	gb:NM_002087.1			
200680 x at	2.05E-04	gb:NM_002128.1 /DEF=Homo	NM_002128		NP_002119
		sapiens high-mobility group			_
		(nonhistone chromosomal) protein		, ,	
,	1.	1 (HMG1), mRNA. /FEA=mRNA			
		/GEN=HMG1 /PROD=high-mobility			
		group (nonhistone	r - i		- 20
· <del>'</del> ·		chromosomal)protein 1	440		
		/DB_XREF=gi:4504424			
*		/UG=Hs.274472 high-mobility	- 1.1		
		group (nonhistone chromosomal)	**************************************		
8		protein 1 /FL=gb:BC003378.1			
		gb:NM_002128.1 gb:D63874.1			*
200682_s_at	1.26E-04	Consensus includes	NM_003347	2. T. T.	NP_003338
- <del></del>	1	gb:BG531983 /FEA=EST		1	
,		/DB_XREF=gi:13523521			
		/DB_XREF=est:602561007F1			
		/CLONE=IMAGE:4699176		İ	
		/UG=Hs.108104 ubiquitin-			
1.		conjugating enzyme E2L 3	ŀ		
		/FL=gb:NM_003347.1			
200687_s_at	0.027633	gb:NM 012426.1 /DEF=Homo	NM 012426	1 - 200-0	NP 036558
	**	sapiens splicing factor 3b,	_	· · · · · · · · · · · · · · · · · · ·	<u> </u>
9.5	· ·	subunit 3, 130kD (SF3B3),			ì
		mRNA. /FEA=mRNA		`	
	1	/GEN=SF3B3 /PROD=splicing		,	1.
	;	factor 3b, subunit 3, 130kD	*		* * * * * * * * * * * * * * * * * * * *
		/DB_XREF=gi:11034822		1	
		/UG=Hs.195614 splicing factor			
	1 ' '	3b, subunit 3, 130kD			+ .
		/FL=gb:NM_012426.1			
		gb:BC000463.1 gb:BC003146.1			
- A A		gb:D13642.1 gb:D87686.1		*	

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
	[	<u> </u>	No.	No.	No.
200693_at	0.013223	gb:NM_006826.1 /DEF=Homo	NM_006826		NP_006817
	)	sapiens tyrosine 3-		***	
0		monooxygenasetryptophan 5-			
		monooxygenase activation			
		protein, theta polypeptide			
		(YWHAQ), mRNA. /FEA=mRNA		, ,	
		/GEN=YWHAQ /PROD=tyrosine 3-			8 (
		monooxygenasetryptophan5-			
	- 4	monooxygenase activation		<b>i</b>	
	-	protein, theta polypeptide			
<i>i</i> =		/DB_XREF=gi:5803226		^	
100		/UG=Hs.74405 tyrosine 3-		41	
*	- :	monooxygenasetryptophan 5-	Î		
		monooxygenase activation	110		
		protein, theta polypeptide			
		/FL=gb:NM_006826.1			
200696_s_at	7 58E-04	gb:NM 000177:1 /DEF=Homo	NM 000177		NP 000168
		sapiens gelsolin (amyloidosis,			
		Finnish type) (GSN), mRNA.			
		/FEA=mRNA /GEN=GSN			
		/PROD=gelsolin (amyloidosis,	. *	. X	
	1	Finnish type)			3
*		/DB_XREF=gi:4504164		* .	
*		/UG=Hs.290070 gelsolin	- Y		
	<b>,</b>	(amyloidosis, Finnish type)			
		/FL=gb:NM_000177.1			
200697_at	1 26E 04	gb:NM_000177.1	NM 000188	1 11 11 11	NP 277035
200091_at	1.20L-04	sapiens hexokinase 1 (HK1),	14141_000100		1117_277033
		nuclear gene encoding			
	*		Ī		
	* *	mitochondrial protein, mRNA.	*0		0.
		/FEA=mRNA /GEN=HK1 /PROD=hexokinase 1	1 1 1		Ci.
					1 1 1 1 1 1 1 1 1 1 1 1 1
		/DB_XREF=gi:4504390 /UG=Hs.118625 hexokinase 1			
4		/FL=gb:M75126.1			
200000 -1	2.055.04	gb:NM_000188.1	NINA COCCEA		ND 000045
200698_at	2.05E-04	Consensus includes gb:AL542253	NIVI_006854		NP_006845
		/FEA=EST			
	,	/DB_XREF=gi:12874115	1	·. ·	
		/DB_XREF=est:AL542253			e
*		/CLONE=CS0DE008YC08 (3			
		prime) /UG=Hs.118778 KDEL			
		(Lys-Asp-Glu-Leu) endoplasmic	1		
*	e- *	reticulum protein retention	1		
· · · · · · · · · · · · · · · · · · ·		receptor 2 /FL=gb:NM_006854.2		ē	

G ne Identifi r	p-value	Description	Gen	Unigene	Protein
. *			Acc ssion	Accession	Accession
			No.	No.	No.
200699_at	0.005852	Consensus includes gb:BE962456	NM_006854		NP_006845
**	1	/FEA=EST	**		19-0
		/DB_XREF=gi:11765376			
		/DB_XREF=est:601655751R1			
		/CLONE=IMAGE:3846156			
		/UG=Hs.118778 KDEL (Lys-Asp-			
•		Glu-Leu) endoplasmic reticulum	*		* /
* (**)		protein retention receptor 2			
		/FL=gb:NM_006854.2			<u> </u>
200700_s_at	0.02145	gb:NM_006854.2 /DEF=Homo	NM_006854		NP_006845
	32	sapiens KDEL (Lys-Asp-Glu-Leu)			
		endoplasmic reticulum protein			
		retention receptor 2 (KDELR2),		* * * * * *	
		mRNA. /FEA=mRNA	. ***		
		/GEN=KDELR2 /PROD=KDEL	^-		
		receptor 2 /DB_XREF=gi:8051609			
3.		/UG=Hs.118778 KDEL (Lys-Asp-			
		Glu-Leu) endoplasmic reticulum	* (1)		
		protein retention receptor 2			
		/FL=gb:NM_006854.2			
				70.0	
200701_at	0.016934	gb:NM_006432.1 /DEF=Homo	NM_006432		NP 006423
		sapiens epididymal secretory			
- ()		protein (19.5kD) (HE1), mRNA.			
		/FEA=mRNA /GEN=HE1		(a) (b) (c)	
	9	/PROD=epididymal secretory			- **
		protein (19.5kD)		9	-00-
		/DB_XREF=gi:5453677			· ·
		/UG=Hs.119529 epididymal			0.*
		secretory protein (19.5kD)	* *		
		/FL=gb:BC002532.1		- *	
		gb:NM 006432.1			
200703_at	0.005852	gb:NM_003746.1 /DEF=Homo	NM 003746		NP_003737
		sapiens dynein, cytoplasmic, light			' T
		polypeptide (PIN), mRNA.	<u> </u>		
		/FEA=mRNA /GEN=PIN			
		/PROD=dynein, cytoplasmic, light			· ·
		polypeptide			· ·
		/DB_XREF=gi:4505812			
		/UG=Hs.5120 dynein, cytoplasmic,			4 4 4 4
I	l '	light polypeptide /FL=gb:U32944.1	1	1	:
		HIGHE DOLYPEDINE /FL-05:032944. I		1	The second second
		gb:NM_003746.1			

Gene ld ntifier	p-value	Description	G ne	Unigene	Protein
*			Accession	Accession	Accession
			No.	No.	No.
200706_s_at	0.026891	gb:NM_004862.1 /DEF=Homo	NM_004862		NP_004853
		sapiens LPS-induced TNF-alpha	, pro-		
		factor (PIG7), mRNA		,	
		/FEA=mRNA /GEN=PIG7			
		/PROD=LPS-induced TNF-alpha	0.00		- '-
	1	factor /DB_XREF=gi:4758913			
		/UG=Hs.76507 LPS-induced TNF-			:
		alpha factor /FL=gb:AB034747.1	÷		-3
		gb:U77396:1 gb:AF010312.1	** *	*	
		gb:NM 004862.1			
200707 at	0.013088		NM 1002743	1	NP 002734
200707_40	0.010000	sapiens protein kinase C			141 _0027 04
	- × .	substrate 80K-H (PRKCSH),	(		
	*	mRNA /FEA=mRNA	*		*
, ss **		/GEN=PRKCSH /PROD=protein	0		
	1	kinase C substrate 80K-H			
			*		
	8 8	/DB_XREF=gi:4506076	*		-
*		/UG=Hs.1432 protein kinase C	* /		
		substrate 80K-H /FL=gb:J03075.1			
		gb:NM_002743.1 gb:AF144075.1		200	
000700	4.005.04	11111 000001 20000	111111111111111111111111111111111111111		100100
200709_at	1.26E-04	gb:NM_000801.1 /DEF=Homo			NP_463460
		sapiens FK506-binding protein 1A			
		(12kD) (FKBP1A), mRNA.			
		/FEA=mRNA /GEN=FKBP1A			
		/PROD=FK506-binding protein 1A	+		
		(12kD) /DB_XREF=gi:4503724		,	
	/:	/UG=Hs.752 FK506-binding	·		
	.0, .	protein 1A (12kD)			.00-
*		/FL=gb:BC001925.1 gb:M34539.1			
		gb:NM_000801.1	}		
		<u> </u>			
200712_s_at	0.004341	microtubule-associated protein,	AI633566		NP: 036457
		RP/EB family, member 1		Hs.234279	
200713_s_at	1.26E-04	gb:NM_012325.1 /DEF=Homo	NM_012325		NP_036457
		sapiens microtubule-associated			
		protein, RPEB family, member 1			2
		(MAPRE1), mRNA. /FEA=mRNA		, *	
		/GEN=MAPRE1			ŀ
	- ·	/PROD=microtubule-associated			
		protein, RPEB family,member 1	*,		
	6.4	/DB_XREF=gi:6912493	,		
		/UG=Hs.234279 microtubule-			
*	1	associated protein, RPEB family,		0.2	
		member 1 /FL=gb:NM_012325.1			
		gb:U24166.1			
		95.524100.1			
	L	<del></del>		<u> </u>	L

G ne Identifier	p-value	Description	Gen	Unigen	Prot in
•			Accession	Accession	Accession
• '			No.	No.	No.
200714_x_at	0.013223	gb:NM_006812.1 /DEF=Homo	NM_006812		NP_006803
		sapiens amplified in			
		osteosarcoma (OS-9), mRNA.			
		/FEA=mRNA /GEN=OS-9	• :		
		/PROD=amplified in			
		osteosarcoma			0.00
		/DB_XREF=gi:5803108			10
		/UG=Hs.76228 amplified in		٠.	
	,	osteosarcoma /FL=gb:U41635.1			
* •	į.	gb:AB002806.1 gb:NM_006812.1			
200715_x_at	0.026891	gb:BC000514.1 /DEF=Homo	BC000514		NP 036555
		sapiens, ribosomal protein L13a,		4.5	_
	1	clone MGC;8547, mRNA,	38		
,	10	complete cds. /FEA=mRNA			
		/PROD=ribosomal protein L13a			
•		/DB_XREF≔gi:12653484			•
		/UG=Hs.119122 ribosomal protein			
		L13a /FL=gb:BC000514.1			
		gb:NM 012423.1	* 1		, · · · •
	Y				
200716_x_at	0.007779	gb:NM_012423.1 /DEF=Homo	NM_012423		NP 036555
	,	sapiens ribosomal protein L13a		*	
		(RPL13A), mRNA. /FEA=mRNA	= 1		
	٠,	/GEN=RPL13A /PROD=ribosomal			
		protein L13a	500 A		
; 8		/DB_XREF=gi:6912633			
		/UG=Hs.119122 ribosomal protein	-00		
		L13a /FL=gb:BC000514.1			
e		gb:NM_012423.1			
					× 20 .
200717_x at	0.041055	gb:NM_000971.1 /DEF=Homo	NM 000971	1	NP 000962
<del></del>	1	sapiens ribosomal protein L7			_
		(RPL7), mRNA. /FEA=mRNA	*		
		/GEN=RPL7 /PROD=ribosomal		-	
		protein L7 /DB_XREF=gi:4506658			
		/UG=Hs.153 ribosomal protein L7			
14		/FL=gb:L16558.1 gb:NM_000971.1	a ·	•	*
					00-

Gene Identifier	p-value	Description	Gen	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
200721 s at	0.007779	gb:NM_005736.2 /DEF=Homo	NM 005736		NP_005727
	* .	sapiens ARP1 (actin-related		Ψ.	
		protein 1, yeast) homolog A		. 0	00
*		(centractin alpha) (ACTR1A),		<i>'</i>	
		mRNA. /FEA=mRNA		5 y 2	
		/GEN=ACTR1A /PROD=actin-		*	•
		related protein 1A		, , , , , , , , , , , , , , , , , , ,	
		/DB_XREF=gi:13325058	,		
		/UG=Hs.153961 ARP1 (actin-			
		related protein 1, yeast) homolog			
*		A (centractin alpha)			
		/FL=gb:BC000693.1	*	*	
		gb:NM_005736.2			1.
200723 s at	5.03F-04	gb:NM_005898.1 /DEF=Homo	NM 005898	<del></del>	NP 005889
200120_3_ut	0.002 04	sapiens membrane component,	11111_0000000		
		chromosome 11, surface marker		. 3	0.
0		1 (M11S1), mRNA. /FEA≃mRNA			
		/GEN=M11S1 /PROD=membrane			,
	7	component, chromosome 11,		• • •	.*
		surfacemarker 1	i i	* 1	·Yo
					* *
		/DB_XREF=gi:5174502	• •		÷
		/UG=Hs.278672 membrane			• •
· ·	1	component, chromosome 11,			
***		surface marker 1		1 10 *:	
* *		/FL=gb:BC001731.1	<b>∤</b> `.	2	
600705		gb:NM_005898.1			
200725_x_at	0.00228	gb:NM_006013.1 /DEF=Homo	NM_006013	.,	NP_006004
,		sapiens ribosomal protein L10		· .	
	1	(RPL10), mRNA. /FEA=mRNA			11.
		/GEN=RPL10 /PROD=ribosomal		1 :	
		protein L10		1, 3	\$ 1
		/DB_XREF=gi:5174430			
		/UG=Hs.29797 ribosomal protein		*	· .
* .		L10 /FL=gb:BC003358.1			
		gb:M73791.1 gb:M64241.1			
7		gb:NM_006013.1			
200728_at	3.26E-04	ARP2 actin-related protein 2	AA699583		NP_005713
,		homolog (yeast)		Hs.42915	*
200729_s_at	0.005852	gb:NM_005722.1 /DEF=Homo	NM_005722		NP_005713
•		sapiens ARP2 (actin-related			
	,	protein 2, yeast) homolog			£
ý.	}	(ACTR2), mRNA. /FEA=mRNA	1	]	
		/GEN=ACTR2 /PROD=ARP2			
		(actin-related protein 2, yeast)	}		
* .		homolog /DB_XREF=gi:5031570			
	}	/UG=Hs.42915 ARP2 (actin-	*		}
		related protein 2, yeast) homolog	1		•
	}	/FL=gb:AF006082.1			9
TY-		gb:NM_005722.1		- 3	
	<u> </u>	ISP. MIN DOOLET. I	<u> </u>	ب ب	L

Gene Identifier	p-value	Description	Gen	Unigene	Protein
1			Accession	Accession	Accession
*		N *	No.	No.	No.
200731_s_at	0.033381	protein tyrosine phosphatase type	BF576710		NP_003454
		IVA, member 1		Hs.227777	-
200732_s_at	7.58E-04	protein tyrosine phosphatase type	BF576710	7.00	NP 003454
		IVA, member 1		Hs.227777	<del>-</del> , :
200733 s_at	5.03E-04	gb:U48296.1 /DEF=Homo sapiens	U48296	<del></del>	NP_003454
7		protein tyrosine phosphatase			- y
		PTPCAAX1 (hPTPCAAX1)			!
*		mRNA, complete cds.			
	· .	/FEA=mRNA /GEN=hPTPCAAX1		·	
		/PROD=protein tyrosine		•	
		phosphatase PTPCAAX1			
. *		/DB_XREF≃gi:1777754			
		/UG=Hs.227777 protein tyrosine			
		phosphatase type IVA, member		λ.	
		1 /FL=gb:U48296.1	ė ,		
		gb:NM 003463.1	-		
		<u>-</u>			
200734 s at	2.05E-04	ADP-ribosylation factor 3	BG341906	Hs.119177	NP 001650
200736_s_at		gb:NM 000581.1 /DEF=Homo	NM 000581	,	NP 000572
	1	sapiens glutathione peroxidase 1	_, , , , , ,		
*		(GPX1), mRNA. /FEA=mRNA			1.
		/GEN=GPX1 /PROD=glutathione			Į.
		peroxidase 1	U	- (1)	•
		/DB_XREF=gi:10834975			<u>.</u> .
		/UG=Hs.76686 glutathione	-00		
		peroxidase 1		*	
Ē.,	1 . :	/FL=gb:NM_000581.1			
		gb:BC000742.1 gb:M21304.1			*
200737 at	1.26F-04	gb:NM 000291.1 /DEF=Homo	NM_000291		NP_000282
200701_at	1.202 07	sapiens phosphoglycerate kinase	14141_000231	·	111 _000202
, , ,		1 (PGK1), mRNA. /FEA=mRNA			
		/GEN=PGK1			
		/PROD=phosphoglycerate kinase		·	
		1 /DB_XREF=gi:4505762			
	1.	/UG=Hs.78771 phosphoglycerate		1	
( )		kinase 1 /FL=gb:NM_000291.1	*		
200738 s at	1.26F_04	gb:NM_000291.1 /DEF=Homo	NM_000291		NP_000282
200730_3_at	1.202-07	sapiens phosphoglycerate kinase	14141_000251	- 3	141 _000202
	1	1 (PGK1), mRNA. /FEA=mRNA			
		/GEN=PGK1		100	
÷	[-	/PROD=phosphoglycerate kinase			
100	<b>-</b>	1 /DB_XREF=gi:4505762	- 3.0		,
	]				10
, ,		/UG=Hs.78771 phosphoglycerate	. ②		]
200720+	7 505 04	kinase 1 /FL=gb:NM_000291.1	DC220520		ND 000007
200739_s_at	1.50E-04	SMT3 suppressor of mif two 3	BG338532	Un 05110	NP_008867
	1,	homolog 1 (yeast)	L	Hs.85119	L

Gene Identifier	p-value	Description	Gene	Unigene	Prot in
			Accession	Accession	Acc ssion
			No.	No.	No.
200740_s_at	5.03E-04	gb:NM 006936.1 /DEF=Homo	NM 006936		NP_008867
		sapiens SMT3 (suppressor of mif			
		two 3, yeast) homolog 1	and the second		
		(SMT3H1), mRNA /FEA=mRNA			
		/GEN=SMT3H1 /PROD=SMT3			
		(suppressor of mif two 3, yeast)	*		
		homolog 1 /DB_XREF=gi:5902095			
		/UG=Hs.85119 SMT3 (suppressor			
	·	of mif two 3, yeast) homolog 1	4		
		/FL=gb:BC000036.1		, .	
		gb:NM_006936.1			
		19b.11111_000000.1			• • · ·
200742 s at	1.26F-04	ceroid-lipofuscinosis, neuronal 2,	BG231932	7	NP_000382
2007 12_0_4	1.202 0,1	late infantile (Jansky-Bielschowsky	B0201002		
		disease)		Hs.20478	
200743_s_at	1.26E-04	gb:NM 000391.2 /DEF=Homo	NM 000391	113.20-70	NP 000382
2007 40_0_4	1.202	sapiens ceroid-lipofuscinosis,		* .	141 _000002
		neuronal 2, late infantile (Jansky-			
		Bielschowsky disease) (CLN2),		37	
	1	mRNA. /FEA=mRNA,/GEN=CLN2	Ç.		
*		/PROD=ceroid-lipofuscinosis,			
		neuronal 2, lateinfantile (Jansky-	1.		
	ļ .	Bielschowsky disease)	ir.		
		/DB_XREF≈gi:5597012	· ·		٠.
		/UG=Hs.20478 ceroid-	· : .		
	:	lipofuscinosis, neuronal 2, late			
		infantile (Jansky-Bielschowsky			
8.4	- 1	disease) /FL=gb:AF017456.1			
		gb:NM 000391.2			
	]* .	gb.14141_000391.2			]
200744 s at	7 58E 04	Consensus includes gb:AI741124	NIM 002074		NP 002065
200744_5_at	7.30L-04	/FEA=EST /DB_XREF=gi:5109412	NIVI_002074		NF_002005
- 7					
4		/DB_XREF=est:wg19c04.x1 /CLONE=IMAGE:2365542			
		/UG=Hs.215595 guanine			
		nucleotide binding protein (G	*	. 2	
	1				, ,
	}	protein), beta polypeptide 1			
		/FL=gb:NM_002074.1	, ·		
	, ×	gb:BC004186.1			
	<u> </u>	<u> </u>			` :

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Acc ssion	Accession	Accession
			No.	No.	No.
200746_s_at	2.05E-04	gb:NM_002074.1 /DEF=Homo	NM_002074		NP_002065
		sapiens guanine nucleotide	-1	* 44	
		binding protein (G protein), beta			
y		polypeptide 1 (GNB1), mRNA.	0.		
		/FEA=mRNA /GEN=GNB1			* . * *
		/PROD=guanine nucleotide			
		binding protein (G protein),beta			
	* * * * * * * * * * * * * * * * * * * *	polypeptide 1			
* .*:	· · · · ·	/DB_XREF=gi:11321584			
		/UG=Hs.215595 guanine	. (2)		
		nucleotide binding protein (G			
		protein), beta polypeptide 1		١.	
		/FL=gb:NM_002074.1			
		gb:BC004186.1	1		
200753_x_at		hypothetical protein ET	BE866585	Hs.73965	NP_003007
200757_s_at	0.034221	gb:NM_001219.2 /DEF=Homo	NM_001219		NP_001210
		sapiens calumenin (CALU),			
		mRNA /FEA=mRNA /GEN=CALU	-		-
300		/PROD=calumenin precursor	*	7 . 4	
		/DB_XREF=gi:6005991		<u> </u>	
		/UG=Hs.7753 calumenin			
	0.00	/FL=gb:U67280.1 gb:AF013759.1			
	- Tage 1	gb:NM_001219.2			
200760_s_at	0.041055	vitamin A responsive, cytoskeleton	N92494		NP_006398
		related		Hs.92384	
200764_s_at	0.003171	catenin (cadherin-associated	AI826881		NP_001894
		protein), alpha 1, 102kDa		Hs.178452	
200765_x_at	7.58E-04	10 -	NM_001903		NP_001894
		sapiens catenin (cadherin-	1		
	0 ()	associated protein), alpha 1			
3		(102kD) (CTNNA1), mRNA.			
	1	/FEA=mRNA /GEN=CTNNA1			
		/PROD=catenin (cadherin-	la de la composición de la composición de la composición de la composición de la composición de la composición		
		associated protein), alpha			
		1(102kD) /DB_XREF=gi:4503126		*	
		/UG=Hs.178452 catenin (cadherin-	1		
````	·	associated protein), alpha 1			
	*	(102kD) /FL=gb:L23805.1			
*		gb:NM_001903.1			
1 1			*	1.	
200772_x_at	0.004341	prothymosin, alpha (gene sequence	BF686442		NP_002814
	<u> </u>	[28]	, ,	Hs.250655	<u> </u>

Gene Identifier	p-value	Description	G ne	Unig ne	Prot in
			Accession	Accession	Accession
			No.	No.	No.
200777_s_at	7.58E-04	gb:NM_014670.1 /DEF=Homo	NM_014670		NP 055485
		sapiens KIAA0005 gene product			<del>-</del> "
		(KIAA0005), mRNA. /FEA=mRNA	1		
		/GEN=KIAA0005		å	
5 g , 2		/PROD=KIAA0005 gene product	*		0
	7.	/DB XREF=gi:7661849			. *
₩**		/UG=Hs.155291 KIAA0005 gene	0		
		product /FL=gb:D13630.1			
		gb:NM_014670:1	f A		-
200778_s_at	0.041055	neural precursor cell expressed,	Al191427		NP 004395
200170_0_dt	0.0 11000	developmentally down-regulated 5	/110142/	Hs.155595	141 _004000
200780_x_at	0.00228	gb:NM_000516.2 /DEF=Homo	NM_000516	113.100000	NP_536351
200700_X_at	0.00220	sapiens guanine nucleotide	14141_000510		141-230231
		binding protein (G protein), alpha	*		0
		stimulating activity polypeptide 1			*
		(GNAS1), mRNA. /FEA=mRNA	8	/	
		/GEN=GNAS1 /PROD=guanine			D &
					•
		nucleotide binding protein (G		,	* * * * * * * * * * * * * * * * * * * *
		protein),alpha stimulating activity			
3		polypeptide 1			:
		/DB_XREF=gi:8659565		,	
		/UG=Hs.273385 guanine			
		nucleotide binding protein (G			
		protein), alpha stimulating activity			
		polypeptide 1 /FL=gb:BC002722.1			
		gb:AF088185.1 gb:NM_000516.2	• . •		*
200781_s_at	0.004341	19.	NM_001019		NP_001010
* *		sapiens ribosomal protein S15a			
		(RPS15A), mRNA. /FEA=mRNA	0.	*.	
	30	/GEN=RPS15A /PROD=ribosomal	. *		
		protein S15a			
		/DB_XREF=gi:4506688	* *		- 100
		/UG=Hs.2953 ribosomal protein			·
		S15a /FL=gb:BC001697.1	·		
		gb:NM_001019.1			
200782_at	1.26E-04	gb:NM_001154:2 /DEF=Homo	NM_001154		NP_001145
		sapiens annexin A5 (ANXA5),		· '	
	***	mRNA. /FEA=mRNA	**		ζ
*	,	/GEN=ANXA5 /PROD=annexin V			
*		/DB_XREF=gi:4809273	50		,
		/UG=Hs.300711 annexin A5	) <sup>-</sup>		
		/FL=gb:BC001429.1		3	· ·
		gb:BC004993.1 gb:M18366.1			
		gb:J03745.1 gb:M21731.1			*
		gb:M19384.1 gb:D00172.1			
		gb.NM 001154.2			
	<u> </u>	19-11-11-			

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
200785_s_at	7.58E-04	gb:NM_002332.1 /DEF=Homo	NM_002332		NP_002323
		sapiens low density lipoprotein-			8
	100	related protein 1 (alpha-2-			
*		macroglobulin receptor) (LRP1),			-
		mRNA. /FEA=mRNA /GEN=LRP1	1 4		
		/PROD=low density lipoprotein-			
		related protein 1(alpha-2-			
		macroglobulin receptor)		* 1	
	-	/DB_XREF=gi:4758685	ne i		·
		/UG=Hs.89137 low density			
		lipoprotein-related protein 1		. :	
0		(alpha-2-macroglobulin receptor)	8		
		/FL=gb:NM_002332.1			
200786_at	0.00161	gb:NM_002799.1 /DEF=Homo	NM_002799		NP 002790
		sapiens proteasome (prosome,			_
		macropain) subunit, beta type, 7			i.
		(PSMB7), mRNA. /FEA=mRNA			
		/GEN=PSMB7			. :
		/PROD=proteasome (prosome,		37 °	
		macropain) subunit, betatype, 7		1. At 1.	
*		/DB_XREF=gi:4506202			
, (i)		/UG=Hs.118065 proteasome	- X		
		(prosome, macropain) subunit,	-	* *	
		beta type, 7 /FL=gb:BC000509.1			
		gb:D38048.1 gb:NM_002799.1		1	
	*				
200789 at	0.002313	gb:NM 001398.1 /DEF=Homo	NM_001398		NP 001389
		sapiens enoyl Coenzyme A			
		hydratase 1, peroxisomal (ECH1),			
	, ,	mRNA. /FEA=mRNA /GEN=ECH1			
* *		/PROD=peroxisomal enoyl-			
1 1 1		coenzyme A hydratase-likeprotein			
	*	/DB_XREF=gi:4503446		-	100
( ·		/UG=Hs.196176 enoyl Coenzyme	,		* *
* *		A hydratase 1, peroxisomal			
		/FL=gb:NM_001398.1			. (
		gb:U16660.1			· ·
	0.			1 47	
		8		1	i
	·	·			

Gene Identifier	p-value	Description	Gene	Unig ne	Protein
			Accession	Accession	Accession
			No.	No.	No.
200791_s_at	5.03E-04	gb:NM_003870.1 /DEF=Homo	NM_003870	.,	NP_003861
		sapiens IQ motif containing			
		GTPase activating protein 1		0. <sup>3</sup>	1
. "	* 1	(IQGAP1), mRNA. /FEA=mRNA	*		
-		/GEN=IQGAP1 /PROD=IQ motif.		*	
	0.5	containing GTPase activating			
		protein 1 /DB_XREF=gi:4506786		1	
		/UG=Hs.1742 IQ motif containing		*	
		GTPase activating protein 1	· ·		
		/FL=gb:NM_003870.1 gb:L33075.1			
200792_at	0.026891	gb:NM_001469.1 /DEF=Homo	NM_001469		NP_001460
·		sapiens thyroid autoantigen 70kD			
		(Ku antigen) (G22P1), mRNA.		N - 1	
		/FEA=mRNA /GEN=G22P1			
. *		/PROD=thyroid autoantigen 70kD			
		(Ku antigen)			
		/DB_XREF=gi:4503840		1	
*		/UG=Hs.197345 thyroid			, a * *
· · · · · · · · · · · · · · · · · · ·		autoantigen 70kD (Ku antigen)		<b>l</b> .	₹ · · ÷
V.		/FL=gb:J04611.1 gb:M32865.1	Ň		
200704 2 -4	0.00404	gb:J04607.1 gb:NM_001469.1	NIM 04 4704		ND OFFE
200794_x_at	0.00161	gb:NM_014764.1 /DEF=Homo	NM_014764		NP_055579
		sapiëns DAZ associated protein			
4.7		2 (DAZAP2), mRNA.	}		1
	l'	/FEA=mRNA /GEN=DAZAP2	- 1		
		/PROD=DAZ associated protein 2			
		/DB_XREF=gi:7661885 /UG=Hs.75416 DAZ associated		٠.	
-		protein 2 /FL=gb:BC002334.1			-
		gb:D31767.1 gb:NM_014764.1	* ,		
200799 at	7.58E-04		NM_005345		NP 005336
200133_at	7.JOL-04	sapiens heat shock 70kD protein	Name		LO03336
		1A (HSPA1A), mRNA.			
		//FEA=mRNA /GEN=HSPA1A			
		/PROD=heat shock 70kD protein			
		1A /DB_XREF=gi:5579469		{	
* .		/UG=Hs.8997 heat shock 70kD	*** 1.8		- "
		protein 1A /FL=gb:BC002453.1	-0		
		gb:NM 005345.3	108	-	
•	1	32,0000 10.0			
	<u></u>	L	L		L

Gene Identifi r	p-value	Description	Gene	Unig ne	Protein
			Accession	Acc ssion	Accession
			No.	No.	No.
200800_s_at	2.05E-04	gb:NM_005345.3 /DEF=Homo	NM_005345		NP_005336
		sapiens heat shock 70kD protein		11	7
		1A (HSPA1A), mRNA.			
		/FEA=mRNA /GEN=HSPA1A			,
*		/PROD=heat shock 70kD protein			
		1A /DB_XREF=gi:5579469	100		
		/UG=Hs.8997 heat shock 70kD		8.1	
		protein 1A /FL=gb:BC002453.1			
*	-	gb:NM_005345.3			
200803_s_at	3.26E-04	gb:AF033095.1 /DEF=Homo	AF033095	,	NP_003208
		sapiens testis enhanced gene			
		transcript protein (TEGT) mRNA,			
		complete cds. /FEA=mRNA			ŀ
		/GEN=TEGT /PRQD=testis	,	1	
*		enhanced gene transcript protein	. *		4
		/DB_XREF=gi:2645728			
		/UG=Hs.74637 testis enhanced		0	
<i>y</i>		gene transcript (BAX inhibitor 1)			* 1
	4	/FL=gb:BC000916.1			
		gb:AF033095.1 gb:NM_003217.1			
		gaaaa			
200804_at	0.033381	gb:NM_003217.1 /DEF=Homo	NM_003217		NP 003208
	*	sapiens testis enhanced gene			_
* *		transcript (TEGT), mRNA.		· .	
		/FEA=mRNA /GEN=TEGT	980		
* "		/PROD=testis enhanced gene			
	. 3	transcript /DB_XREF=gi:4507432		`	
		/UG=Hs.74637 testis enhanced			
		gene transcript (BAX inhibitor 1)			
		/FL=gb:BC000916.1	*		
		gb:AF033095.1 gb:NM_003217.1		*	
200814_at	0.004341	gb.NM_006263.1 /DEF=Homo	NM_006263		NP_788955
		sapiens proteasome (prosome,			
	,	macropain) activator subunit 1			
		(PA28 alpha) (PSME1), mRNA.			
			1		1
		I/FEA=mRNA /GEN=PSME1			
		/FEA=mRNA /GEN=PSME1 /PROD=proteasome (prosome.			
		/PROD=proteasome (prosome,			
		/PROD=proteasome (prosome, macropain) activatorsubunit 1	*		
		/PROD=proteasome (prosome, macropain) activatorsubunit 1 (PA28 alpha)	*		
		/PROD=proteasome (prosome, macropain) activatorsubunit 1 (PA28 alpha) /DB_XREF=gi:5453989	*		
		/PROD=proteasome (prosome, macropain) activatorsubunit 1 (PA28 alpha) /DB_XREF=gi:5453989 /UG=Hs.75348 proteasome	*		
		/PROD=proteasome (prosome, macropain) activatorsubunit 1 (PA28 alpha) /DB_XREF=gi:5453989 /UG=Hs.75348 proteasome (prosome, macropain) activator			
		/PROD=proteasome (prosome, macropain) activatorsubunit 1 (PA28 alpha) /DB_XREF=gi:5453989 /UG=Hs.75348 proteasome			

Gene Identifier	p-value	Description	Gene Accession	Unigene Accession	Prot in Accession
			No.	No.	No.
200815_s_at	1.26E-04	gb:L13386.1 /DEF=Homo sapiens (clone 47) Miller-Dieker		*	NP_000421
		lissencephaly protein (LIS1)			
		mRNA, complete cds. /FEA=mRNA /GEN=LIS1			
		/PROD=Miller-Dieker lissencephaly protein /DB_XREF=gi:349825		*	
		/UG=Hs.77318 platelet-activating			
		factor acetylhydrolase, isoform lb, alpha subunit (45kD)			
		/FL=gb:L13385.1 gb:L13386.1 gb:NM_000430.2		*()	
			. ,		
200820_at	1.26E-04	gb:NM_002812:1 /DEF=Homo sapiens proteasome (prosome,	NM_002812		NP_002803
		macropain) 26S subunit, non-			
		ATPase, 8 (PSMD8), mRNA. /FEA=mRNA /GEN=PSMD8		) 0	- )
		/PROD=proteasome (prosome, macropain) 26S subunit,non-			
		ATPase, 8 /DB_XREF=gi:4506232	ı	* * *	,
* * *		/UG=Hs.78466 proteasome (prosome, macropain) 26S	-		*
		subunit, non-ATPase, 8 // /FL=gb:D38047.1 gb:BC001164.1			
		gb:NM_002812.1			
200821_at	5.03E-04	gb:NM_013995.1 /DEF=Homo	NM_013995		NP_054701
		sapiens lysosomal-associated membrane protein 2 (LAMP2),			
		transcript variant LAMP2B,			
		mRNA. /FEA=mRNA /GEN=LAMP2 /PROD=lysosomal-		· · · · · · · · · · · · · · · · · · ·	
		associated membrane protein 2precursor /DB_XREF=gi:7669502			
	× .	/UG=Hs.8262 lysosomal-			
		associated membrane protein 2 /FL=gb:U36336.1 gb:BC002965.1 gb:NM_013995.1			
		gb.14i4i_010990,1	* * *		

Gene Identifi r	p-value	D scription	Gene	Unigene	Protein
		1.00	Accession	Accession	Accession
			No.	No.	No.
200822_x_at	0:001116	gb:NM_000365.1 /DEF=Homo	NM_000365		
	7	sapiens triosephosphate	7		
	l	isomerase 1 (TPI1), mRNA	ļ·		
		/FEA=mRNA /GEN=TPI1			
* * *		/PROD=triosephosphate			
		isomerase 1		<i>'</i>	
		/DB_XREF=gi:4507644		·-	
*		/UG=Hs.83848 triosephosphate			
÷ '''		isomerase 1 /FL=qb:BC004230.1			
0 0 0		gb:NM 000365.1	,	*	
					** *
200823 x_at	0.00228	gb:NM 000992.1 /DEF=Homo	NM_000992	*	NP_000983
= = = = = = = = = = = = = = = = = = = =		sapiens ribosomal protein L29			
		(RPL29), mRNA /FEA=mRNA			
		/GEN=RPL29 /PROD=ribosomal			
24		protein L29			:
		/DB_XREF=gi:4506628			
		/UG=Hs.183698 ribosomal protein			
		L29 /FL=gb:U49083.1			
		gb:NM_000992.1 gb:U10248.1			
200827 at	0.004341	gb:NM_000302.1 /DEF=Homo	NM 000302		NP 000293
200021_at	0:004341	sapiens procollagen-lysine, 2-	NIVI_000302		NP_000293
	1	oxoglutarate 5-dioxygenase (lysine		*	Y
		hydroxylase, Ehlers-Danlos			î
	0.				
		syndrome type VI) (PLOD),		}	9
		mRNA. /FEA=mRNA /GEN=PLOD		0	
		/PROD=procollagen-lysine 5-			
* * * *		dioxygenase			
		/DB_XREF=gi:4557836			
1		/UG=Hs 75093 procollagen-lysine,			
		2-oxoglutarate 5-dioxygenase	1		Q a
		(lysine hydroxylase, Ehlers-Danlos			
		syndrome type VI)		-	
1	0000	/FL=gb:L06419.1 gb:NM_000302.1			<del>-</del>
				<u></u>	
200829_x_at	3.26E-04	gb:NM_003457.1 /DEF=Homo	NM_003457		NP_003448
		sapiens zinc finger protein 207			۵.
		(ZNF207), mRNA /FEA=mRNA			
		/GEN=ZNF207 /PROD=zinc finger			* ×
		protein 207		: 1.	
	}	/DB_XREF=gi:4508016	¥	1	
		/UG=Hs.62112 zinc finger protein			
		207 /FL=gb:AF046001.1			
		gb:NM_003457.1		0.00	· 4

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Acc ssion	Accession	Accession
*	, · · · .	*	No.	No.	No.
200830_at	1.26E-04	gb:NM_002808.1 /DEF=Homo	NM_002808		NP_002799
		sapiens proteasome (prosome,		· .	7
		macropain) 26S subunit, non-			
		ATPase, 2 (PSMD2), mRNA.			
,		/FEA=mRNA /GEN=PSMD2			
*	, ,	/PROD=proteasome (prosome,	*		
		macropain) 26S subunit,non-			6
		ATPase, 2 /DB_XREF=gi:4506226			3
		/UG=Hs:74619 proteasome			
		(prosome, macropain) 26S			
*		subunit, non-ATPase, 2			
*		/FL=gb:D78151.1 gb:BC002368.1	V 00	;	
		gb:BC002997.1 gb:NM_002808.1	g = 20 ·		
		gb:U18247.1 gb:U12596.1	* :	* * *	
			· · · · · · · · · · · · · · · · · · ·		
200833_s_at	0.033381	gb:NM_015646.1 /DEF=Homo	NM 015646		NP 056461
		sapiens RAP1B, member of RAS			-
		oncogene family (RAP1B),			1 N. 1
14 1		mRNA. /FEA=mRNA			
* .		/GEN=RAP1B		32	
		/PROD=DKFZP586H0723 protein			
		/DB_XREF=gi;7661677		*	
		/UG=Hs.156764 RAP1B, member			
*		of RAS oncogene family			
		/FL=gb:BC000176.2	7		
	1	gb:NM_015646.1		. *	
200838_at	7 58F-04	gb:NM_001908:1 /DEF=Homo	NM 001908	5,	NP 680093
200000_at	1.002 0	sapiens cathepsin B (CTSB),			
	1	mRNA. /FEA=mRNA /GEN=CTSB			
		/PROD=cathepsin B			*
		/DB_XREF=gi:4503138	2	8	
		/UG=Hs.297939 cathepsin B	*		
		//FL=gb:M14221.1 gb:L16510.1			
ter yet a di		gb:NM 001908.1			
200839_s_at	3.26F-04	gb.NM_001908.1 /DEF=Homo	NM 001908		NP_680093
200003_5_4	0.202	sapiens cathepsin B (CTSB),	11111_001000		
	1	mRNA. /FEA=mRNA /GEN=CTSB		=	
		/PROD=cathepsin B			
		//DB_XREF=gi:4503138			
*		//UG=Hs.297939 cathepsin B.	j	<u>.</u>	
		/FL=gb:M14221.1 gb:L16510.1			
:		gb:NM_001908.1			
200844 5 5	1 265 04	anti-oxidant protein 2 (non-	BE869583		NP_004896
200844_s_at	1.200-04	selenium glutathione peroxidase,	PEOOSOO		111-004090
	. *	acidic calcium-independent	· ·		
	*			Hs.120	
	1	phospholipase A2)	<del></del>	1115,120	1

Gene Identifier	p-value	Description	Gn	Unigene	Protein
			Accession	Accession	Accession
	,		No.	No.	No
200845_s_at	0.003171	gb:NM_004905.1 /DEF=Homo	NM 004905		NP_004896
=====================================		sapiens anti-oxidant protein 2	<u> </u>		_, _,
·		(non-selenium glutathione			
		peroxidase, acidic calcium-	••		
		independent phospholipase A2)			
	1	(KIAA0106), mRNA. /FEA=mRNA			
· 5,	/:	/GEN=KIAA0106 /PROD=anti-		3	
				:	
		oxidant protein 2 (non-selenium		4.5	
* .		glutathioneperoxidase, acidic			
		calcium-independent	1 1		
9		phospholipase A2)			-
		/DB_XREF=gi:4758637			
141		/UG=Hs.120 anti-oxidant protein		. 8	,
	1	2 (non-selenium glutathione			
		peroxidase, acidic calcium-			
	r i	independent phospholipase A2)	**		
		/FL=gb:D14662.1			
	1:	gb:NM_004905.1	4		
200850 s at	0.003171	gb:NM 006621.1 /DEF=Homo	NM 006621		NP 006612
		sapiens S-adenosylhomocysteine			
		hydrolase-like 1 (AHCYL1),		1	
		mRNA. /FEA=mRNA			
		/GEN=AHCYL1 /PROD=S-			
£ *		adenosylhomocysteine hydrolase-		: '	
40		like 1 /DB_XREF=gi:5729723	* 1 E	1.	-
· = =	1	/UG=Hs.4113 S-		0	
		adenosylhomocysteine hydrolase-			
	] •			·	
		like 1 /FL=gb:U82761.1			
* 1		gb:NM_006621.1			
200050	0.55.04	1 100 100 1 10 EE	1111 000100		NE COCCE
200853_at	2.05E-04	gb:NM_002106.1 /DEF=Homo	NM_002106		NP_002097
		sapiens H2A histone family,			
	4 4	member Z (H2AFZ), mRNA.	:		
	-	/FEA=mRNA /GEN=H2AFZ			
		/PROD=H2A histone family,		·	
· ·		member Z /DB_XREF=gi:4504254		1	
		/UG=Hs.119192 H2A histone			
*		family, member Z	* .		
		/FL=gb:M37583.1	*	ľ	
		gb:NM_002106.1			
	1				

Gene Identifier	p-value	Description	Gene	Unig n	Protein
	·		Accession	Accession	Accession
	1	*	No.	No.	No.
200854_at	1.26E-04	Consensus includes	NM_006311		NP_006302
* .		gb.AB028970.1 /DEF=Homo			_
		sapiens mRNA for KIAA1047		1	· .
		protein, partial cds. /FEA=mRNA		. *	
		/GEN=KIAA1047	,		
		/PROD=KIAA1047 protein			
		/DB_XREF=gi:5689430	-		
*		/UG=Hs.144904 nuclear receptor	~		
		co-repressor 1			
		/FL=gb:AF044209.1			. \
		gb:NM_006311.1			
200855_at	1.26F-04	Consensus includes	NM_006311		NP 006302
at	1.202.04	gb:AW771910 /FEA=EST		*	_000002
		/DB_XREF=gi:7703971			``
		/DB_XREF=est:hn66c11.x1			
		/CLONE=IMAGE:3032852			×.
		/UG=Hs.144904 nuclear receptor			
		co-repressor 1			
y				4	
i i e		/FL=gb:AF044209.1			
000000	0.00445	gb:NM_006311.1	NINA 000044	m 2 m	ND 000000
200856_x_at	0.02145	Consensus includes gb:BF437948	NM_006311		NP_006302
		/FEA=EST			
*		/DB_XREF=gi:11450465			
		/DB_XREF=est:7q63b10.x1			
	· .	/CLONE=IMAGE:3702882			
*		/UG=Hs.144904 nuclear receptor			
		co-repressor 1			000
		/FL=gb:AF044209.1			
		gb:NM_006311.1		1	**
200857_s_at	0.00161	gb:NM_006311.1 /DEF=Homo	NM_006311		NP_006302
.00		sapiens nuclear receptor co-			
•		repressor 1 (NCOR1), mRNA.			
*	*	/FEA=mRNA /GEN=NCOR1		3	
	,	/PROD=nuclear receptor co-		*	
. 4		repressor 1	* *		
. *		/DB_XREF=gi:5454137			
		/UG=Hs.144904 nuclear receptor	<b>[</b> ·	,	:
	:	co-repressor 1	1		
		/FL=gb:AF044209.1		10	
•		gb:NM_006311.1			
200860_s_at	1.26E-04		BC000779		NP_057368
-		sapiens, Similar to KIAA1007		, ,	· - ··
*,		protein, clone MGC:692, mRNA,	]		
,	1	complete cds. /FEA=mRNA			
		/PROD=Similar to KIAA1007	1		I
0 00		protein /DB_XREF=gi:12653966			
		/UG=Hs.279949 KIAA1007 protein			-[
	1	/FL=gb:BC000779.1	*	<b>{</b>	-
•		gb:AF110778.1 gb:NM_016284.1	1	1 .	
1			·		

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
200861_at	2.05E-04	gb:NM_016284.1 /DEF=Homo	NM_016284		NP_057368
1		sapiens KIAA1007 protein			-
*	•	(KIAA1007), mRNA. /FEA=mRNA		!	1
· · · · · ·		/GEN=KIAA1007			
		/PROD=KIAA1007 protein			
		/DB XREF=gi:7706213	• •	Ċ	
		/UG=Hs.279949 KIAA1007 protein	÷		*
	٠.	/FL=gb:BC000779.1			
		gb:AF110778.1 gb:NM_016284.1			
200863_s_at	2.05E-04		Al215102		NP 004654
		family	, 112 10 102	Hs.75618	00 100 1
200864 s at	5 03F-04	gb:NM_004663.1 /DEF=Homo	NM 004663		NP 004654
	J.00L 07	sapiens RAB11A, member RAS	0030,00		_004004
et j		oncogene family (RAB11A),		*	
	- **	mRNA. /FEA=mRNA			
		/GEN=RAB11A /PROD=RAB11A,	, Y 9		
		member RAS oncogene family			
		/DB XREF=gi:4758983			
	* (	/UG=Hs.75618 RAB11A, member			304
		RAS oncogene family	*		
1 1	: 1	/FL=gb:AF000231.1			
		gb:NM_004663.1			
200869_at	0.00228	gb:NM_000980.1:/DEF=Homo	NM_000980		NP_000971
		sapiens ribosomal protein L18a	V		
		(RPL18A), mRNA. /FEA=mRNA			
		/GEN=RPL18A /PROD=ribosomal			
		protein L18a	a ·		
		/DB_XREF=gi:11415025			
*		/UG=Hs.163593 ribosomal protein			
	. >	L18a /FL=gb:NM_000980.1			
		gb:L05093.1			
					0
200870_at	7.58E-04	gb:NM_007178.1 /DEF=Homo	NM_007178	**********	NP_009109
		sapiens unr-interacting protein		·	
		(UNRIP), mRNA. /FEA=mRNA		,	
		/GEN=UNRIP /PROD=unr-		:	Ξ
	į	interacting protein			
		/DB_XREF=gi:6005931		~	
	- 1	/UG=Hs.3727 unr-interacting	. :		* 9
		protein /FL=gb:BC000162.1			
		II	1	1	ı
		gb:AB024327.1 gb:NM 007178.1			. (;

Gene Identifier	p-value	Description	Gene Accession	Unigen Accession	Protein Accession
*			No.	No.	No.
200876_s_at	0.00228	gb:NM_002793.1 /DEF=Homo	NM_002793	<del>dia kana an</del>	NP 002784
		sapiens proteasome (prosome,		* *	<del>-</del>
		macropain) subunit, beta type, 1	* .		
		(PSMB1), mRNA. /FEA=mRNA	•	* · · · · · · · · · · · · · · · · · · ·	
		/GEN=PSMB1	The state of the s	. ,	
e		/PROD=proteasome (prosome,			
		macropain) subunit, betatype, 1			
m	6	/DB_XREF=gi:4506192			3
· · · · ·		/UG=Hs.75748 proteasome		8	
		(prosome, macropain) subunit,			
		beta type, 1 /FL=gb:BC000508.1			
	, O	gb:NM_002793.1	*		
	10				*
200880_at	0.004341	DnaJ (Hsp40) homolog, subfamily	AL534104		NP_001530
	1	A, member 1		Hs.94	
200881_s_at	1,26E-04	gb:NM_001539.1' /DEF=Homo	NM_001539		NP_001530
*		sapiens heat shock protein,			
		DNAJ-like 2 (HSJ2), mRNA			F
, ,		/FEA=mRNA /GEN=HSJ2	*		
		/PROD=heat shock protein, DNAJ			
*		like 2 /DB_XREF=gi:4504510	*		
	* :	/UG=Hs.94 DnaJ (Hsp40)			
		homolog, subfamily A, member 1			
		/FL=gb:D13388.1 gb:L08069.1			
*		gb:NM_001539.1			
200882_s_at	0.02145	gb:NM_002810.1 /DEF=Homo	NM_002810		NP_722544
		sapiens proteasome (prosome,	1.0		
		macropain) 26S subunit, non-	· (x)		
		ATPase, 4 (PSMD4), mRNA.			
	- 1	/FEA=mRNA /GEN=PSMD4	·	6	
		/PROD=proteasome (prosome,			A.C.
		macropain) 26S subunit,non-			
		ATPase, 4 /DB_XREF=gi:5292160			
0.0		/UG=Hs.148495 proteasome			
		(prosome, macropain) 26S			
		subunit, non-ATPase, 4			
*		/FL=gb:BC002365.1 gb:U24704.1			
		gb:NM_002810.1			

Gene Identifier	p-value	Description	Gene	Unigene	Protein
	Î		Accession	Accession	Accession
			No.	No.	No.
200883_at	0.02145	gb:NM_003366.1 /DEF=Homo	NM_003366		NP_003357
		sapiens ubiquinol-cytochrome c	• • • • • • • • • • • • • • • • • • • •		
		reductase core protein II	* , )		
		(UQCRC2), mRNA /FEA=mRNA			
5	2.	/GEN=UQCRC2 /PROD=ubiquinol-			
		cytochrome c reductase core			. 6
		proteinII /DB_XREF=gi:4507842			
		/UG=Hs.173554 ubiquinol-			
		cytochrome c reductase core			***
		protein: II /FL=gb:BC000484.1		. )	
		gb:BC003136.1 gb:J04973.1			
		gb:NM_003366.1		. * 6	
	A .				
200886_s_at	1.26E-04	gb:NM_002629:1 /DEF=Homo	NM_002629	1	NP_002620
		sapiens phosphoglycerate mutase			al al
		1 (brain) (PGAM1), mRNA.			
· .		/FEA=mRNA /GEN=PGAM1	-)(-		
*		/PROD=phosphoglycerate mutase			
		1 (brain) /DB_XREF=gi:4505752			
* 1		/UG=Hs.181013 phosphoglycerate			
	-8-	mutase 1 (brain)		n	
		/FL=gb:BC000455.1			
		gb:NM_002629.1 gb:J04173.1	=		
200889_s_at	3.26E-04	signal sequence receptor, alpha	AI016620		NP_003135
		(translocon-associated protein			
	2010000	alpha)		Hs 250773	
200891_s_at	0.010205	gb:NM_003144.2 /DEF=Homo	NM_003144		NP_003135
		sapiens signal sequence			-3
		receptor, alpha (translocon-			
		associated protein alpha) (SSR1),			
		mRNA. /FEA=mRNA /GEN=SSR1			-30-
		/PROD=signal sequence receptor,		-	
i		alpha /DB_XREF=gi:6552340			
		/UG=Hs.250773 signal sequence			
		receptor, alpha (translocon-			
	ŀ	associated protein alpha)		. (	*
		/FL=gb:AF156965.1	*		0. 0
* .	*	gb:NM_003144.2		-	
	1		<u> </u>	L	1.

Gene Identifier	p-value	D scription	Gene	Unigen	Protein
		*	Accession	Accession	Accession
			No.	No.	No.
200896_x_at	7.58E-04	gb:NM_004494.1 /DEF=Homo	NM_004494		NP 004485
		sapiens hepatoma-derived growth	- :/		- , ,
		factor (high-mobility group protein	,	٠,	
		1-like) (HDGF), mRNA			
		/FEA=mRNA /GEN=HDGF		-	1 11
×		/PROD=hepatoma-derived growth	*		0.0
		factor (high-mobilitygroup protein			
		1-like) /DB_XREF=gi:4758515			. 50
		/UG=Hs.89525 hepatoma-derived	0		
* * *		growth factor (high-mobility group			
		protein 1-like)		,	
		/FL=gb:NM_004494.1			
		gb:D16431.1			
200899 s at	0.02145	gb:NM_012215.1 /DEF=Homo	NM 012215	The same of the sa	NP 036347
77		sapiens meningioma expressed	· · · · · <del>-</del> · · · · · · · ·		
		antigen 5 (hyaluronidase)			(3
		(MGEA5), mRNA. /FEA=mRNA	Y .		-1
		/GEN=MGEA5			-
		/PROD=meningioma expressed			
		antigen 5 (hyaluronidase)			. 3
		/DB_XREF=gi:11024697	. 00	*	. 4
* = :	00	/UG=Hs.5734 meningioma	a	:	
		expressed antigen 5		٠.	1
4.		(hyaluronidase)	* :	r <sup>i</sup> .	a.a. V
		/FL=gb:AF036144.2	a. *	* "	
	: '	gb:NM_012215.1			
200902_at	1 26F-04	gb:NM_004261.1 /DEF=Homo	NM_004261		NP_004252
200002_40	1.202.01	sapiens 15 kDa selenoprotein	14141_00-1201		-004232
.00		(SEP15), mRNA. /FEA=mRNA			
		/GEN=SEP15:/PROD=15 kDa.			
7		selenoprotein	*		
		/DB_XREF=gi:4759095		*	-
	0 1	/UG=Hs.90606:15 kDa	· X-		
		selenoprotein /FL=gb:AF288991.1		1	• •
	1 1	gb:BC005294.1 gb:AF051894.1	-	1	
		gb:NM 004261.1	ė .	-	
		gb.14141_004201.1			* 1
200909 s at	0.003171	gb:NM_001004.1 /DEF=Homo	NM 001004		NP_000995
200303_3_at	0.003171	sapiens ribosomal protein, large	14141_001004		141 _000993
		P2 (RPLP2), mRNA.	,		
,		/FEA=mRNA /GEN=RPLP2			
()	1/1	/PROD=ribosomal protein, large			.
ļ		P2 /DB_XREF=gi:4506670			
	·	/UG=Hs.119500 ribosomal		2	
		protein, large P2		N-	,
		/FL=gb:BC005354.1 gb:M17887.1			
	L	gb:NM_001004.1			

Gene Identifier	p-value	Description	G ne	Unig ne	Prot in
			Accession	Acc ssion	Acc ssion
*			No.	No.	No.
200911_s_at	0.033381	gb:NM_006283.1 /DEF=Homo	NM_006283	-	NP_006274
		sapiens transforming, acidic	<del></del>		_
		coiled-coil containing protein 1		<b>:</b> .	<b>i</b> .
	ļ. ·	(TACC1), mRNA /FEA=mRNA			
* .		/GEN=TACC1		-)(-*	
		/PROD=transforming, acidic coiled	:-		0
		coil containingprotein 1			
·		/DB_XREF=gi:5454099	V 2 0		
		/UG=Hs.173159 transforming,			
		acidic coiled-coil containing			
		protein 1 /FL=gb:AF049910.1			
		gb:NM 006283.1	.***		
200914_x at	1.26E-04	kinectin 1 (kinesin receptor)	BF589024	Hs.211577	
200918 s at		gb:NM_003139.1 /DEF=Homo	NM 003139		NP_003130
		sapiens signal recognition particle		3 7	
0)		receptor (docking protein)		*	
	1	(SRPR), mRNA. /FEA=mRNA	, .	* 73	
*(		/GEN=SRPR /PROD=signal		1.	
and the second s		recognition particle receptor		*	
*		(dockingprotein)			
	4.	/DB_XREF=gi:4507222			
		/UG=Hs.75730 signal recognition			*
		particle receptor (docking protein)			
		/FL=gb:BC001162.1			
		gb:NM_003139.1			
		3			t a vi v
200920 s at	1.26E-04	B-cell translocation gene 1, anti-	AL535380		NP_001722
		proliferative		Hs.77054	
200925_at	1.26E-04	gb:NM_004373.1 /DEF=Homo	NM 004373	17	NP_004364
-		sapiens cytochrome c oxidase			_90.001
		subunit VIa polypeptide 1		, , ,	
		(COX6A1), mRNA. /FEA=mRNA			
		/GEN=COX6A1		÷	
		/PROD=cytochrome c oxidase		- " "	
		subunit VIa polypeptide 1			*
		/DB_XREF=gi:10047079			*
		/UG=Hs.180714 cytochrome c			
		oxidase subunit VIa polypeptide			
* '		1 /FL=gb:NM 004373.1			*
200927_s_at	1.26E-04	RAB14, member RAS oncogene	AA919115		NP_057406
		family		Hs.5807	_55, 750
	L	pranting.		1113.0007	L

Gene Identifier	p-value	Description	Gene	Unigene	Protein
		*	Accession	Accession	Accession
		-	No.	No.	No.
200929_at	5.03E-04	gb:NM_006827.1 /DEF=Homo	NM_006827		NP_006818
	-	sapiens transmembrane trafficking			
		protein (TMP21), mRNA.	4.		
		/FEA=mRNA /GEN=TMP21			
		/PROD=transmembrane trafficking			30
		protein /DB_XREF=gi:5803200			• * :
		/UG=Hs.74137 transmembrane		. (	**.
		trafficking protein	10		· • • ·
*		/FL=gb:BC001825.1	. :		
, , , , ,		gb:NM_006827.1	,		
				•	
* 19 =1 f × ×	20.0				
200931_s_at	0.005852	gb:NM_014000.1 /DEF=Homo	NM_014000		NP_054706
		sapiens vinculin (VCL), transcript			
		variant meta-VCL, mRNA.	•		
		/FEA=mRNA /GEN=VCL		• • • • • • • • • • • • • • • • • • • •	
		/PROD=VCL isoform meta-VCL		1 1 4	
		/DB_XREF=gi:7669549			• 7
		/UG=Hs.75350 vinculin			
		/FL=gb:NM_014000.1			
000000	4 505 04				
200932_s_at	1.58E-04	gb:NM_006400.2 /DEF=Homo	NM_006400		NP_006391
		sapiens dynactin 2 (p50)			,
		(DCTN2), mRNA. /FEA=mRNA			
		/GEN=DCTN2 /PROD=dynactin 2		*	
, ;	4	/DB_XREF=gi:13259506			
	3	/UG=Hs.84153 dynactin 2 (p50)			
territoria.		/FL=gb:U50733.1 gb:BC000718.1		14	i.
200026 -4	0.002474	gb:NM_006400.2	NIM 000072	٠	ND 450044
200936_at	0.003171	gb:NM_000973.1 /DEF=Homo	NM_000973	,	NP_150644
		sapiens ribosomal protein L8	*		*
		(RPL8), mRNA. /FEA=mRNA	č.	+	
		/GEN=RPL8 /PROD=ribosomal		*	
		protein L8 /DB_XREF=gi:4506662			
		/UG=Hs.178551 ribosomal protein			3
		L8 /FL=gb:BC000077.1		, -	
		gb:NM_000973.1			
200941_at	0.003171	Consensus includes	AK026575	. ,	NP 001528
200941_at	0.003171	gb:AK026575.1 /DEF=Homo	AK020373		NP_001520
	-	sapiens cDNA: FLJ22922 fis,	,		*
* .		cione KAT06722. /FEA=mRNA			
	-	/DB_XREF=gi:10439459		:	, 1
	•	/UG=Hs.250899 heat shock	10° 1		
[		factor binding protein 1	Å		
		/FL=gb:AF068754.1	^ "	ĺ	0,1,1
		gb:NM_001537.1			
	L	[gu.14141_001337.1			<u> </u>

Gene Identifier	p-value	D scription	Gene	Unig ne	Protein
	1	*	Accession	Accession	Accession
			No.	No.	No.
200942_s_at	1.26E-04	gb:NM_001537.1 /DEF=Homo	NM_001537	1.8	NP_001528
		sapiens heat shock factor	_		<del>17</del>
	.: /	binding protein 1 (HSBP1),		. `.	
· · · · · · ·		mRNA. /FEA=mRNA	. *		,
		/GEN=HSBP1 /PROD=heat shock	*		
		factor binding protein 1			
		/DB_XREF=gi:4557646	,		
		/UG=Hs.250899 heat shock			
, - · · · ·		factor binding protein 1			
	i '	/FL=gb:AF068754.1			
*		gb:NM 001537.1		4.00	• • •
200943_at	0.013223	gb:NM 004965.1 /DEF=Homo	NM_004965		NP 004956
	1 3 3 3 3 3	sapiens high-mobility group			
*	,	(nonhistone chromosomal) protein			1.5.5
4		14 (HMG14), mRNA.			
		/FEA=mRNA /GEN=HMG14	*		
		/PROD=high-mobility group	a .		
7 7 7		(nonhistone chromosomal)protein	:8		-
*		14 /DB_XREF=gi:4826757			*
*		/UG=Hs.251064 high-mobility			
* *		group (nonhistone chromosomal)			
		protein 14 /FL=gb:BC000075.1	0		
		gb:J02621.1 gb:NM_004965.1	Y		
200950_at	1.26F-04	gb:NM_006409.1 /DEF=Homo	NM_006409		NP_006400
200000_at	1.202 0 1	sapiens actin related protein 23	1000 100		
		complex, subunit 1A (41 kD)			
		(ARPC1A), mRNA /FEA=mRNA			
	1	/GEN=ARPC1A /PROD=actin			*
		related protein 23 complex,			·
	•	subunit 1A(41 kD)			<u></u>
		/DB_XREF=gi:5454077	-,		
:		/UG=Hs.90370 actin related	:	*	- 0
8	1	protein 23 complex, subunit 1A	e	•	
		(41 kD) /FL=gb:NM_006409.1			
200953_s_at	0.016034	gb:NM_001759.1 /DEF=Homo	NM 001759		NP_001750
200933_S_at	0.010934	sapiens cyclin D2 (CCND2),	114101_001739	*	NF_001/50
	1	mRNA. /FEA=mRNA			
· .					
		/GEN=CCND2 /PROD=cyclin D2	1 · X		
100	]	/DB_XREF=gi:4502616			
*		/UG=Hs.75586 cyclin D2			(
-		/FL=gb:M90813.1 gb:D13639.1			
	1	gb:NM_001759.1			

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
	*		No.	No.	No.
200954_at	0.041795	gb:NM_001694.1 /DEF=Homo	NM_001694		NP_001685
		sapiens ATPase, H+ transporting,		-0.	
		lysosomal (vacuolar proton pump)			• • • •
		16kD (ATP6L), mRNA.			•
		/FEA=mRNA /GEN=ATP6L		**************************************	- 8 ·
		/PROD=ATPase, H+ transporting,			- *
		lysosomal (vacuolarproton pump)			
		16kD /DB_XREF=gi:4502312	: 1		
		/UG=Hs.76159 ATPase, H+			
		transporting, lysosomal (vacuolar			*
	1 ,	proton pump) 16kD		) •	
		/FL=gb:BC004537.1 gb:M62762.1			
		gb:NM_001694.1	ļ · · · ; ;		
200958_s_at	0.010205	gb:NM_005625.1 /DEF=Homo	NM_005625		NP_005616
8		sapiens syndecan binding protein			
		(syntenin) (SDCBP), mRNA.	- 3,		
		/FEA=mRNA /GEN=SDCBP			
		/PROD=syndecan binding protein		, ,	
		(syntenin) /DB_XREF=gi:5032082			
		/UG=Hs.8180 syndecan binding			- * *
		protein (syntenin)			*
		/FL=gb:AF000652.1	*	1	
	1.0	gb:NM_005625.1		()	. *
				, ,	
200960_x_at	7.58E-04	17 . — 1	NM_007096		NP_009027
		sapiens clathrin, light polypeptide		*	
		(Lca) (CLTA), transcript variant			
		brain-specific, mRNA.			30 - 1 - 1
		/FEA=mRNA /GEN=CLTA			
	•	/PROD=clathrin, light polypeptide			. ,
		A (Lca) isoform b			- 7
		/DB_XREF=gi:6005992			*
		/UG=Hs.104143 clathrin, light			j
	· .	polypeptide (Lca)		*	
; ;		/FL=gb:M20471.1		. 1	
		gb:NM_007096.1			
200961_at	1.26E-04	9	NM_012248		NP_036380
		sapiens selenophosphate		*	0
		synthetase 2 (SPS2), mRNA.			
	*	/FEA=mRNA /GEN=SPS2			
		/PROD=selenophosphate	*	* *	· .
* .		synthetase 2			
*		/DB_XREF=gi:7657612			
* (8	-	/UG=Hs.118725 selenophosphate	100		
		synthetase 2 /FL=gb:BC002381.1			ļ
		gb:U43286.1 gb:NM_012248.1			
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Gene Identifi r	p-valu	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
*	** ** *		No.	No.	No.
200964_at	0.007779	gb:NM_003334.1 /DEF=Homo	NM_003334		NP_695012
		sapiens ubiquitin-activating	•	1.8	-
	· .	enzyme E1 (A1S9T and BN75			
- ,		temperature sensitivity			-8-
* . *,		complementing) (UBE1), mRNA.		1	
		/FEA=mRNA /GEN=UBE1			
		/PROD=ubiquitin-activating			1 * *
		enzyme E1 (A1S9T and		i .	= .
· .	*	BN75temperature sensitivity		•	
		complementing)	•		100
		/DB_XREF=gi:4507762	- "		
		/UG=Hs.2055 ubiquitin-activating	***		** ,
		enzyme E1 (A1S9T and BN75			00
	71.:	temperature sensitivity			
		complementing) /FL=gb:M58028.1	8 7 1 1		
* "	-	gb:NM_003334.1			. */
	0.004040	1 1111 2000 1 1000			VIET 000000
200968_s_at	0.001618	gb:NM_000942.1 /DEF=Homo	NM_000942		NP_000933
		sapiens peptidylprolyl isomerase		1	
,		B (cyclophilin B) (PPIB), mRNA.			
		/FEA=mRNA /GEN=PPIB		·	
·		/PROD=peptidylprolyl isomerase B		0	
	1	(cyclophilin B)			
		/DB_XREF=gi:4758949	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		
	-	/UG=Hs.699 peptidylprolyl	0		
		isomerase B (cyclophilin B)			
		/FL=gb:BC001125.1 gb:M60857.1			
		gb:M63573.1 gb:NM_000942.1	·		
,	1 .	,			,
				, , , , , , , , , , , , , , , , , , ,	*
200970 s at	0.00228	gb:AL136807.1 /DEF=Homo	AL136807		NP 055260
:		sapiens mRNA; cDNA	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		
* *	1	DKFZp434L1621 (from clone			
		DKFZp434L1621); complete cds.		· ·	
		/FEA=mRNA			
		/GEN=DKFZp434L1621			0
*		/PROD=hypothetical protein	÷		
, · · ·		/DB_XREF=gi:12053124		12 mm	÷
		/UG=Hs.76698 stress-associated			
*			2		
		endoplasmic reticulum protein 1;		16.	1
		ribosome associated membrane		·	
		protein 4 /FL=gb:AL136807.1			
		gb:AF136975.1 gb:AB022427.1			
i '		gb:NM_014445.1			y.
· <u>:</u>					13.79

Gene Identifier	p-valu	D scription	Gene	Unigene	Protein
	:		Accession	Accession	Acc ssion
		*	No.	No.	No.
200971' s at	5.03E-04	gb:NM_014445.1 /DEF=Homo	NM 014445		NP_055260
	,	sapiens stress-associated			000200
		endoplasmic reticulum protein 1;	* *		
		ribosome associated membrane		-	10 miles
		protein 4 (SERP1), mRNA.			* *
		/FEA=mRNA /GEN=SERP1		70	*
		/PROD=stress-associated			* 1 T
	7	endoplasmic reticulum protein1;			
*		ribosome associated membrane		*,	
		protein 4 /DB_XREF=gi:7657551			
		/UG=Hs.76698 stress-associated			ı
		endoplasmic reticulum protein 1;	1		*
		ribosome associated membrane		*	. •
		protein 4 /FL=gb:AL136807.1	4	1	x * 6
		gb:AF136975.1 gb:AB022427.1		V	
		gb:NM_014445.1			
		<b>3</b> 5913330.1			9
200975_at	5.03E-04	gb:NM_000310.1 /DEF=Homo	NM 000310	1.2	NP_000301
200070_at	0.002.04	sapiens palmitoyl-protein	14141_000010	,	_000501
		thioesterase 1 (ceroid-	<u>.</u>		
		lipofuscinosis, neuronal 1,		*	
		infantile) (PPT1), mRNA.	e .		
- 1 - 6 - 1 - 1 - 1 - 1	(X)	/FEA=mRNA /GEN=PPT1			
		/PROD=palmitoyl-protein			
		thioesterase 1(ceroid-	* *		· .
		lipofuscinosis, neuronal 1,		<b>'</b>	
		infantile) /DB_XREF=gi:4506030			
		/UG=Hs.3873 palmitoyl-protein			ę i
		thioesterase 1 (ceroid-			n=)(=
		lipofuscinosis, neuronal 1,			•
		infantile) /FL=gb:U44772.1			Q **
	1	gb:NM_000310.1			
200976_s_at	0.004341	gb:NM_006024.2 /DEF=Homo	NM_006024		NP_006015
1=00010_3_at	0.007041	sapiens Tax1 (human T-cell	1 4141_000024	·	
		leukemia virus type I) binding			1 2
		protein 1 (TAX1BP1), mRNA.		*	
	1)	/FEA=mRNA /GEN=TAX1BP1		1	
	;· ,	/PROD=Tax1 (human T-cell			
		leukemia virus type I)binding	, , , , , , , , , , , , , , , , , , ,	4X - 1	
		protein 1 /DB XREF=gi:5803188	8	•	. =
		/UG=Hs.5437 Tax1 (human T-cell		<u> </u>	. 9.
		leukemia virus type I) binding			
	000				
		protein 1 /FL=gb:U33821.2			
*		gb:NM_006024.2 gb:AF090891.1			
W	1.	gb:AF268075.1		,	
200070 -+	0.00000	byrujoto dobudeo se se se se	DE720070	10	
200979_at	0.00228	pyruvate dehydrogenase	BF739979	Un 1000	
Ļ	1	(lipoamide) alpha 1	L	Hs.1023	l

Gene Identifier	p-value	Description	Gene	Unigen	Protein
			Accession	Accession	Accession
			No.	No.	No.
200980_s_at	3.26E-04	gb:NM_000284.1 /DEF=Homo	NM_000284		NP_000275
		sapiens pyruvate dehydrogenase			
		(lipoamide) alpha 1 (PDHA1),	-		-3-
		mRNA. /FEA=mRNA			- 1
		/GEN=PDHA1 /PROD=pyruvate			
		dehydrogenase (lipoamide) alpha	,		
		1 /DB_XREF=gi:4505684			
	,	/UG=Hs.1023 pyruvate	* (*		
		dehydrogenase (lipoamide) alpha	· ,		
	Ċ	1 /FL=gb:L48690.1		1).	*
		gb:BC002406.1 gb:J03575.1			
		gb:M24848.1 gb:L13318.1	3		
*	*	gb:NM_000284:1			· .
200981 x at	7 50E 04	gb:NM_016592.1 /DEF=Homo	NM 016592	11/100	ND E2C2E4
200961_X_at	7.30E-04		14141_010295		NP_536351
		sapiens neuroendocrine secretory		- T	
		protein' 55 (NESP55), mRNA.			
	•0	/FEA=mRNA /GEN=NESP55			
		/PROD=neuroendocrine secretory		1 11 1 10	
		protein 55 /DB:XREF=gi:7706588		1	* *
	· ·	/UG=Hs.113368 neuroendocrine			
00		secretory protein 55			. 3
		/FL=gb:AF105253.1			
		gb:NM_016592.1	'	* .	,
	* * * * * * * * * * * * * * * * * * * *			A-	
	1	A Company of the second of the			
200983_x_at	0.00161	Consensus includes gb:BF983379	NM_000611		NP_000602
		/FEA=EST			
	8-	/DB_XREF=gi:12386191	*	Ł	
		/DB_XREF=est:602305270F1		. 0	
	G . Y	/CLONE=IMAGE:4396576	* . *		
		/UG=Hs.119663 CD59 antigen			
		p18-20 (antigen identified by		·	ŀ
		monoclonal antibodies 16.3A5,			
	*	EJ16, EJ30, EL32 and G344)			
		/FL=gb:NM_000611.1			
	*	gb:M34671.1		9	
200984_s_at	0.003171	Consensus includes gb:X16447.1	NM_000611		NP_000602
		/DEF=Human mRNA for CD59,	1	<u> </u>	
,		an LY-6-like protein regulating		. :	
		complement membrane attack.			
		/FEA=mRNA /PROD=precursor			1
		polypeptide (AA -25 to 103)			
w		/DB XREF=gi:29805	***	,	
		/UG=Hs.119663 CD59 antigen			C**
, ,	ľ	p18-20 (antigen identified by			
*		monoclonal antibodies 16.3A5,			
		EJ16, EJ30, EL32 and G344)	* !	í e	]
	:	/FL=gb:NM_000611.1		-	
		igb:M34671.1			
·L	1	L	- A 4		L

Gene Identifier	p-value	Description	G ne	Unigene	Protein
. *	1		Accession	Accession	Accession
			No.	No.	No.
200985_s_at	1.26E-04	gb:NM_000611.1 /DEF=Homo	NM_000611		NP_000602
	ľ	sapiens CD59 antigen p18-20			
,		(antigen identified by monoclonal			,
· · · ×	ļ.	antibodies 16.3A5, EJ16, EJ30,	*		
*		EL32 and G344) (CD59), mRNA.			
	1	/FEA=mRNA /GEN=CD59			
,		/PROD=CD59 antigen p18-20	*		
• •		(antigen identified bymonoclonal			
		antibodies 16.3A5, EJ16, EJ30,	÷ *		
		EL32 and G344)		100	
	i .	/DB_XREF=gi:10835164	,		
	1	/UG=Hs.119663 CD59 antigen	*		
		p18-20 (antigen identified by		7	
		monoclonal antibodies 16.3A5,			
		EJ16, EJ30, EL32 and G344)			
		/FL=gb:NM 000611.1			
		gb:M34671.1			
		4, 1		* * * *	
200987_x_at	0.021165	proteasome (prosome, macropain)	AA758755		NP_789839
		activator subunit 3 (PA28 gamma;			
		Ki)		Hs.152978	
200988_s_at	0.003171	gb:NM_005789.1 /DEF=Homo	NM_005789		NP_789839
		sapiens proteasome (prosome,			
		macropain) activator subunit 3			
		(PA28 gamma; Ki) (PSME3),	* ,		
		mRNA. /FEA=mRNA			. **.
		/GEN=PSME3			1 1
		/PROD=proteasome (prosome,			
		macropain) activatorsubunit 3			
. (1)		(PA28 gamma; Ki)			
		/DB_XREF=gi:5031996			<b>\</b>
		/UG=Hs.152978 proteasome			
÷		(prosome, macropain) activator			
		subunit 3 (PA28 gamma; Ki)			1.
a *		/FL=gb:NM_005789.1		1	
	1	gb:U11292.1			

Gene Identifier	p-value	Description	Gene	Unigene	Protein
	x' ,		Accession	Accession	Accession
• :		*	No.	No.	No.
200989_at	0.005852	gb:NM_001530.1 /DEF=Homo	NM_001530		NP_851397
		sapiens hypoxia-inducible factor	0		
		1, alpha subunit (basic helix-loop-	. 1	4.	
		helix transcription factor) (HIF1A),			
		mRNA. /FEA=mRNA			
•		/GEN=HIF1A /PROD=hypoxia-			
		inducible factor 1, alpha subunit			
		(basichelix-loop-helix transcription			
A. A.	1 .	factor) /DB_XREF=gi:4504384			'
		/UG=Hs.197540 hypoxia-inducible			
		factor 1, alpha subunit (basic			
		helix-loop-helix transcription			- T
		factor) /FL=gb:U29165.1			8
		gb:AF304431.1 gb:NM 001530.1			
		gb:AF207601.1 gb:AF207602.1		*	
		gb:U22431.1		: ×'	
					1
200996_at	5.03E-04	gb:NM_005721.2 /DEF=Homo	NM 005721	1.	NP 005712
		sapiens ARP3 (actin-related	7		_
		protein 3, yeast) homolog			
		(ACTR3), mRNA. /FEA=mRNA			100
		/GEN=ACTR3 /PROD=ARP3		*	
		(actin-related protein 3, yeast)	1		] `.
		homolog /DB_XREF=gi:7262289			
00		/UG=Hs.5321 ARP3 (actin-related		. , ,	
		protein 3, yeast) homolog			
·	,	/FL=gb:AF006083.1			
	-	gb:NM_005721.2			
200997_at	0.016934	gb:NM_002896.1 /DEF=Homo	NM_002896		NP_002887
•		sapiens RNA binding motif	_		1 E
		protein 4 (RBM4), mRNA.			27
		/FEA=mRNA/GEN=RBM4			, ,
		/PROD=RNA binding motif			
	] .	protein 4 /DB_XREF=gi:4506444	1.0		
		/UG=Hs.6106 RNA binding motif	~		
•	,	protein 4 /FL=gb:BC000307.1			
) * *		gb:U89505.1 gb:NM_002896.1			
·Y-	* * * * * * * * * * * * * * * * * * * *				
			<del></del>		

Gene Identifier	p-value	D scription	Gn	Unigene	Protein
***	-		Accession	Acc ssion	Accession
		* *	No.	No.	No.
200999_s_at	5.03E-04	gb:NM_006825.1 /DEF=Homo	NM_006825		NP_006816
		sapiens transmembrane protein	·	-	· -
		(63kD), endoplasmic			
**		reticulumGolgi intermediate	*		5,
		compartment (P63), mRNA.			1
		/FEA=mRNA /GEN=P63			
	-	/PROD=transmembrane protein			
		(63kD), endoplasmicreticulumGolgi			-
		intermediate compartment	- 1		
		/DB_XREF=gi:5803112			1.
3 3 4	•	/UG=Hs.74368 transmembrane			
	,	protein (63kD), endoplasmic			
		reticulumGolgi intermediate			
		compartment			
		/FL=gb:NM_006825.1		11	
	- 31	21.43			
201002_s_at	0.007779	gb:U39361.1 /DEF=Homo sapiens	U39361	* 12 (* * * * * * * * * * * * * * * * * * *	NP_071887
		DNA-binding protein (CROC-1B)			
		mRNA, complete cds.			
**	·	/FEA=mRNA /GEN=CROC-1B			
		/PROD=DNA-binding protein	0.00		
		/DB_XREF=gi:1066081		1(0	
4		/UG=Hs.75875 ubiquitin-	* * *		*
*	1	conjugating enzyme E2 variant 1			
		/FL=gb:U39361.1	. 1		
		gb:NM_003349.2 gb:BC000468.1		-	
201003_x_at	0.026891		NM 003349	11/2	NP 071887
		sapiens ubiquitin-conjugating		y 000	
••••		enzyme E2 variant 1 (UBE2V1),	*		
		transcript variant 2, mRNA.		le .	. * .
		/FEA=mRNA /GEN=UBE2V1		1	X
		/PROD=ubiquitin-conjugating			
		enzyme E2 variant 1,isoform b			
	1-	/DB_XREF=gi:12025659		•	*
•		/UG=Hs.75875 ubiquitin-		. 🤞	
		conjugating enzyme E2 variant 1			, ,
		/FL=gb:U39361.1	0.		
		gb:NM_003349.2 gb:BC000468.1		`	
	*	gb.ivivi_003348.2	*		. :
*	1	L	<u>'</u>	· · ·	<u> </u>

Gene Identifier	p-value	Description	Gene	Unigene	Protein
	-		Accession	Accession	Accession
	*		No.	No.	No.
201007_at	3.26E-04	gb:NM_000183.1 /DEF=Homo	NM_000183		NP_000174
		sapiens hydroxyacyl-Coenzyme A			
	1	dehydrogenase3-ketoacyl-			7.
	* )	Coenzyme A thiolaseenoyl-		100	ļ. <sup>*</sup>
		Coenzyme A hydratase		1	
		(trifunctional protein), beta subunit			
		(HADHB), mRNA. /FEA=mRNA	4.		191
*		/GEN=HADHB		d	
		/PROD=hydroxyacyl-Coenzyme			
	; ;	Adehydrogenase3-ketoacyl-			
		Coenzyme Athiolaseenoyl-			
		Coenzyme A hydratase		1	
		(trifunctionalprotein), beta subunit			
		/DB XREF=gi:4504326		*	
		/UG=Hs 146812 hydroxyacyl-			
		Coenzyme A dehydrogenase3-	*.	8	
		ketoacyl-Coenzyme A			
		thiolaseenoyl-Coenzyme A			
		hydratase (trifunctional protein),			- 1 - 10 - m
		beta subunit /FL=gb:AF113209.1	111	,	
		gb:NM_000183.1 gb:D16481.1			
201009_s_at	0.00161	Consensus includes gb:Al439556	NM_006472		NP 006463
201003_3_at	0.00101	/FEA=EST /DB_XREF=gi:4305149	14141_000412	*	141 _000403
		/DB_XREF=est:tc90c12.x1			*
( )	-	/CLONE=IMAGE:2073430	1 m		
		/UG=Hs.179526 upregulated by			
1.00		1,25-dihydroxyvitamin D-3		* * *	-
		/FL=gb:NM_006472.1 gb:S73591.1	-		:
		/FL=gb.NW_000472.1_gb.575591.1			
201011 at	0.003171	gb:NM_002950.1 /DEF=Homo	NM 002950	1001111	NP_002941
201011_at	0.003174	sapiens ribophorin I (RPN1),	NN_002930		NP_002941
		mRNA. /FEA=mRNA /GEN=RPN1			9
	2 *			N	N .
		/PROD=ribophorin 1			
s		/DB_XREF=gi:4506674	8		
* * * * * * * * * * * * * * * * * * * *		/UG=Hs.2280 ribophorin I			
201012 at	0.00164	/FL=gb:NM_002950.1	NINA 000700		ND 000604
201012_at	0.00101	gb:NM_000700.1 /DEF=Homo	NM_000700		NP_000691
	*	sapiens annexin A1 (ANXA1),			
*		mRNA. /FEA=mRNA			
- 1	i	/GEN=ANXA1 /PROD=annexin I			
,		/DB_XREF=gi:4502100			
, •		/UG=Hs.78225 annexin A1	·	-	
• •		/FL=gb:BC001275.1		~	·
004047	0.000555	gb:NM_000700.1	DE5 4655 :	-	NB 604465
201017_at	0.003529	eukaryotic translation initiation	BE542684	11. 45.45	NP_001403
		factor 1A	<u> </u>	Hs.4310	

G n ld ntifier	p-value	D scription	Gene	Unigene	Protein
			Accession	Acc ssion	Accession
			No.	No.	No.
201019_s_at	0.003171	gb:NM_001412.1 /DEF=Homo	NM_001412		NP 001403
		sapiens eukaryotic translation	. 2. 7		<del></del>
	i.	initiation factor 1A (EIF1A),			÷
		mRNA. /FEA=mRNA /GEN=EIF1A			
χ.		/PROD=eukaryotic translation			*
	-	initiation factor 1A			
		/DB_XREF=gi:4503498			÷ .
*	* *	/UG=Hs.4310 eukaryotic	-		9
		translation initiation factor 1A		3	
		/FL=gb:BC000793.1 gb:L18960.1			
		gb:NM_001412.1		•	*
201020_at	1 26F-04	gb:NM_003405.1 /DEF=Homo	NM 003405		NP 003396
20.1020_01	1.202.0	sapiens tyrosine 3-	11111_000400		141 _000000
		monooxygenasetryptophan 5-			
		monooxygenase activation			
		protein, eta polypeptide			1
		(YWHAH), mRNA /FEA=mRNA			
		/GEN=YWHAH /PROD=tyrosine 3-		*	*
	· . · · · · · · · · · ·				
		monooxygenasetryptophan5-			
		monooxygenase activation	* *	0	;
· ·		protein, eta polypeptide		9	
		/DB_XREF=gi:4507950			
		/UG=Hs.75544 tyrosine 3-			
		monooxygenasetryptophan 5-		· .	-4
×		monooxygenase activation			
		protein, eta polypeptide	0		*
	٠,"	/FL=gb:BC003047.1 gb:L20422.1			
	-	gb:NM_003405.1	1		• • • •
201023_at	0.041055	gb:NM_005642.1 /DEF=Homo	NM_005642	**	NP_005633
		sapiens TATA box binding			
	•	protein (TBP)-associated factor,		. *	
		RNA polymerase II, F, 55kD		* *	1(3)
		(TAF2F), mRNA. /FEA=mRNA	* *	• • • •	
		/GEN=TAF2F /PROD=TATA box			7
		binding protein (TBP)-			
		associatedfactor, RNA	,	*. *	-
		polymerase II, F, 55kD			
(	٠.	/DB_XREF=gi:5032148	1. The second of the second of		
n		/UG=Hs.155188 TATA box			
		binding protein (TBP)-associated	. X		
l			ľ	-33	1
		factor, RNA polymerase II. F.			- ,
	,	factor, RNA polymerase II, F, 55kD /FL=gb:NM_005642.1			· .

Gene Identifier	p-value	Description	Gen	Unigene	Protein
		7 *	Accession	Accession	Accession
			No.	No.	No.
201032_at	0.033381	gb:NM_006698.1 /DEF=Homo	NM_006698	* * * * * * * * * * * * * * * * * * * *	NP_006689
1		sapiens bladder cancer			-
		associated protein (BLCAP),	1.		. '
	,	mRNA. /FEA=mRNA			
. *		/GEN=BLCAP /PROD=bladder			
- 5		cancer associated protein	4 .		
•		/DB_XREF=gi:5729737			14 · ·
		/UG=Hs.5300 bladder cancer		-	
		associated protein	8	• •	
, ,		/FL=gb:AF053470.1		• .	*
		gb:NM 006698.1			*
201038_s_at	2.05E-04	ESTs, Highly similar to putative	BE560202		
		human HLA class II associated			
		protein I; cerebellar leucine rich		- TY	
		acidic nuclear protein [Homo			
		sapiens] [H.sapiens]		Hs.356089	
201047 x at	1 26F-04	gb:BC003617.1 /DEF=Homo	BC003617	113.00000	NP_002860
2010-7-X-at	1.202 04	sapiens, RAB6, member RAS	10000017		002000
		oncogene family, clone			
*	•	MGC:1654, mRNA, complete cds.	**	. ".	
*		/FEA=mRNA /PROD=RAB6,			X
		member RAS oncogene family	3.9		
		/DB_XREF=gi:13177663	1. 1.		
		/UG=Hs.5636 RAB6A, member		,	
*			* · ·		
		RAS oncogene family			
		/FL=gb:BC003617.1	· · · · · · · · · · · · · · · · · · ·		
		gb:NM_002869.1 gb:AF130986.1	4		
		gb:AF130122.1 gb:M28212.1			Co.
*		gb:AF119836.1 gb:AF198616.1			
0040403	0.044070				115 00000
201048_x_at	0.041973	gb:NM_002869.1 /DEF=Homo	NM_002869		NP_002860
0 (X)		sapiens RAB6, member RAS			
ř		oncogene family (RAB6), mRNA.	•		
		/FEA=mRNA /GEN=RAB6	1		-
*		/PROD=RAB6, member RAS			**
	* -	oncogene family	· -		
· - ·		/DB_XREF=gi:4506372			* '
0 0		/UG=Hs.5636 RAB6A, member		· ·	
•	, , , , , , , , , , , , , , , , , , ,	RAS oncogene family		* N.	* /
		/FL=gb:BC003617.1			-
		gb:NM_002869.1 gb:AF130986.1	* :	* (	
10		gb:AF130122.1 gb:M28212.1			
·		gb:AF119836.1 gb:AF198616.1	<u> </u>		

Gene Identifier	p-value	Description	Gene	Unigene Accession	Protein :
,	· .	*	Accession	No.	Accession
201049_s_at	0.012222	gb:NM 022551,1 /DEF=Homo	No.	NO.	No.
201049_s_at	0.013223		NM_022551		NP_072045
		sapiens ribosomal protein S18			
		(RPS18), mRNA. /FEA=mRNA			
/ * 'X'		/GEN=RPS18 /PROD=ribosomal	*		
v **		protein S18		-27	
		/DB_XREF=gi:11968181	, , , , , , , , , , , , , , , , , , ,		
*		/UG=Hs.275865 ribosomal protein	0		,
	_	S18 /FL=gb:NM_022551.1	- "		
201051_at	5.03E-04	ESTs, Highly similar to putative	BE560202		*
		human HLA class II associated			\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
		protein I; cerebellar leucine rich			
		acidic nuclear protein [Homo			
*		sapiens] [H.sapiens]		Hs.356089	
201052 s at	1.26E-04	proteasome (prosome, macropain)	BG029917		NP_848694
		inhibitor subunit 1 (PI31)		Hs.75925	
201053 s_at	0.001911	gb:NM_006814.1 /DEF=Homo	NM_006814		NP 848694
		sapiens proteasome (prosome,			
*		macropain) inhibitor subunit 1			
	1	(PI31) (PSMF1), mRNA.			1.
		/FEA=mRNA /GEN=PSMF1	,		-7
	1	/PROD=proteasome inhibitor			,
		/DB_XREF=gi:5803122			
		/UG=Hs.75925 proteasome			10
		(prosome, macropain) inhibitor			
		subunit 1 (Pl31) /FL=gb:D88378.1			
		gb:NM_006814.1			
		gb.NW_000614.1	· :		
201050 -4	0.000746		NEŠ470	15.	1 2
201056_at	0.009716	golgi autoantigen, golgin subfamily	N53479		X.
•. • • • • • • • • • • • • • • • • • •	*	b, macrogolgin (with		115 7044	
2040001	2.005.04	transmembrane signal), 1	A1507007	Hs:7844	ND 004000
201060_x_at	3.26E-04	guanine nucleotide binding protein	AI537887	115 400 400	NP_004090
004004	1 005 04	10	1404005	Hs.160483	115 00 1000
201061_s_at	1.26E-04	gb:M81635.1 /DEF=Homo sapiens	M81635		NP_004090
•		erythrocyte membrane protein			
9		mRNA, complete cds.			
		/FEA=mRNA /GEN=stomatin			- 1
·		peptide /PROD=stomatin peptide			
÷		/DB_XREF=gi:181183			
Φ <sub>3</sub>		/UG=Hs.160483 erythrocyte			
		membrane protein band 7.2			
		(stomatin) /FL=gb:M81635.1		1	* .
		gb:NM_004099.1			

Gene Identifier	p-value	Description	Gene	Unigene	Prot in
		×	Accession	Accession	Accession
	" :		No.	No.	No.
201065_s_at	0.005852	gb:NM_001518.1 /DEF=Homo	NM_001518		NP_127496
	4. •	sapiens general transcription		*	
	]	factor II, i (GTF2I), mRNA.			
		/FEA=mRNA /GEN=GTF2I			
12		/PROD=general transcription	<i>*</i>	*	
		factor II, i /DB_XREF=gi:4504202		9	* *
		/UG=Hs.278589 general	1	χ.	
		transcription factor II, i		-	4
		/FL=gb:U77948.1 gb:AF015553.1	A		
A STATE OF THE STA		gb:AF038969.1 gb:NM: 001518.1			
		gb., (**00000; ** gb.**(**)			
201069 at	0.011725	gb:NM_004530:1 /DEF=Homo	NM_004530		NP_004521
201000_at	0.011123	sapiens matrix metalloproteinase	14101_004000	*	_004321
7 s	1	2 (gelatinase A, 72kD gelatinase,			
		72kD type IV collagenase)			
-1-	•	(MMP2), mRNA /FEA=mRNA			C (20)
		the state of the s		ne jin er.	
	1	/GEN=MMP2 /PROD=matrix			
	:	metalloproteinase 2 preproprotein	,		·
*		/DB_XREF=gi:11342665			*
		/UG=Hs.111301 matrix	[ • • • •		
		metalloproteinase 2 (gelatinase A,			
		72kD gelatinase, 72kD type IV		*	
	- !	collagenase) /FL=gb:NM_004530.1			
		gb:BC002576.1			
	ļ. · · ·			1.	j .
			Syr T	*	
			•		
201070_x_at	0.003529	splicing factor 3b, subunit 1,	AI739389		NP_036565
		155kDa		Hs.334826	- -
201075_s_at	0.02145	gb:NM_003074.1 /DEF=Homo	NM 003074		NP 003065
, <u> </u>		sapiens SWISNF related, matrix	_		10 J
144. V.		associated, actin dependent	3	20.4	•*
	-5-	regulator of chromatin, subfamily	-		
ŧ		c, member 1 (SMARCC1),	Control of the contro		•
		mRNA /FEA=mRNA	-	* *	
		/GEN=SMARCC1		:	*
		/PROD=SWISNF related, matrix			
		associated, actindependent			
·		regulator of chromatin, subfamily			
•					
	1	c, member 1			٠.
		/DB_XREF=gi:4507078			:
	,	/UG=Hs.172280 SWISNF related,	·	1	
		matrix associated, actin			
	Į.	dependent regulator of chromatin,			
		subfámily c, member 1	9		
		/FL=gb:U66615.1			
	l · .	gb:NM_003074.1		1	1

Gene Identifi r	p-value	Description	Gene	Unigene	Protein
			Accession	Accession No.	Accession
201076 at	0.013223	gb:NM_005008.1 /DEF=Homo	No. NM_005008	NO.	<b>No.</b> NP 004999
2010/0_at	0.013223	sapiens non-histone chromosome	14161-002000		1117_004999
			·		
•		protein 2 (S. cerevisiae)-like 1		)	
	*	(NHP2L1), mRNA /FEA=mRNA			, V
*		/GEN=NHP2L1 /PROD=non-			
		histone chromosome protein 2			
		(S.cerevisiae)-like 1			
	· • •	/DB_XREF=gi:4826859			
	a. 1	/UG=Hs.182255 non-histone			[
	1. 1. 1	chromosome protein 2 (S.	-		
jaj e j	- *	cerevisiae)-like 1			*
		/FL=gb:BC005358.1 gb:D50420.1			
1	***	gb:AF091076.1 gb:NM_005008.1	* .		
•	1.1 \$1 5	gb:AF155235.1		1	1 * ::
•					
201078_at	1.26E-04	gb:NM_004800.1 /DEF=Homo	NM 004800		NP_004791
:		sapiens transmembrane 9			
	47	superfamily member 2 (TM9SF2),			
ier'		mRNA. /FEA=mRNA			
		/GEN=TM9SF2			
		/PROD=transmembrane 9			•• -
		superfamily member 2			
	-	/DB XREF=gi:4758873			٠.\
		/UG=Hs.28757 transmembrane 9			
· · · · · ·					
		superfamily member 2	1		
		/FL=gb:U81006.1			
war and a second second	2 Sec. 1	gb:NM_004800.1		S	
201086_x_at	7.58E-04	gb:NM_003103.1 /DEF=Homo	NM_003103		NP_620305
		sapiens SON DNA binding			
		protein (SON), mRNA.			1
	2	/FEA=mRNA /GEN=SON	· .		-
*		/PROD=SON DNA binding			*
	5	protein /DB_XREF=gi:4507152			
		/UG=Hs.92909 SON DNA binding	•		
		protein /FL=gb:NM_003103.1			0
		J	· ·		
201087 at	0.026891	gb:NM 002859.1 /DEF=Homo	NM 002859		NP_002850
		sapiens paxillin (PXN), mRNA.		1	-332300
		/FEA=mRNA /GEN=PXN	*.*		
, « Q.		/PROD=paxillin			
· Se.	1	//DB_XREF=gi:4506344			-
				٠.	
		/UG=Hs.102497 paxillin			
· · · · · · · · · · · · · · · · · · ·		/FL=gb:NM_002859.1			8 72
		gb:U14588.1			

Gene ld ntifier	p-value	D scription	Gene	Unigene	Prot in
			Accession	Accession	Acc ssion
			No.	No.	No.
201088 at	0.00161	gb:NM 002266.1 /DEF=Homo	NM 002266		NP 002257
· · ·		sapiens karyopherin alpha 2	-		
		(RAG cohort 1, importin alpha 1)		Ē	
		(KPNA2), mRNA. /FEA=mRNA		·	
.*		/GEN=KPNA2 /PROD=karyopherin		- "	
		alpha 2 /DB_XREF=gi:4504896		·	
	:	/UG=Hs.159557 karyopherin			
		alpha 2 (RAG cohort 1, importin			
	00 -3	alpha 1) /FL=gb:NM_002266.1			~
			7	*	
	* * * *	gb:U09559.1 gb:U28386.1			8 0
20100	0.00.01				
201089_at	0.00161	gb:NM_001693.1 /DEF=Homo	NM_001693	* .	NP_001684
		sapiens ATPase, H+ transporting,			
		lysosomal (vacuolar proton		*	
		pump), beta polypeptide, 5658kD,			
	1,1	isoform 2 (ATP6B2), mRNA.		1.45	
	: · · · · .	/FEA=mRNA /GEN=ATP6B2			
*	0	/PROD=ATPase, H+ transporting,			
		lysosomal (vacuolarproton pump),	- 0.0		
		beta polypeptide, 5658kD,			
		isoform 2 /DB_XREF=gi:4502310	*		
		/UG=Hs.1697 ATPase, H+			
		transporting, lysosomal (vacuolar			•
		proton pump), beta polypeptide,	,		
		5658kD, isoform 2	*		
		/FL=gb:BC003100.1	4.	10.	
en en grant of the contract of		gb:NM_001693.1 gb:L35249.1			
*		gb.14W_001099.1 gb.E33249.1			
201000 v at	3.26E-04	gb:NM_006082.1 /DEF=Homo	NM 006082		NP 006073
201090_x_at	3.200-04		INIVI_UUUUUZ		NE_000073
		sapiens tubulin, alpha, ubiquitous			
		(K-ALPHA-1), mRNA.	4		
		/FEA=mRNA /GEN=K-ALPHA-1		* 1	
·		/PROD=tubulin, alpha, ubiquitous			
		/DB_XREF=gi:5174476			
		/UG=Hs.278242 tubulin, alpha,	1	ŀ	
		ubiquitous /FL=gb:BC000696.1		* *	
		gb:BC001128.1 gb:BC001209.1			, ,
-		gb:K00558.1 gb:AF081484.1			
		gb:NM_006082.1			
· · ·					-
201091_s_at	3.26E-04	chromobox homolog 3 (HP1	BE748755	0 1 - W 71	NP_057671
201001 <u></u> 3 at					

Gene Identifier	p-value	Description	Gn	Unig ne	Protein
			Acc ssion	Accession	Accession
			No.	No.	No.
201094_at	0.041055	gb:NM_001032.1 /DEF=Homo	NM_001032		NP_001023
		sapiens ribosomal protein S29		,	
		(RPS29), mRNA. /FEA=mRNA			
		/GEN=RPS29 /PROD=ribosomal	· · · · · · · · · · · · · · · · · · ·	:	
		protein S29	1	*	
		/DB_XREF=gi:4506716			
	10	/UG=Hs.539 ribosomal protein	-		
		S29 /FL=gb:L31610.1	*		
004000	0.004000	gb:NM_001032.1 gb:U14973.1	1111 60 100 1		ND 004005
201095_at	0.001323	gb:NM_004394.1 /DEF=Homo	NM_004394		NP_004385
		sapiens death-associated protein			-
		(DAP), mRNA. /FEA=mRNA		<u> </u>	
		/GEN=DAP /PROD=death- associated protein			
		/DB_XREF=gi:4758119			
		/UG=Hs.75189 death-associated	*		
	×	protein /FL=gb:BC002726.1			
		gb:NM 004394.1	X-		
201096 s at	2 05F-04	ADP-ribosylation factor 4	AL537042	Hs.75290	NP 001651
201097 s at		gb:NM 001660.2 /DEF=Homo	NM_001660	1.0.7 0200	NP 001651
	V	sapiens ADP-ribosylation factor 4		1	
		(ARF4), mRNA. /FEA=mRNA		}	,
		/GEN=ARF4 /PROD=ADP-			
		ribosylation factor 4	b.,		
		/DB_XREF=gi:6995998	11.		
	37%	/UG=Hs.75290 ADP-ribosylation	,		
		factor 4 /FL=gb:BC003364.1			
		gb:M36341:1 gb:NM_001660.2			
201098_at	1.26E-04	gb:NM_004766.1 /DEF=Homo	NM_004766	1	NP_004757
		sapiens coatomer protein			
		complex, subunit beta 2 (beta		*	
<i>i</i>		prime) (COPB2), mRNA.			
*		/FEA=mRNA /GEN=COPB2			
		/PROD=coatomer protein			
, , , , , , , , , , , , , , , , , , ,	1	complex, subunit beta 2			
		(betaprime)			
		/DB_XREF=gi:4758031 /UG=Hs.75724 coatomer protein		a a	· .
		complex, subunit beta 2 (beta			
		prime) /FL=gb:BC000326.1	1	+	
		gb:NM_004766.1	1	•	
201099 at	1.26F-04	ubiquitin specific protease 9, X	AA824386		
	1.202.07	chromosome (fat facets-like	7 132 1000		
		terresidente fractionera into	JI		

Gene Identifier	p-value	Description	Gene Accession	Unigene Accession	Protein Accession
	1		No.	No.	No.
201100_s_at	5.025.04	gb:NM 004652.2 /DEF=Homo	NM 004652	140.	NP_068706
201100_S_at	5.03E-04	sapiens ubiquitin specific	14141_004052		NF_000/00
		protease 9, X chromosome			
		(Drosophila fat facets related)			
	1	(USP9X), transcript variant 1,			
	· · · · · ·	mRNA /FEA=mRNA			
		/GEN=USP9X:/PROD=Drosophila	Ò	*	
		fat facets related, X-linked,	* 0		·
		isoform1 /DB_XREF=gi:11641424			
	` - (	/UG=Hs.77578 ubiquitin specific	*		
		protease 9, X chromosome	* -: · · · · · · · · · · · · · · · · · ·		·
		(Drosophila fat facets related)	0.00		1.
		/FL=gb:NM_004652.2			1.00
201102_s_at	0.003171	gb:NM_002626.1 /DEF=Homo	NM_002626		NP_002617
		sapiens phosphofructokinase, liver	* * * * * *		· ·
		(PFKL), mRNA. /FEA=mRNA			*
		/GEN=PFKL		* .	
	10.0	/PROD=phosphofructokinase, liver	*** * *		
		/DB_XREF=gi:4505746	1		*
•		/UG=Hs.155455	,	3 y.	-x-
		phosphofructokinase, liver			
		/FL=gb:BC004920.1 gb:X15573.1			
		gb:NM_002626.1			
201103_x_at	0.013223	hypothetical protein	BE299495		NP_775909
	1 -1 - 1 - 1 - 1	DJ328E19.C1.1	×	Hs.323463	_
201104 x at	0.007052	gb:NM_015383.1 /DEF=Homo	NM 015383		NP 056198
		sapiens hypothetical protein			
		(DJ328E19.C1.1), mRNA.	* *		
		/FEA=mRNA			
	*	/GEN=DJ328E19.C1.1	* . · ·	2	
4, 4		/PROD=hypothetical protein	1.00	* ? .	
		//DB_XREF=gi:7657016		1	
	00				
- 1	·	//UG=Hs.218329 hypothetical			
204405 -4	0.000001	protein /FL=gb:NM_015383.1	NIM 000005	<del>                                     </del>	NP_002296
201105_at	0.026891	gb:NM_002305.2 /DEF=Homo	NM_002305		NP_002296
		sapiens lectin, galactoside-	F-1		
		binding, soluble, /1 (galectin 1)			
V. *		(LGALS1), mRNA /FEA=mRNA			
		/GEN=LGALS1 /PROD=beta-			
19.		galactosidase binding lectin			
	-	precursor /DB_XREF=gi:6006015			
	1 .	/UG=Hs.227751 lectin,			
		galactoside-binding, soluble, 1			
	,	(galectin 1) /FL=gb:BC001693.1		1.	,
		gb:J04456.1 gb:NM_002305.2			

Gen Identifier	p-value	Description	Gene	Unig ne	Protein
	1		Accession	Acc ssion	Accession
			No.	No.	No.
201114_x_at	0.001116	gb:NM_002792.1 /DEF=Homo	NM_002792		NP 689468
		sapiens proteasome (prosome,	. –		
10	1.	macropain) subunit, alpha type, 7		*	
*		(PSMA7), mRNA. /FEA=mRNA		· ·	
		/GEN=PSMA7			
		/PROD=proteasome (prosome,			
	*	macropain) subunit, alphatype, 7			
		/DB XREF=gi:4506188			
		/UG=Hs.233952 proteasome			
		(prosome, macropain) subunit,		-	*
	1 . Y			100	
		alpha type, 7 /FL=gb:BC004427.1			
	8	gb:AF022815.1 gb:AF054185.1	<b>]</b> .		
		gb:NM_002792.1	8		- X
554445	0.000004				
201118_at	0.033381	gb:NM_002631.1 /DEF=Homo	NM_002631		NP_002622
		sapiens phosphogluconate			
		dehydrogenase (PGD), mRNA		4	.,.
		/FEA=mRNA /GEN=PGD			
		/PROD=phosphogluconate	*		
•	* * * * * * * * * * * * * * * * * * * *	dehydrogenase			· .
• • • •		/DB_XREF=gi:4505758			1
	-11	/UG=Hs.75888 phosphogluconate			6
		dehydrogenase	8:		
* * *		/FL=gb:BC000368.1			
9		gb:NM_002631.1 :gb:U30255.1			
	1				
201119_s_at	0.003171	gb:NM_004074.1 /DEF=Homo	NM 004074		NP 004065
		sapiens cytochrome c oxidase	<b>√</b> <del>-</del>		
		subunit VIII (COX8), nuclear	* -		
*	· ·	gene encoding mitochondrial		ar e e	
3		protein, mRNA: /FEA=mRNA	j .		
		/GEN=COX8 /PROD=cytochrome		,	,
* * * * * * * * * * * * * * * * * * * *		c oxidase subunit VIII	8- V - V		*
		/DB_XREF=gi:4758043	= ); =	1.	* 0
					* (
		/UG=Hs.81097 cytochrome c			
		oxidase subunit VIII		1	l:
. 7		/FL=gb:NM_004074.1	1		

Gene Identifi r	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
201126_s_at	0.026891	gb:NM_002406.2 /DEF=Homo	NM 002406		NP_002397
		sapiens mannosyl (alpha-1,3-)-			_
*.	, , , )	glycoprotein beta-1,2-N-			. 1
	•	acetylglucosaminyltransferase		· ·	
		(MGAT1), mRNA. /FEA=mRNA			3.4
×		/GEN=MGAT1 /PROD=mannosyl			
		(alpha-1,3-)-glycoproteinbeta-1,2-N-			
		acetylglucosaminyltransferase			
	4.	/DB_XREF=gi:6031182			
		/UG=Hs.151513 mannosyl (alpha-			
		1,3-)-glycoprotein beta-1,2-N-	)		
		acetylglucosaminyltransferase			·
		/FL=gb:M55621.1			'
		1		. 1	
204420 3 104	0.00464	gb:NM_002406.2	NIM ODIOOC		ND 004007
201128_s_at	0.00 161	gb:NM_001096.1 /DEF=Homo	NM_001096		NP_001087
		sapiens ATP citrate lyase	*		* * *
		(ACLY), mRNA. /FEA=mRNA	••		
		/GEN=ACLY /PROD=ATP citrate		7-2	*
	+ +	lyase /DB_XREF=gi:4501864			0.0
	00	/UG=Hs.174140 ATP citrate lyase			* *
(1)		/FL=gb:NM_001096.1	**		
		ħ.		: -	
201129_at	0.004341	gb:NM_006276.2 /DEF=Homo	NM_006276		NP_006267
		sapiens splicing factor,	*	. 2	
		arginineserine-rich 7 (35kD)	. *	, já	
,		(SFRS7), mRNA: /FEA=mRNA		*	i .
		/GEN=SFRS7 /PROD=splicing			
11.		factor, arginineserine-rich 7			
1		(35kD) /DB_XREF=gi:6857827		-	
	-	/UG=Hs.184167 splicing factor;			
		arginineserine-rich 7 (35kD)			v =)(=
	,	/FL=gb:BC000997.2 gb:L22253.1	•		ļ
		gb:NM_006276.2			
201132_at	1.26E-04		NM_019597		NP_062543
		sapiens heterogeneous nuclear		· ·	
	• 00	ribonucleoprotein H2 (H)	) *		i .
·		(HNRPH2), mRNA. /FEA=mRNA	* .		
		/GEN=HNRPH2			
		/PROD=heterogeneous nuclear			
*		ribonucleoprotein H2 (H)		_	• •
	- 1	/DB_XREF=gi:9624997			
· · · · · · · · · · · · · · · · · · ·		/UG=Hs.278857 heterogeneous			
,		<u> </u>		. ( ;	
·		nuclear ribonucleoprotein H2 (H)			
201122	0.004440	/FL=gb:NM_019597.1	A A 4 40000	Ha 070040	ND 055024
201133_s_at	1 0.001116	KIAA0438 gene product	AA142966	Hs.279849	NP_055634

Gene Identifier		Description	Gn	Unigene	Protein
(a)	p-value		Accession	Accession	Accession
	•	×	No.	No.	No.
201136_at	5.03E-04	gb:NM_002668.1 /DEF=Homo	NM_002668		NP_002659
		sapiens proteolipid protein 2			_
		(colonic epithelium-enriched)		6	
		(PLP2), mRNA. /FEA=mRNA			
14.	-	/GEN=PLP2 /PROD=proteolipid			
		protein 2 (colonicepithelium-	· · · · ·		
0		enriched) /DB XREF=gi:4505892			*
		/UG=Hs.77422 proteolipid protein			- 1
	*	2 (colonic epithelium-enriched)	: :	16	
		/FL=gb:L09604.1 gb:NM_002668.1		*	
		3		· · · · · · ·	
201138_s_at	0.005852	Sjogren syndrome antigen B	BG532929	7	NP_003133
		(autoantigen La)		Hs.83715	
201140 s_at	0.007779	gb:NM_004583.1 /DEF=Homo	NM 004583	14	NP_004574
ए विकास सिक्ता है। इ.स.		sapiens RAB5C, member RAS			<del></del>
		oncogene family (RAB5C),			
		mRNA. /FEA=mRNA			
	* ·	/GEN=RAB5C /PROD=RAB5C,	8 7		
	+ 1	member RAS oncogene family			
		/DB XREF=gi:4759019			
		/UG=Hs.479 RAB5C, member		1	· , .
		RAS oncogene family			5.0
	1.	/FL=gb:NM 004583.1			
		gb:U11293.1 gb:U18420.1			
,		gb:AF141304.1			
201146_at	1 26F-04	gb:NM_006164.1 /DEF=Homo	NM_006164		NP_006155
		sapiens nuclear factor (erythroid-			
	. •	derived 2)-like 2 (NFE2L2),			
		mRNA. /FEA=mRNA			
		/GEN=NFE2L2 /PROD=nuclear			
	4	factor (erythroid-derived 2)-like 2	"		
		/DB_XREF=gi:5453775			
		/UG=Hs.155396 nuclear factor			
		(erythroid-derived 2)-like 2			
		/FL=gb:NM_006164.1	5 x		*
201154_x_at	0.004341	gb:NM_000968.1 /DEF=Homo	NM 000968	*** - 1-1	NP_000959
		sapiens ribosomal protein L4	_		<del>-</del> .
	. *	(RPL4), mRNA. /FEA=mRNA	*		•
		/GEN=RPL4 /PROD=ribosomal			٠.
		protein L4 /DB_XREF=gi:4506652	0		
4		/UG=Hs.286 ribosomal protein L4			
*		/FL=gb:BC001365.1 gb:L20868.1			
		gb:D23660.1 gb:NM 000968.1	*	1 .	
	-8-		* (1)		
				•	

Gene Identifier	p-value	Description	G ne	Unigen	Protein
	*	*	Accession	Accession	Accession
			No.	No.	No.
201155_s_at	0.013223	gb:NM_014874.1 /DEF=Homo	NM 014874		NP 055689
<del></del>		sapiens KIAA0214 gene product			
		(KIAA0214), mRNA. /FEA=mRNA		*	
		/GEN=KIAA0214		_	
		/PROD=KIAA0214 gene product	- 1		,
•		/DB_XREF=gi:7662003			
•		/UG=Hs.3363 KIAA0214 gene			
,		product /FL=gb:D86987.1			
		gb:AF036536.1 gb:NM_014874.1	*		
201156 s at	0.04734	Consensus includes	AF141304	-	NP 004574
201100_0_d(	0.01701	gb:AF141304.1 /DEF=Homo	/ 11 14 1004		_004374
er en en en		sapiens small GTPase (RAB5C)		8 0	
		mRNA, complete cds. /FEA=CDS			
		/GEN=RAB5C /PROD=small		9	
		GTPase /DB_XREF=gi:7672664			
		/UG=Hs.479 RAB5C, member			•
	1,1	RAS oncogene family		* * * * * * * * * * * * * * * * * * * *	
	-	/FL=gb:NM_004583.1			
		gb:U11293.1 gb:U18420.1			
		gb:AF141304.1			-x
201160_s at	1.26E.04	cold shock domain protein A	AL556190	Hs.198726	NP 003642
201161 s at		gb:NM 003651.1 /DEF=Homo	NM 003651	113.130720	NP 003642
201101_3_at	1.412-04	sapiens cold shock domain	14141_003031		147_003042
	·.	protein A (CSDA), mRNA		· · ·	
		/FEA=mRNA /GEN=CSDA			
		/PROD=cold shock domain	* 0	1.0	÷
		protein A /DB_XREF=gi:4503070 /UG=Hs.1139 cold shock domain		1	
				. 1	* -
		protein A /FL=gb:NM_003651.1		e. i	÷.
201162 - 64	2.265.04		NIA ODAFEO	7* 1 2 2	ND 004544
201163_s_at	3.26E-04	gb:NM_001553.1 /DEF=Homo	NM_001553		NP_001544
		sapiens insulin-like growth factor		-	*
		binding protein 7 (IGFBP7),			
		mRNA. /FEA=mRNA	1		
		/GEN=IGFBP7 /PROD=insulin-like	.=:	*	
		growth factor binding protein 7	1		
		/DB_XREF=gi:4504618		*	. * .
		/UG=Hs.119206 insulin-like	*	9	;
		growth factor binding protein 7		-y-	
		/FL=gb:L19182.1 gb:NM_001553.1			1
201165_s_at	1.26E-04	pumilio homolog 1 (Drosophila)	BG474429	Hs.153834	

Gene Identifier	p-valu	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
		*	No.	No.	No.
201166_s_at	0.004341	gb:NM_014676.1 /DEF=Homo	NM_014676.		NP_055491
		sapiens pumilio (Drosophila)			_
		homolog 1 (PUM1), mRNA.	*		
		/FEA=mRNA /GEN=PUM1			`,'
	8	/PROD=pumilio (Drosophila)	3		
		homolog 1			
		/DB_XREF=gi:13491165			
	-	/UG=Hs.153834 pumilio			
	,	(Drosophila) homolog 1			
		/FL=gb:AF315592.1	***	*	
		gb:NM_014676.1			
201170 s at	0.005852	gb:NM_003670.1 /DEF=Homo	NM_003670		NP_003661
		sapiens basic helix-loop-helix			
		domain containing, class B, 2	•		
	,	(BHLHB2), mRNA. /FEA=mRNA			*
	* 1	/GEN=BHLHB2			
		/PROD=differentiated embryo		,	
		chondrocyte expressed gene1			
		/DB_XREF=gi:4503298	v <sup>a</sup>		
		/UG=Hs.171825 basic helix-loop-			
		helix domain containing, class B,			
		2 /FL=gb:AB004066.1			
		gb:NM_003670.1			
201172_x_at	7.58E-04		NM_003945		NP 003936
		sapiens ATPase, H+ transporting,			- <del>-</del> -
		lysosomal (vacuolar proton pump)		* *	
		9kD (ATP6H), mRNA.			** *
	*	/FEA=mRNA:/GEN=ATP6H			
		/PROD=ATPase, H+ transporting,	+		
		lysosomal (vacuolarproton pump)	4 1 2		
		9kD /DB_XREF=gi:4502318			
1		/UG=Hs.24322 ATPase, H+			
		transporting, lysosomal (vacuolar			
		proton pump) 9kD			*
		/FL=gb:NM_003945.1			
			•		
201173_x_at	7.58E-04	gb:NM_006600.1 /DEF=Homo	NM_006600		NP_006591
		sapiens nuclear distribution gene		* 1	
		C (A.nidulans) homolog (NUDC),			* 3
	:	mRNA. /FEA=mRNA			,
	. *	/GEN=NUDC /PROD=nuclear			*
		distribution gene C		ļ	B
		(A.nidulans)homolog			
	*	/DB_XREF=gi:5729952	. *		÷
		/UG=Hs.263812 nuclear	,	* =	
·	0	distribution gene C (A.nidulans)	8	ē	ė G
2		homolog /FL=gb:BC002399.1		* 1	
		gb:BC003132.1 gb:AB019408.1			
	. /:	gb:AF130736.1 gb:AF125465.1			
		gb:AF100760.1 gb:NM_006600.1			4.0

Gene Identifier	p-value	Description	G n	Unigene	Protein
			Acc ssion	Accession	Acc ssion
* 1 ·			No.	No.	No.
201174_s_at	5.03E-04	gb:NM_018975.1 /DEF=Homo	NM_018975		NP_061848
		sapiens TRF2-interacting			_
		telomeric RAP1 protein (RAP1),			
		mRNA. /FEA=mRNA /GEN=RAP1		· γ .	
		/PROD=TRF2-interacting telomeric			•
		RAP1 protein			
		/DB XREF=gi:9507032	*		
		/UG=Hs.274428 TRF2-interacting			
	.]	telomeric RAP1 protein			
	*	/FL=gb:BC004465.1			
		gb:AF262988.1 gb:NM_018975.1			
201176_s_at	0.00161	gb:NM_001655.2 /DEF=Homo	NM 001655		NP 001646
		sapiens archain 1 (ARCN1),			
		mRNA. /FEA=mRNA		* .	
		/GEN=ARCN1 /PROD=archain			
		/DB_XREF=gi:11863153			٠
		/UG=Hs.33642 archain 1			
		/FL=gb:NM_001655.2			
201178 at	1 26F-04	gb:NM_012179.1 /DEF=Homo	NM 012179	THE STATE OF THE STATE OF	NP 036311
201110_ut	1,202.01	sapiens F-box only protein 7	0 .2		
. 0		(FBXO7), mRNA. /FEA=mRNA			
		/GEN=FBXO7 /PROD=F-box only			
* · · ·		protein 7 /DB_XREF=gi:7106310	7. 4 - 10		
		/UG=Hs.5912 F-box only protein		y Single	
0 - 1		7 /FL=gb:AF129537.1			
		gb:NM_012179.1 gb:AF233225.1			
		gb./4//_0/2173.1 gb./4 233223.1			
201179_s_at	0.00228	gb:J03005.1 /DEF=Human	J03005		NP 006487
201110_3_at	0.00220	alternative guanine nucleotide-			1.11 _000-07.
		binding regulatory protein (G)			*
		alpha-inhibitory-subunit mRNA,	, .		
* ()		complete cds. /FEA=mRNA			
*		/GEN=GNAI1	*		
		/DB_XREF=gi:183183	*	1	
		//UG=Hs.73799 guanine nucleotide			
*	7	binding protein (G protein), alpha		* * * * * * * * * * * * * * * * * * * *	
		inhibiting activity polypeptide 3	. *	* 1	
*		/FL=gb:J03005.1 gb:J03198.1			
	, ,	gb:M27543.1 gb:J03238.1		:	4 2
		lgb:NM 006496.1			
L		[gb.14141_000490. ]	<u> </u>		

G n ld ntifi r	p-valu	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
*		*	No.	No.	No.
201180_s_at	1.26E-04	gb:J03198.1 /DEF=Human	J03198	,	NP_006487
-		stimulatory G protein (of receptor-			
		regulated K+ channels) alpha			
		subunit mRNA, complete cds.			y .
* .		/FEA=mRNA			
7		/DB_XREF=gi:183224	-	(-	
*		/UG=Hs.73799 guanine nucleotide			
		binding protein (G protein), alpha			
		inhibiting activity polypeptide 3		' '	
30.00	-,	/FL=gb:J03005.1 gb:J03198.1			-
		gb:M27543.1 gb:J03238.1			
* * * * * * * * * * * * * * * * * * * *	*	gb:NM 006496.1			
201181_at	0.001116	gb:NM 006496.1 /DEF=Homo	NM 006496	×	NP 006487
		sapiens guanine nucleotide			
		binding protein (G protein), alpha			
		inhibiting activity polypeptide 3	fa .		
	9	(GNAI3), mRNA. /FEA=mRNA			
,		/GEN=GNAI3 /PROD=guanine			
	, T	nucleotide binding protein (G			
		protein),alpha inhibiting activity			
(i)		polypeptide 3		j),	
	2	/DB_XREF=gi:5729849		·)(-	••
		/UG=Hs.73799 guanine nucleotide			
		binding protein (G protein), alpha			
×	* .	inhibiting activity polypeptide 3			
		/FL=gb:J03005:1 gb:J03198.1			
	*	gb:M27543.1 gb:J03238.1			
		gb:NM_006496.1			- 0
201183_s_at	0.004341	chromodomain helicase DNA	AI761771	- 10	NP_001264
1201100_3_at	0.00-0-1	binding protein 4	707,01771	Hs.74441	_00120-
201186 at	3.26F-04	gb:NM_002337.1 /DEF=Homo	NM 002337	113.74447	NP 002328
201100_at	0.200 04	sapiens low density lipoprotein-	1111_002007	1	_002020
		related protein-associated protein			
		1 (alpha-2-macroglobulin receptor-		0	
		associated protein 1) (LRPAP1),		<b>!</b> *	*
<u></u>		mRNA. /FEA=mRNA	. *		
		/GEN=LRPAP1 /PROD=low		*	
**		density lipoprotein-relatedprotein-	1	*	
		associated protein 1 (alpha-2-			
*		macroglobulinreceptor-associated	-		
<u>'</u>		protein 1) /DB_XREF=gi:4505020		·	
		/UG=Hs.75140 low density	1.		
		lipoprotein-related protein-		=Cv.	*
	, ,	associated protein 1 (alpha-2-			
		macroglobulin receptor-associated			
		protein 1) /FL=gb;M63959.1			
V-		gb:NM_002337.1			- 4
		go.14191_002007.1			
			1		
L	<u></u>		1	Ļ	<u> </u>

Gene Identifier	p-valu	Description	G ne	Unigene	Prot in
			Accession	Accession	Accession
			No.	No.	No.
201190_s_at	0.00228	phosphotidylinositol transfer protein	H15647		NP 006215
201130_5_at	0.00220		1113047	Hs.409367	MF_000213
201191 at	0.004400	phosphotidylinositol transfer protein	LIAEGAZ	115.409307	NP 006215
201.191_at	0.001109		1304 <i>1</i>	Un 400267	NP_000215
204400 - 54	2.055.04	ChiNIM 000004 4 (DEE-11	NIM OCCOOL	Hs.409367	ND 000045
201192_s_at	2.05E-04	gb:NM_006224.1 /DEF=Homo	NM_006224		NP_006215
		sapiens phosphotidylinositol	· .	*	
	13	transfer protein (PITPN), mRNA.		-	J .
3	2 -	/FEA=mRNA /GEN=PITPN			
		/PROD=phosphotidylinositol			·
	1	transfer protein			0
	4 5	/DB_XREF=gi:5453907		1	· · · · · · ·
		/UG=Hs.79709 phosphotidylinositol			
	1:	transfer protein /FL=gb:D30036.1			-
1		gb:M73704.1 gb:NM_006224.1			
201193_at	1.26E-04	gb:NM_005896.1 /DEF=Homo	NM_005896	1.0	NP_005887
		sapiens isocitrate dehydrogenase	_	,	
*		1 (NADP+), soluble (IDH1),	*		
		mRNA: /FEA=mRNA /GEN=IDH1			
		/PROD=isocitrate dehydrogenase	Q 0		
		1 (NADP+), soluble			
		/DB_XREF=gi:5174470	_		- 30
		/UG=Hs.11223 isocitrate	_ ×		
		dehydrogenase 1 (NADP+),			1
		soluble /FL=gb:AF020038.1			
8.		gb:AF113917.1 gb:NM_005896.1		*	
		gb:AL136702.1			-0.0
004404					
201194_at	0.022795	gb:NM_003009.1 /DEF=Homo	NM_003009		NP_003000
_	- (0)	sapiens selenoprotein W, 1			
1	1 1 1 1 1 1 1 1	(SEPW1), mRNA /FEA=mRNA		***	. •
		/GEN=SEPW1		* .	
	, Y	/PROD=selenoprotein W, 1	**		
		/DB_XREF=gi:4506886			
• • 00		/UG=Hs.14231 selenoprotein W,	,		, , ,
		1 /FL=gb:U67171.1			
		gb:AF015283.1 gb:NM_003009.1		1	
201196_s_at	5.03E-04	gb:M21154.1 /DEF=Human S-	M21154		NP 001625
_ <b></b>		adenosylmethionine decarboxylase			<del>-</del>
		mRNA, complete cds.	) ·	1	
	1 3	/FEA=mRNA /GEN=AMD2			
	: *	/DB XREF=gi:178517	8		
	[-	/UG=Hs.262476 S-			
٠.		adenosylmethionine decarboxylase			
1		1 /FL=gb:BC000171.2			
				. :	
		gb:M21154.1 gb:NM_001634.3	17-3		. 9
L.,		L <sub>_</sub>	<u>L</u>	<u> </u>	l

G ne Identifier	p-valu	Description	Gene	Unigene	Protein
			Acc ssion	Accession	Accession
	-	*	No.	No.	No.
201199 s at .	0.041795	gb:NM_002807.1 /DEF=Homo	NM_002807		NP_002798
= -		sapiens proteasome (prosome,	<del>-</del>		-
		macropain) 26S subunit, non-			·
		ATPase, 1 (PSMD1), mRNA.			,
- 3		/FEA=mRNA /GEN=PSMD1			
		/PROD=proteasome (prosome,			
		macropain) 26S subunit,non-	* *		
4		ATPase, 1 /DB_XREF=gi:4506224	*		: '
		/UG=Hs.3887 proteasome	80		
		(prosome, macropain) 26S	в.	* /	
		subunit, non-ATPase, 1			
		/FL=gb:D44466.1			3
8		gb:NM 002807.1			
		gb.NW_002007.1			
201200 at	3 26E 04	gb:NM_003851.1 /DEF=Homo	NM 003851		NP 003842
201200_at	3.20E-04	sapiens cellular repressor of E1A			INP_003642
		stimulated genes (CREG), mRNA. /FEA=mRNA			
					***
	ų.	/GEN=CREG /PROD=cellular		* * *	
		repressor of E1A-stimulated			ر از از از از از از از از از از از از از
		genes /DB_XREF=gi:4503036			
		/UG=Hs.5710 cellular repressor		* ** 1	1
		of E1A-stimulated genes	17 - 17 - 17 - 17 - 17 - 17 - 17 - 17 -		
	$v = \tilde{e_{i,j}} \cdot v = e(v)$	/FL=gb:AF084523.1			
		gb:NM_003851.1	1		
201201_at	0.016934	gb:NM_000100.1 /DEF=Homo	NM_000100		NP_000091
	٠.	sapiens cystatin B (stefin B)	·		
		(CSTB), mRNA. /FEA=mRNA			
		/GEN=CSTB /PROD=cystatin B			8.4
		(stefin B) /DB_XREF=gi:4503116	÷ .,		
	*	/UG=Hs.695 cystatin B (stefin B)			
	,	/FL=gb:BC003370.1 gb:L03558.1			*
	4,	gb:NM_000100.1			
201202_at	5.03E-04	gb:NM_002592.1 /DEF=Homo	NM_002592		NP_002583
	e T	sapiens proliferating cell nuclear		1	
		antigen (PCNA), mRNA.			
		/FEA=mRNA /GEN=PCNA			
		/PROD=proliferating cell nuclear			1
		antigen /DB_XREF=gi:4505640	,	· ·	2
<del>.</del> .		/UG=Hs.78996 proliferating cell	× 00 ,		
		nuclear antigen			* .
*		/FL=gb:BC000491.1 gb:M15796.1			
		,	1		

Gene Identifier	p-value	Description	Gene	Unigene	Protein
. 4			Accession	Accession	Accession
. *			No.	No.	No.
201214_s_at	0.005852	gb:NM_002712.1 /DEF=Homo	NM_002712		NP_002703
		sapiens protein phosphatase 1,			
		regulatory subunit 7 (PPP1R7),			·
		mRNA. /FEA=mRNA			
		/GEN=PPP1R7 /PROD=protein		٦.	
·		phosphatase 1, regulatory subunit	,		
*		7 /DB_XREF=gi:4506012			*
	_	/UG=Hs.36587 protein		a	1000
	]	phosphatase 1, regulatory subunit			
		7 /FL=gb:BC000910.1			
201217_x_at	0.022291	gb:NM_002712.1 gb:NM_000967.1 /DEF=Homo	NM 000967	Service production of the service of	NP_000958
201217_x_at	0.033361	sapiens ribosomal protein L3	NIVI_000967		MP_000930
		(RPL3), mRNA. /FEA=mRNA			
And the second		/GEN=RPL3 /PROD=ribosomal			
		protein L3 /DB_XREF=gi:4506648			
		/UG=Hs.119598 ribosomal protein			
		L3 /FL=gb:BC002408.1			
		gb:BC004323.1 gb:NM_000967.1			*
201218_at	0.004341	Consensus includes gb:N23018	NM_001329		NP_073713
		/FEA=EST /DB_XREF=gi:1137168	- 4		
		/DB_XREF=est:yx65d12.s1		*	* * * * * * * * * * * * * * * * * * * *
		/CLONE=IMAGE:266615			
**		/UG=Hs.171391 C-terminal	e.		* * *
		binding protein 2			
		/FL=gb:AF016507.1			
		gb:NM_001329.1	1	-	
201221 s at	7 50E 04	gb:NM_003089:1 /DEF=Homo	NM_003089		NP 003080
201221_S_at	7.56E-04	sapiens small nuclear	IAINI_003089		INP_003080
1 m		ribonucleoprotein 70kD			1
V	·	polypeptide (RNP antigen)			
		(SNRP70), mRNA. /FEA=mRNA			-
	e .	/GEN=SNRP70 /PROD=small			-
		nuclear ribonucleoprotein 70kD	*		*
		polypeptide(RNP antigen)			
		/DB_XREF=gi:4507118	*	*	
		/UG=Hs.174051 small nuclear	·		
, i i	,	ribonucleoprotein 70kD		* ****	
		polypeptide (RNP antigen)			
		/FL=gb:BC000342.1 gb:M22636.1			
		gb:NM_003089.1			
201222_s_at	1.26E-04	RAD23 homolog B (S. cerevisiae)	AL527365	Hs.178658	NP_002865

Gene Identifier	p-valu	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201223_s_at	5.03E-04	gb:NM_002874.1 /DEF=Homo	NM_002874		NP_002865
:		sapiens RAD23 (S. cerevisiae)	-		
•		homolog B (RAD23B), mRNA.	0	,	
		/FEA=mRNA /GEN=RAD23B			
		/PROD=RAD23 (S. cerevisiae)			
		homolog B		, 0	
	**	/DB XREF=gi:4506386			7.8
		/UG=Hs 178658 RAD23 (S.	Q		
* (4)		cerevisiae) homolog B			٠.
		/FL=gb:NM_002874.1			
		gb:D21090.1			
201234 at	6.68E-04	I V	NM 004517	65 100	NP 004508
—————————————————————————————————————	4,1 -, -, -, -, -, -, -, -, -, -, -, -, -,	sapiens integrin-linked kinase	· -		
	-	(ILK), mRNA. /FEA=mRNA			
		/GEN=ILK /PROD=integrin-linked		120	-1 .
		kinase /DB XREF=gi:4758605	. 10		
	, ,	/UG=Hs.6196 integrin-linked			
	100	kinase /FL=gb:U40282.1			
	·	gb.NM 004517.1	*		
201235 s at	0.033428	BTG family, member 2	BG339064	Hs.75462	NP 006754
201237_at		capping protein (actin filament)	AV685920		NP 006127
	1	muscle Z-line, alpha 2		Hs.75546	
201238 s at	2.05E-04	gb:BC005338.1 /DEF=Homo	BC005338	1	NP 006127
	1	sapiens, capping protein (actin			
		filament) muscle Z-line, alpha 2,		×	
94		clone MGC:12426, mRNA,			
		complete cds. /FEA=mRNA			. ••
		/PROD=capping protein (actin			
		filament) muscle Z-line,alpha 2			
		/DB_XREF=gi:13529130			
		/UG=Hs.75546 capping protein	*		. *
		(actin filament) muscle Z-line,		].	
		alpha 2 /FL=gb:BC005338.1			
		gb:NM_006136.1 gb:U03269.1			
201239_s_at	0.003171	ESTs, Highly similar to	BF530535	0 1	
a.	0.005171	SP25_HUMAN Microsomal signal			. *
· ·		peptidase 25 kDa subunit (SPase			
		25 kDa subunit (SPase			
		[H.sapiens]		Hs.381155	-
940		[[ri.sapieris]	<u> </u>	[F18.30 F135] _	

Gene Identifier	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201248_s_at	0.020456	gb:NM_004599.1 /DEF=Homo	NM_004599		NP_004590
		sapiens sterol regulatory element			
		binding transcription factor 2			
*		(SREBF2), mRNA. /FEA=mRNA			
	0	/GEN=SREBF2 /PROD=sterol			
***		regulatory element binding		•	
		transcriptionfactor 2	40		
*		/DB_XREF=gi:4759169	*	-	:
		/UG=Hs.108689 sterol regulatory			
,		element binding transcription			
		factor 2 /FL=gb:U02031.1	1,00		
	-	gb:NM 004599.1			-
		95			
201251 at	0.041055	gb:NM 002654.1 /DEF=Homo	NM 002654		NP 002645
7, 7, 7,		sapiens pyruvate kinase, muscle			
* *	-	(PKM2), mRNA. /FEA=mRNA			
		/GEN=PKM2 /PROD=pyruvate		= + 4	
		kinase, muscle			ъ
**		/DB_XREF=gi:4505838			
	e de la companya de l	/UG=Hs.198281 pyruvate kinase,	v		
		muscle /FL=gb:BC000481.1			-, · ·
	***	gb:M23725.1 gb:M26252.1			
		gb:NM_002654.1	n		
, in it is less		gs.:\\\\_002004.\		0 *	
201252 at	0.043703	gb:NM_006503.1 /DEF=Homo	NM_006503	<del></del>	NP_694546
201202_dt	0.040700	sapiens proteasome (prosome,	11111_000000		
		macropain) 26S subunit, ATPase,	*	· .	
	* 1	4 (PSMC4), mRNA. /FEA=mRNA			
		/GEN=PSMC4	<u> </u>		
		/PROD=proteasome (prosome,			
	1	macropain) 26S subunit,ATPase,			
		4 /DB XREF=gi:5729990			
		/UG=Hs.211594 proteasome			
		(prosome, macropain) 26S			
		subunit, ATPase, 4			· ·
		/FL=gb:BC000343.1	ļ		` -
*		gb:AF038965.1 gb:AF020736.1			
		gb:U27515.1 gb:NM_006503.1			
			L		

Gene Identifier	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
		· '	No.	No.	No.
201253_s_at	0.016934	gb:NM_006319.1 /DEF=Homo	NM_006319		NP_665695
		sapiens CDP-diacylglycerol			*
	· ·	inositol 3-phosphatidyltransferase			
ev .		(phosphatidylinositol synthase)	]-		
		(CDIPT), mRNA. /FEA=mRNA			
		/GEN=CDIPT /PROD=CDP-			
		diacylglycerolinositol3-			
		phosphatidyltransferase			
		(phosphatidylinositol synthase)			*
	· .	/DB_XREF=gi:5453905			
1 1 1 1 1	· ·	/UG=Hs.227107 CDP-			
* "		diacylglycerolinositol 3-	-	,	a y
		phosphatidyltransferase			
	*	(phosphatidylinositol synthase)			
-		/FL=gb:BC001444.1			
**		gb:AF014807.1_gb:NM_006319.1			* * * * * * * * * * * * * * * * * * * *
201254_x_at	0.041055	gb:NM_001010.1 /DEF=Homo	NM_001010		NP_001001
	1	sapiens ribosomal protein S6			
		(RPS6), mRNA: /FEA=mRNA	1.5		
		/GEN=RPS6 /PROD=ribosomal	<b>\</b>		
		protein S6 /DB_XREF=gi:4506730		*	
		/UG=Hs.241507 ribosomal protein	101		
		S6 /FL=gb:M20020.1			
		gb:NM_001010.1	:		
201255_x_at	0.016934	gb:NM_004639.1 /DEF=Homo	NM_004639		NP_542434
0 ,		sapiens HLA-B associated			
		transcript-3 (D6S52E), mRNA.	- 33		
		/FEA=mRNA /GEN=D6S52E		8	100
	. ',,	/PROD=HLA-B associated		=	
	1	transcript-3	9		
	· ·	/DB_XREF=gi:4758109			
	8	/UG=Hs.274348 HLA-B			
		associated transcript-3			
		/FL=gb:M33519.1			
		gb:NM_004639.1			
201256_at	2.05E-04	gb:NM_004718.1 /DEF=Homo	NM_004718		NP_004709
		sapiens cytochrome c oxidase	, ·· ·	1 1	
	*	subunit VIIa polypeptide 2 like			
	,	(COX7A2L), mRNA. /FEA=mRNA			
		/GEN=COX7A2L			
	<b>↓</b>	/PROD=cytochrome c oxidase	ļ		} ·
		subunit VIIa polypeptide 2like			8
		/DB_XREF=gi:4758041			,
	1	/UG=Hs.30888 cytochrome c	1		
		oxidase subunit VIIa polypeptide	1	* .	
i i	3	2 like /FL=gb:BC005251.1		. x	
	1	gb:AB007618.1 gb:NM_004718.1			<b>)</b>
·			<u></u>	<u> </u>	<u></u>

Gen Identifier	p-value	Description	Gene	Unig n	Protein
×			Accession	Acc ssion	Accession
			No.	No.	No.
201257_x_at	0.033381	gb:NM_001006.1 /DEF=Homo	NM_001006		NP_000997
		sapiens ribosomal protein S3A			,
,		(RPS3A), mRNA./FEA=mRNA	,		
*	. :	/GEN=RPS3A /PROD=ribosomal			- "
		protein S3A			
· · ·		/DB_XREF=gi:4506722			
8,		/UG=Hs.77039 ribosomal protein			
		S3A /FL=gb:BC000204.1			
70	* * )	gb:BC001708.1 gb:BC004981.1			* · · ·
	Ÿ	gb:M84711.1 gb:M77234.1			3
		gb:L13802.1 gb:NM_001006.1			
201260_s_at	0.033381	•	NM_006754	* ***	NP_006745
		sapiens synaptophysin-like protein			
* * =		(SYPL), mRNA: /FEA=mRNA			
		/GEN=SYPL			
<u>.</u>		/PROD=synaptophysin-like protein		· .	V
	,	/DB_XREF=gi:5803184		e)(e	
		/UG=Hs.80919 synaptophysin-like	*	T-2	=
		protein /FL=gb:NM_006754.1			4 *
201001					
201261_x_at	0.021045	gb:BC002416.1 /DEF=Homo	BC002416		NP_001702
*		sapiens, biglycan, clone			
		MGC:2298, mRNA, complete cds.		-0.5	
		/FEA=mRNA /PROD=biglycan	*		
		/DB_XREF=gi:12803216		0	ſ
		/UG=Hs.821 biglycan	l. :		
		/FL=gb:BC002416.1			· .
		gb:BC004244.1: gb:J04599.1			
		gb:NM_001711.1		٠.	
201264 ot	6 70E 04	ch:NM 007262.1 /DEE-Homo	NIM 007262		ND 000404
201264_at	0.79E-04	gb:NM_007263.1 /DEF=Homo	NM_007263		NP_009194
		sapiens coatomer protein			*
		complex, subunit epsilon (COPE), mRNA. /FEA=mRNA	÷ .		
		/GEN=COPE /PROD=coatomer		i E	
		protein complex, subunit epsilon	e i		* "
1		DB_XREF=gi:6005734			9
, ,		/UG=Hs.10326 coatomer protein	8		
		complex, subunit epsilon			·
		/FL=gb:AL136928.1	1 ::		7 .
		gb:BC003155.1 gb:NM_007263.1			٠.
L		[gb.bc003133.1 gb.NW_007263.1	L	L	

G ne Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201266_at	1.26E-04	gb:NM_003330.1 /DEF=Homo	NM_003330		NP_003321
		sapiens thioredoxin reductase 1			
		(TXNRD1), mRNA /FEA=mRNA	1		
		/GEN=TXNRD1			
,		/PROD=thioredoxin reductase 1	4.		
1.1		/DB_XREF=gi:4507746			1,13
	* *	/UG=Hs.13046 thioredoxin			
		reductase 1 /FL=gb:D88687.1		,	
		gb;AF077367.1 gb:NM_003330.1			
	, ,	gb:AF208018.1			
201268_at	0.02145	gb:NM_002512.1 /DEF=Homo	NM 002512	F 30 T Ex	NP_002503
		sapiens non-metastatic cells 2,			_
		protein (NM23B) expressed in	*	, F	0. "
**		(NME2), nuclear gene encoding		* -	
"		mitochondrial protein, mRNA.			
		/FEA=mRNA /GEN=NME2			
		/PROD=non-metastatic cells 2,			
		protein (NM23B)expressed in			
		/DB_XREF=gi:4505408	4		
		/UG=Hs.275163 non-metastatic			
		cells 2, protein (NM23B)			· ·
		expressed in /FL=gb BC002476.1			
		gb:M36981.1 gb:L16785.1		*.	1 -
		gb:NM_002512:1			
				-	
201273_s_at	5.03E-04	gb:NM_003133:1 /DEF=Homo	NM_003133		NP_003124
	.:	sapiens signal recognition particle			
		9kD (SRP9), mRNA.	t-	ā.:	
		/FEA=mRNA /GEN=SRP9			9
		/PROD=signal recognition particle			
		9kD /DB_XREF=gi:4507216			
		/UG=Hs.75975 signal recognition	*		_
		particle 9kD /FL=gb:NM_003133.1			**
		gb:U20998.1	[93]		
, * * .	,	* *	*		0
				_	

Gene ld ntifi r	p-value	Description	Gene	Unigen	Protein
	(		Accession	Accession	Accession
			No.	No.	No.
201275 at	2.05E-04	gb:NM 002004.1 /DEF=Homo	NM 002004		NP 001995
	,	sapiens farnesyl diphosphate	_		-7.
	·	synthase (farnesyl pyrophosphate			
=		synthetase,			)
		dimethylallyltranstransferase,			
		geranyltranstransferase) (FDPS),		: 7	
	ļ ·	mRNA. /FEA=mRNA /GEN=FDPS			
		/PROD=farnesyl_diphosphate			
*		synthase (farnesylpyrophosphate		• •	<i>y</i>
		synthetase,		0	
	1.3	dimethylallyltranstransferase,gerany			
	ET.	Iltranstransferase)			
	·	/DB_XREF=gi:4503684			
	9	/UG=Hs.77393 farnesyl		***	
		diphosphate synthase (farnesyl			· ·
				*	
		pyrophosphate synthetase,			
		dimethylallyltranstransferase,			
8		geranyltranstransferase)		΄,	*
		/FL=gb:J05262.1 gb:D14697.1		* *	
		gb:NM_002004.1			eles e
				12	
201277_s_at	3.26E-04	gb:NM_004499.1 /DEF=Homo	NM_004499		NP_112556
		sapiens heterogeneous nuclear			1
		ribonucleoprotein AB (HNRPAB),			
		mRNA /FEA=mRNA		. 4	
		/GEN=HNRPAB			
		/PROD=heterogeneous nuclear			
	. (0)	ribonucleoprotein AB			
: 1	•	/DB_XREF=gi:4758541			,
		/UG=Hs.81361 heterogeneous			
		nuclear ribonucleoprotein AB			
*		/FL=gb:BC002625.1	1 1 ×		. (
3		gb:BC004561.1 gb:M65028.1	1.5		
	*	gb:NM_004499.1			
201278_at	0.041055	disabled homolog 2, mitogen-	N21202		1
_		responsive phosphoprotein			
		(Drosophila)		Hs.81988	
201285 at	1.26E-04	gb:NM 013446.1 /DEF=Homo	NM 013446		NP_038474
· -	:	sapiens makorin, ring finger	,	*	_
*	1	protein, 1 (MKRN1), mRNA.			
·		/FEA=mRNA /GEN=MKRN1	1		
		/PROD=makorin, ring finger			
		protein, 1 /DB_XREF=gi;7305272		ŀ	
		/UG=Hs.7838 makorin, ring finger	Į ·		
		protein, 1 /FL=gb.AL136812.1			
		gb:AF192784.1 gb:NM_013446.1		1	
· · ·	1:		1	,	*
L	<u></u>		L.,,		<u> </u>

Gene Identifier	p-valu	Description	Gene	Unigene	Protein
			Acc ssion	Accession	Accession
		×	No.	No.	No.
201290_at	0.004341	gb:NM_014300.1 /DEF=Homo	NM_014300		NP_055115
4		sapiens signal peptidase complex			
,		(18kD) (SPC18), mRNA.		· ·	
	1	/FEA=mRNA /GEN=SPC18			
	*.*	/PROD=signal peptidase complex			
* .		(18kD) /DB_XREF=gi:7657608			
		/UG=Hs 9534 signal peptidase	* * * *	6.	
		complex (18kD)	] :		
/ - /		/FL=gb:BC000359.1			
		gb:AF061737.1 gb;AF108945.1			-
		gb:NM_014300.1			
				1.7	D
201296_s_at	0.00228	gb:NM_015626.1 /DEF=Homo	NM 015626	35.	NP 599027
77.		sapiens DKFZP564A122 protein	T		_
		(DKFZP564A122), mRNA.			ý *
		/FEA=mRNA	8 " 8		
		/GEN=DKFZP564A122			
		/PROD=DKFZP564A122 protein			
		/DB_XREF=gi:7661595			
	#	/UG=Hs.187991 DKFZP564A122	*	1	
		protein /FL=gb:AF106684.1	*		
		gb:NM_015626.1			
201297 s at	0.00228	Consensus includes	NM 018221	45	NP 060691
		gb:AK023321.1 /DEF=Homo			_
1. 1. A		sapiens cDNA FLJ13259 fis,			
		clone OVARC1000876,		,	
	*	moderately similar to MOB1			
		PROTEIN. /FEA=mRNA		44	\$ \$-
		/DB_XREF=gi:10435206			
		/UG=Hs.196437 hypothetical		* *	
N 1		protein FLJ10788			
		/FL=gb:AB016839.1			
* * *		gb:BC003398.1 gb:NM_018221.1			`
201298_s_at	2.05E-04		BC003398	1 - 22 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	NP 060691
		sapiens, hypothetical protein		,	
		FLJ10788, clone MGC:4929,			-)(- *
		mRNA, complete cds.	. 9		
		/FEA=mRNA /PROD=hypothetical			
. (		protein FLJ10788		1	
		/DB XREF=gi:13097287		<u> </u>	[
		/UG=Hs.196437 hypothetical			'
	. : ,	protein FLJ10788		*	
	0.00	/FL=gb:AB016839.1		[	·
100		gb:BC003398.1 gb:NM_018221.1			· .
		90.1111_010221.1	***		
L <u>.</u>	<u> </u>	L		<u> </u>	

G ne Identifier	p-value	Description	Gene	Unigene	Prot in
			Accession	Accession	Acc ssion
			No.	No.	No.
201301 s at	1.26E-04	gb:BC000182.1 /DEF=Homo	BC000182		NP_001144
		sapiens, annexin A4, clone			_
		MGC:2271, mRNA, complete cds.			
		/FEA=mRNA /PROD=annexin A4			
. *		/DB_XREF=gi:12652858	8		
* /	,	/UG=Hs.77840 annexin A4			* .
		/FL=gb:D78152.1 gb:BC000182.1	<b>.</b>	· ·	
	-	gb:M82809.1 gb:M19383.1		· :	
	2.8	gb:NM_001153.2			* * * * * * * * * * * * * * * * * * * *
		92.1111_001.100.2		8	• •
201302_at	1.26E-04	gb:NM_001153.2 /DEF=Homo	NM 001153	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NP_001144
20.002_ú	1.202.07	sapiens annexin A4 (ANXA4),	14141_001100		_001144
* *		mRNA. /FEA=mRNA	40% (A)		
		/GEN=ANXA4 /PROD=annexin IV			
		/DB_XREF=gi:4809272		* //	· .
	·	/UG=Hs:77840 annexin A4			
		/FL=gb:D78152.1 gb:BC000182.1			
		gb:M82809.1 gb:M19383.1			
204202 -1	0.055.04	gb:NM_001153:2	NIN 04 4740		ND SEEEE
201303_at	2.05E-04	gb:NM_014740.1 /DEF=Homo	NM_014740		NP_055555
		sapiens KIAA0111 gene product			
		(KIAA0111), mRNA. /FEA=mRNA	3		
		/GEN=KIAA0111	*		
	0	/PROD=KIAA0111 gene product			* (
		/DB_XREF=gi:7661919			
		/UG=Hs.79768 KIAA0111 gene	*		
		product /FL=gb:BC003662.1			·
		gb:BC004386.1 gb:D21853.1			
· · · · · · · · · · · · · · · · · · ·		gb:NM_014740.1			
201311_s_at	1.26E-04	SH3 domain binding glutamic acid-	AL515318	× ***	NP_003013
		rich protein like		Hs.408289	
201312_s_at	2.05E-04	gb:NM_003022/1 /DEF=Homo	NM_003022		NP_003013
		sapiens SH3 domain binding			
		glutamic acid-rich protein like			
1		(SH3BGRL), mRNA. /FEA=mRNA			,
		/GEN=SH3BGRL /PROD=SH3	•	6	
		domain binding glutamic acid-rich			;
,		proteinlike /DB XREF=gi:4506924			
0		/UG=Hs.14368 SH3 domain	· ()		•
1 1		binding glutamic acid-rich protein	(		
		like /FL=qb:AL136718.1			
		gb:AF042081.1 gb:NM_003022.1			
		3			
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Gene Identifier	p-value	Description	Gen	Unigene	Protein
- 8-	1,	"	Accession	Acc ssion	Accession
		*	No.	No.	No.
201317_s_at	5.03E-04	gb:NM_002787.1 /DEF=Homo	NM_002787		NP_002778
-	1	sapiens proteasome (prosome,		· .	-
	1	macropain) subunit, alpha type, 2		ļ .	
	**	(PSMA2), mRNA. /FEA=mRNA	٠.	=	1 1
		/GEN=PSMA2			
		/PROD=proteasome (prosome,			
		macropain) subunit, alphatype, 2			
		/DB_XREF=gi:4506180		•	
*		/UG=Hs.181309 proteasome			
		(prosome, macropain) subunit,			
	10	alpha type, 2			
		/FL=gb:NM_002787.1		* **	·
201318_s_at	1.26E-04	gb:NM_006471.1 /DEF=Homo	NM_006471	- 1	NP 006462
		sapiens myosin, light polypeptide,	<del>-</del> 5 • • • • • •		
	1	regulatory, non-sarcomeric (20kD)		. 1	·.
		(MLCB), mRNA. /FEA=mRNA			
	*	/GEN=MLCB /PROD=myosin, light			
		polypeptide, regulatory,non-			
		sarcomeric (20kD)			
		/DB_XREF=gi:5453739			
*		/UG=Hs.233936 myosin, light			
		polypeptide, regulatory, non-			
		sarcomeric (20kD)		U *	ľ
4 .		/FL=gb:NM_006471.1	'	•	
•		7. 2. g2900			
201319 at	0.010205	gb:NM 006471.1 /DEF=Homo	NM 006471	7 7 7 7 7 7	NP_006462
201010_0	0.010200	sapiens myosin, light polypeptide,	11111_000-17		141 _000402
		regulatory, non-sarcomeric (20kD)		40.7	
		(MLCB), mRNA. /FEA=mRNA	-		
		/GEN=MLCB /PROD=myosin, light			X
* .		polypeptide, regulatory,non-			
		sarcomeric (20kD)	* + +-		
		/DB_XREF=gi:5453739		, a	. "
4		//UG=Hs.233936 myosin, light	-		
		polypeptide, regulatory, non-	*		
	* *	sarcomeric (20kD)		ļ,·	
		/FL=gb:NM_006471.1			
		///L-gb.MM_0004/ 1.1		4:	}
			· ·		1 1

Gene Identifier	p-value	Description	Gene Accession No.	Unigen Accession No.	Protein Acc ssion No.
201322 at	7.58E-04	gb:NM 001686.1 /DEF=Homo	NM 001686		NP 001677
		sapiens ATP synthase, H+	- ·		70.9
•		transporting, mitochondrial F1	3		
		complex, beta polypeptide	8	* ()	/
		(ATP5B), nuclear gene encoding	*	0.7	*
		mitochondrial protein, mRNA.			
		/FEA=mRNA /GEN=ATP5B			
		/PROD=ATP synthase, H+	. •		
*	-	transporting, mitochondrial	* 1		
× .		F1complex, beta polypeptide		* .	
* * * * * * * * * * * * * * * * * * * *	. ** * -	/DB_XREF=gi:4502294 /UG=Hs.25			
		ATP synthase, H+ transporting,			
		mitochondrial F1 complex, beta		, a	.5
	· / · ·	polypeptide /FL=gb:D00022.1			
		gb:NM 001686.1			
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\		[gb.NIVI_UU1000.1			
1					
201000	0.055.04		4155550		
201328_at	2.05E-04	v-ets erythroblastosis virus E26	AL575509		
22722	2*1.142	oncogene homolog 2 (avian)		Hs.85146	
201329_s_at	0.041055	gb:NM_005239.1 /DEF=Homo	NM_005239	;	NP_005230
	1	sapiens v-ets avian			
		erythroblastosis virus E26		~	
*		oncogene homolog 2 (ETS2),			
		mRNA.:/FEA=mRNA /GEN=ETS2	•		1.
2		/PROD=v-ets avian			
		erythroblastosis virus E26			
		oncogenehomolog 2			
,		/DB_XREF=gi:4885220	3		
		/UG=Hs.85146 v-ets avian			
		erythroblastosis virus E26			- i
ı.	ļ ·	oncogene homolog 2			• .
		/FL=gb:J04102.1 gb:NM_005239.1		i.	* _
*					
201331_s_at	0.02145	gb:BC004973.1 /DEF=Homo	BC004973		NP_003144
		sapiens, signal transducer and			
		activator of transcription 6,			
		interleukin-4 induced, clone	,		1
	,	MGC:3649, mRNA, complete cds.			
*		//FEA=mRNA /PROD=signal	* .		·
		transducer and activator of	00.		
		transcription6, interleukin-4			
.0		induced /DB_XREF=gi:13436385			
		/UG=Hs.181015 signal transducer			
· · ·		and activator of transcription 6,			o
1		interleukin-4 induced			
		/FL=gb:BC004973.1			. (
		gb:NM_003153.1 gb:U16031.1			
			,		,

Gene Identifier	p-value	Description	G ne	Unigene	Protein
			Accession No.	Accession No.	Accession No.
201336 at	2.05E-04	gb:BC003570.1 /DEF=Homo	BC003570	110.	NP 004772
<del>,</del>		sapiens, Similar to vesicle-			
		associated membrane protein 3,	,	,	
8.		clone MGC:2110, mRNA,		l ta de de	
		complete cds. /FEA=mRNA			
	d	/PROD=Similar to vesicle-	. **		
		associated membrane protein3		. 0	·
*		/DB XREF=gi:13097737	1.3		
		1 77			
· · · · · · · · · · · · · · · · · · ·	*	/UG=Hs.66708 vesicle-associated			
	V	membrane protein 3 (cellubrevin)			
		/FL=gb:BC003570.1		*	
		gb:NM_004781.2			
201337_s_at	0.042536	gb:NM_004781.2 /DEF=Homo	NM_004781		NP_004772
		sapiens vesicle-associated		1 14	
		membrane protein 3 (cellubrevin)			
* *	*	(VAMP3), mRNA. /FEA=mRNA			
	4	/GEN=VAMP3 /PROD=vesicle-			
1 to 1 to 1 to 1 to 1 to 1 to 1 to 1 to		associated membrane protein 3		)-	
		/DB_XREF=gi:9257252			
		/UG=Hs.66708 vesicle-associated	*	:	
		membrane protein 3 (cellubrevin)			
		/FL=gb:BC003570.1			
		gb:NM_004781.2			
		gb.14141_004761.2			
201339 s_at	0.02145	gb:NM_002979.1 /DEF=Homo	NM 002979		NP 002970
201339_S_at	0.02143		11/10/_002979		INP_002970
	· ·	sapiens sterol carrier protein 2			* 1
		(SCP2), mRNA. /FEA=mRNA		•	
2. *		/GEN=SCP2 /PROD=sterol carrier			*
		protein 2 /DB_XREF=gi:4506822			
	§	/UG=Hs.75760 sterol carrier	40		
	1	protein 2 /FL=gb:M75883.1			4
		gb:M75884.1 gb:M55421.1			
		gb:NM_002979.1	2 -		
201343_at	7.58E-04	Consensus includes gb:BE621259	NM 003339		NP 003330
		/FEA=EST /DB_XREF=gi:9892197			
		/DB XREF=est:601493415F1			1
	. E	/CLONE=IMAGE:3895850	1 *		
·		/UG=Hs.108332 ubiquitin-			
		conjugating enzyme E2D 2			
11.		(homologous to yeast UBC45)	*	]	
		/FL=gb:U39317.1		ļ. , ·	
				*	
		gb:NM_003339.1			
	<u>l'.</u>		1	<u> </u>	<u> </u>

Gene Identifier	p-valu	D scription	Gene	Unigene	Protein
	-	*	Accession	Accession	Accession
	-		No.	No.	No.
201345_s_at	1.26E-04	gb:NM_003339.1 /DEF=Homo	NM_003339	-	NP_003330
<del></del> .	,	sapiens ubiquitin-conjugating	_	, ·	-
		enzyme E2D 2 (homologous to			W
	110	yeast UBC45) (UBE2D2), mRNA.			:
1		/FEA=mRNA /GEN=UBE2D2			
00.5		/PROD=ubiquitin-conjugating			* 1
		enzyme E2D 2 (homologousto	•		
		yeast UBC45)			
		/DB_XREF=gi:4507774			
		/UG=Hs.108332 ubiquitin-		* * 4 , 4	
*		conjugating enzyme E2D 2			*
		(homologous to yeast UBC45)			8
		/FL=gb:U39317.1		**	
		gb:NM_003339.1		**	
201346_at	0.007779	gb:NM_024551.1 /DEF=Homo	NM 024551		NP 078827
		sapiens hypothetical protein			<del>-</del>
		FLJ21432 (FLJ21432), mRNA.	. `		
*		/FEA=mRNA /GEN=FLJ21432	5**		
	4 **	/PROD=hypothetical protein			
		FLJ21432			6
		/DB_XREF=gi:13375714			
		/UG=Hs.11641 hypothetical			
		protein FLJ21432			
	i sa it i	/FL=gb:NM_024551.1	*		
		gb:BC004906:1			
201347_x at	0.033381		NM 012203		NP_036335
7 -		sapiens glyoxylate			
ec) y s		reductasehydroxypyruvate			
**		reductase (GRHPR), mRNA.			
		/FEA=mRNA /GEN=GRHPR			
		/PROD=glyoxylate			
*		reductasehydroxypyruvate	* *		
,		reductase /DB_XREF=gi:6912395			
		/UG=Hs.155742 glyoxylate	* *		
*		reductasehydroxypyruvate			
		reductase /FL=gb:AF113215.1	*		
		gb:BC000605.1 gb:BC003131.1	}		}
		gb:AF146018.1 gb:AF113251.1			
		gb:AF134895.1 gb:NM_012203.1			
201351_s_at	0.001116	gb:AF070656.1 /DEF=Homo	AF070656		NP_647474
		sapiens FtsH homolog mRNA,			
. *		complete cds. /FEA=mRNA			
<b>)</b> ' ' ' '		/PROD=FtsH homolog	1		
		/DB_XREF=gi:4454687	. ,	9	
* *	. «	/UG=Hs.206521 YME1	*** · · · ·		
e e	1	(S.cerevisiae)-like 1			
		/FL=gb:AF070656.1	}		
,	1	igb:NM_014263.1			ļ
<u> </u>	<del> </del>	192	<del></del>		

G ne Identifier	p-value	D scription	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201352_at	2.05E-04	gb:NM_014263.1 /DEF=Homo	NM 014263		NP 647474
· <del>-</del>		sapiens YME1 (S.cerevisiae)-like	-		
*		1 (YME1L1), mRNA.			
	4	/FEA=mRNA /GEN=YME1L1			× .
* 3.,	8.7	/PROD=YME1 (S.cerevisiae),like			
		1 /DB_XREF=gi:7657688			
		/UG=Hs.206521 YME1	,		- "
8-		(S.cerevisiae)-like 1			
*	1	/FL=gb:AF070656.1	*		
	•••	gb:NM_014263.1		<u> </u>	
201354_s_at	0.02141	Consensus includes gb:AA788652	NM_013449	. 7 7	NP_038477
*		/FEA=EST /DB_XREF=gi:2848772			<u>.</u>
		/DB_XREF=est:ah30a09.s1	* * * *		
		/CLONE=1240312 /UG=Hs 277401			
		bromodomain adjacent to zinc			
		finger domain, 2A	* 0		
		/FL=gb:AB032254.1			
		gb:NM_013449.1			
201358_s_at	0.041055	gb:NM_016451.1./DEF=Homo	NM_016451	, Y	NP_057535
		sapiens coatomer protein	41.		
		complex, subunit beta (COPB),	*		
+	8	mRNA. /FEA=mRNA			
		/GEN=COPB /PROD=coatomer			
		protein complex, subunit beta	**		
		/DB_XREF=gi:7705368			/
		/UG=Hs.3059 coatomer protéin		-	19
*		complex, subunit beta		(5)	
	1	/FL=gb:AF084457.1			
		gb:AL136593.1 gb:NM_016451.1		7	
201359_at	3.26E-04	gb:NM_016451.1 /DEF=Homo	NM_016451	18,24	NP_057535
		sapiens coatomer protein	* * **,		
		complex, subunit beta (COPB),			
W.	3.	mRNA. /FEA=mRNA			-00.
*		/GEN=COPB /PROD=coatomer			
	* "	protein complex, subunit beta			
11.00	1 :	/DB_XREF=gi:7705368		ai-	
		/UG=Hs.3059 coatomer protein			
	1 :	complex, subunit beta	-		
Ġe.		/FL=gb:AF084457.1			
1		gb:AL136593.1 gb:NM_016451.1		L	

Gen Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201362_at	0.001116	gb:AF205218.1 /DEF=Homo	AF205218		NP 006460
201002_0,		sapiens NS1-binding protein-like			
		protein mRNA, complete cds.			× ×
		/FEA=mRNA /PROD=NS1-binding			*.
		protein-like protein			· ·
		/DB XREF=gi:12003206			
* _					1000
		/UG=Hs.197298 NS1-binding		**************************************	
()0		protein /FL=gb:AF205218.1			
		gb:AB020657.1 gb:AF161553.1	-00		
004000	4 005 04	gb:NM_016389.1	4B000057		110 000100
201363_s_at	1.26E-04	gb:AB020657.1 /DEF=Homo	AB020657		NP_006460
		sapiens mRNA for KIAA0850			
,		protein, complete cds.			
		/FEA=mRNA /GEN=KIAA0850		-	* *
	1000	/PROD=KIAA0850 protein			
154		/DB_XREF=gi:4240188			
		/UG=Hs.197298 NS1-binding		-	-
		protein /FL=gb:AF205218.1			
		gb:AB020657.1 gb:AF161553.1	* " · · · ·		1 *
		gb:NM_016389.1	*	*	
201369_s_at	6.68E-04	gb:NM_006887.1 /DEF=Homo	NM_006887		NP_008818
		sapiens butyrate response factor			
9*	in a literatura	2 (EGF-response factor 2)			
		(BRF2), mRNA::/FEA=mRNA			
		/GEN=BRF2 /PROD=butyrate	*		
		response factor 2 (EGF-response			
		factor2) /DB_XREF=gi:5901899			
		/UG=Hs.78909 butyrate response		7	i '
		factor 2 (EGF-response factor 2)			
		/FL=gb:BC005010.1		4	
	1. The state of th	gb:NM_006887.1	1.0		
					,
	:				
201370_s_at	0.026891	cullin 3	AU145232	Hs 78946	NP 003581
201370_s_at		gb:AF062537.1 /DEF=Homo	AF062537	113.70340	NP 003581
2013/1_5_at	0.001710	sapiens cullin 3 mRNA, complete			141-7002501
		cds. /FEA=mRNA /PROD=cullin 3			
					Ċ
	1	//DB_XREF=gi:3139078			· ·
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		/UG=Hs.78946 cullin 3			* '
		/FL=gb:AF062537.1		ļ	
•	1	gb:AB014517.1 gb:AF052147.1			
	_	gb:AF064087.1 gb:NM_003590.1	}		
·				-	

Gene Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
		*	No.	No.	No
201375_s_at	2.05E-04	gb:NM_004156.1 /DEF=Homo	NM_004156		NP_004147
-		sapiens protein phosphatase 2		, 1)	
iic ·		(formerly 2A), catalytic subunit,		•	
		beta isoform (PPP2CB), mRNA.			
		/FEA=mRNA /GEN=PPP2CB			-
·		/PROD=protein phosphatase 2			,
	1	(formerly 2A), catalyticsubunit,		}	
		beta isoform			0.0
	1	/DB_XREF=gi:4758951	- 34	3	
		/UG=Hs.80350 protein	*		
		phosphatase 2 (formerly 2A),			
	. 1	catalytic subunit, beta isoform	0	*	•
		/FL=gb:NM_004156.1		,	
201379 s_at	0.033381	gb:NM_003288:1 /DEF=Homo	NM_003288		NP_003279
		sapiens tumor protein D52-like 2		٠	
		(TPD52L2), mRNA. /FEA=mRNA			
	*	/GEN=TPD52L2 /PROD=tumor			
		protein D52-like 2			-
		/DB_XREF=gi:4507642			9.0
		/UG=Hs.154718 tumor protein			
		D52-like 2 /FL=gb:AF004430.1			,
		gb:NM_003288.1	***		
201381_x_at	0.007779	gb:AF057356.1 /DEF=Homo	AF057356		NP_055227
	1.	sapiens calcyclin binding protein			
*		mRNA, complete cds.	1	*	
		/FEA=mRNA /PROD=calcyclin	* E		
		binding protein			
		/DB_XREF=gi:3063652			
*	J. 6	/UG=Hs.27258 calcyclin binding			
		protein /FL=gb:AF314752.1			
		gb:AF057356.1 gb:NM_014412.1			
201382_at	0.046687	gb:NM_014412.1 /DEF=Homo	NM_014412		NP_055227
3		sapiens calcyclin binding protein			
0.00	7	(CACYBP), mRNA, /FEA=mRNA			
	1 1	/GEN=CACYBP /PROD=calcyclin			
	,	binding protein	1		
		/DB_XREF=gi:7656951	,		
		/UG=Hs.27258 calcyclin binding	,	7	0
		protein /FL=gb:AF314752.1			
	Line	gb:AF057356.1 gb:NM_014412.1	THE THE STATE OF T		

Gene Identifi r	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201384 s_at	0.004341	gb:NM_005899.1 /DEF=Homo	NM_005899		NP 114068
	· •	sapiens membrane component,	-		<del>-</del>
		chromosome 17, surface marker	ļ	*	l i
1	* *	2 (ovarian carcinoma antigen			
	+	CA125) (M17S2), mRNA	α		
		/FEA=mRNA /GEN=M17S2			
		/PROD=membrane component,	, ,		
		chromosome 17, surfacemarker 2		· ()	
		(ovarian carcinoma antigen	*		. 00
*	1	CA125) /DB_XREF=gi:5174504		114	
		/UG=Hs.277721 membrane			
		component, chromosome 17,	*		
	7 i	surface marker 2 (ovarian	·		0
		carcinoma antigen CA125)	Property of the second		
		/FL=gb:D30756.1			
		gb:NM 005899.1			l "
		[gb.14]41_003699.1			
201386 s_at	0.012222	ab: A E 2 7 0 9 0 4 1 / DE E - Un ma	AE070004		NID 004240
201300_S_at	0.013223	gb:AF279891.1 /DEF=Homo	AF279891	7	NP_001349
		sapiens dead box protein 15		y 2	
**		mRNA, complete cds.	N	00	
		/FEA=mRNA /PROD=dead box		4	·
		protein 15 /DB_XREF=gi:9624452			
	7 (7 )	/UG=Hs.5683 DEADH (Asp-Glu-			
		Ala-AspHis) box polypeptide 15			· ·
		/FL=gb:AB001636.1		A STATE OF STATE	
		gb:NM_001358.1 gb:AF279891.1	•		
				100	
201390_s_at	0.00161	gb:NM_001320.1 /DEF=Homo	NM_001320		NP_001311
		sapiens casein kinase 2, beta			
:		polypeptide (CSNK2B), mRNA.			
ng.		/FEA=mRNA /GEN=CSNK2B			
	- 30	/PROD=casein kinase 2, beta			
	· ·	polypeptide			
		/DB_XREF=gi:10334850			•
		/UG=Hs.165843 casein kinase 2,	*	X	
		beta polypeptide	. · · ·		
<u> </u>	*	/FL=gb:NM_001320.1			-
201400_at	3.26E-04	gb:NM_002795.1 /DEF=Homo	NM_002795		NP_002786
		sapiens proteasome (prosome,		-0	
()		macropain) subunit, beta type, 3	ļ .	· ·	,
*	,	(PSMB3), mRNA. /FEA=mRNA			. ·
*		/GEN=PSMB3		7	
	,	/PROD=proteasome (prosome,		,	
		macropain) subunit, betatype, 3			
		/DB_XREF=gi:4506196			
, ,		/UG=Hs.82793 proteasome	]		·
		(prosome, macropain) subunit,			
	1	beta type, 3	ľ	:	ì
1		ibela type, 5			
		/FL=gb:NM_002795.1		*	

Gene Identifi r	p-value	Description	Gen	Unigene	Protein
*			Accession	Accession	Accession
			No.	No.	No.
201403 s_at	0.01185	gb:NM_004528.1 /DEF=Homo	NM 004528		NP 004519
		sapiens microsomal glutathione S		7	_
		transferase 3 (MGST3), mRNA.			
		/FEA=mRNA /GEN=MGST3			٠.
		/PROD=microsomal glutathione S-			
	1	transferase 3	**		
*		/DB_XREF=gi:4758713	8 (3)		0.
1.3		/UG=Hs.111811 microsomal		,	
		glutathione S-transferase 3			A-
()	•	/FL=gb:BC000505.1			,
		gb:BC003034.1 gb:AF026977.1			
8		gb:NM_004528.1			
			• • •		y
201407 s_at	0.010205	protein phosphatase 1, catalytic	Al186712	1 2 2 2 2 2	NP_002700
		subunit, beta isoform		Hs.21537	
201408_at	0.026891	protein phosphatase 1, catalytic	AI186712		NP_002700
		subunit, beta isoform		Hs.21537	
201409_s_at	1.26E-04	gb:NM_002709.1 /DEF=Homo	NM_002709		NP_002700
	, , , , , , , , , , , , , , , , , , ,	sapiens protein phosphatase 1,			
	0.0	catalytic subunit, beta isoform			*
		(PPP1CB), mRNA: /FEA=mRNA			
		/GEN=PPP1CB /PROD=protein		·	
		phosphatase 1, catalytic subunit,			έχ.
		betaisoform			N + - 2 - 24
		/DB_XREF=gi:4506004	1		
n - 8	1	/UG=Hs.21537 protein			
		phosphatase 1, catalytic subunit,			
, Million E	0	beta isoform			
		/FL=gb:NM_002709.1			
		gb:AF092905.1			
201410_at		ESTs	AI983043	Hs.409207	171 = 171
201412_at	7.58E-04	gb:NM_014045.1 /DEF=Homo	NM_014045		NP_054764
1		sapiens DKFZP564C1940 protein	*		
0.00		(DKFZP564C1940), mRNA.			1
		/FEA=mRNA	*		
	1	/GEN=DKFZP564C1940			
1	8 .	/PROD=DKFZP564C1940 protein			
	100	/DB_XREF=gi:13027587		:	
	1	/UG=Hs.3804 DKFZP564C1940			
	8	protein /FL=gb:BC000424.1		1	
	<u> </u>	gb:NM_014045.1 gb:AF131760.1	10001	l	L

Gene Identifier	p-valu	D scription	Gene	Unigene	Protein
	197	*	Accession	Accession	Accession
			No.	No.	No.
201422_at	0.001116	gb:NM_006332.1 /DEF=Homo	NM_006332		NP_006323
		sapiens interferon, gamma-			
		inducible protein 30 (IFI30),	l	. 0	
·"	*	mRNA. /FEA=mRNA /GEN=IFI30	1.4		7.
		/PROD=interferon, gamma-		÷	
		inducible protein 30	:		
		/DB_XREF=gi:5453695			
		/UG=Hs.14623 interferon, gamma-			ţ
	· ·	inducible protein 30			
		/FL=gb:J03909.1 gb:NM_006332.1			
		gb:AF097362.1	*		
201423_s_at	0.007779		AL037208	Hs.183874	NP_003580
201425_at	5.03E-04	gb:NM_000690.1 /DEF=Homo	NM_000690°	\$ 20	NP_000681
		sapiens aldehyde dehydrogenase			
		2, mitochondrial (ALDH2), mRNA.			
		/FEA=mRNA /GEN=ALDH2			
*		/PROD=aldehyde dehydrogenase			
		2, mitochondrial			
		/DB_XREF=gi:4502032			4
	8.	/UG=Hs.195432 aldehyde			1.7
	· /,	dehydrogenase 2 family			
1		(mitochondrial)		. '	
		/FL=gb:BC002967.1			
*		gb:NM_000690.1			*,***
201426_s_at	0.007779	vimentin	AI922599	Hs.297753	NP_000995
201429_s_at	0.005852	gb:NM_000998.1 /DEF=Homo	NM_000998		NP_000989
	4	sapiens ribosomal protein L37a			
		(RPL37A), mRNA. /FEA=mRNA			
		/GEN=RPL37A: /PROD=ribosomal			
*		protein L37a		190	
	4	/DB_XREF=gi:4506642		;	
	1 **	/UG=Hs.5566 ribosomal protein			
		L37a /FL=gb:BC000555.1			
	- 30	gb:L06499.1 gb:NM_000998.1			
201433_s_at	0.010205	gb:NM_014754.1 /DEF=Homo	NM_014754		NP_055569
		sapiens phosphatidylserine		l ·	
	1	synthase 1 (PTDSS1), mRNA.			] .
*		/FEA=mRNA /GEN=PTDSS1	-	σ.	
	v.	/PROD=phosphatidylserine			
		synthase 1	,	ļ	
		/DB_XREF=gi:7662646			
		/UG=Hs.77329 phosphatidylserine			
,		synthase 1 /FL=gb:BC004192.1			1
·	1	gb:BC004390.1 gb:D14694.1		Ι, .	
		gb:NM_014754.1			2

Gene ld ntifier	p-value	Description	G ne	Unigene Accession	Protein
			Accession		Accession
0044054	0.004044		No.	No. ^	No.
201435_s_at	0.004341	Consensus includes	NM_001968		NP_001959
		gb:AW268640 /FEA=EST	· ·		
	•	/DB_XREF=gi:6655670			
		/DB_XREF=est:xv52a03.x1	·		
		/CLONE=IMAGE:2816716			
		/UG=Hs.79306 eukaryotic	,		
		translation initiation factor 4E		. *	
	> ;	/FL=gb:M15353.1	*		
	•	gb:NM_001968.1			
201441_at	7.58E-04	gb:NM_001863.2 /DEF=Homo	NM_001863		NP_001854
*	1	sapiens cytochrome c oxidase			
		subunit VIb (COX6B), nuclear			
		gene encoding mitochondrial			
		protein, mRNA. /FEA=mRNA	şir.		
	<i>i</i>	/GEN=COX6B /PROD=cytochrome	0		
		c oxidase subunit VIb			
*		/DB XREF=gi:6680989			
		/UG=Hs.174031 cytochrome c			
		oxidase subunit VIb			*
		/FL=gb:BC001015.1			
		gb:BC002478.1 gb:NM_001863.2	0		
	***	3			
201443_s_at	0.033381	gb:AF248966.1 /DEF=Homo	AF248966		NP 005756
<b></b> ,		sapiens HT028 mRNA, complete	4	*	
	3 4	cds. /FEA=mRNA /PROD=HT028	- * · · · · · · · · · · · · · · · · · ·		
		/DB_XREF=gi:12005668	6.5		
		/UG=Hs.183434 ATPase, H+			
		transporting, lysosomal (vacuolar		*	
		proton pump) membrane sector			
	. <	associated protein M8-9	. 1		
		/FL=gb:AF248966.1		es e	
		gb:NM_005765.1			
		Idouani oo i	*	0.	i .

Gene Identifier	p-value	Description	Gene	Unigen	Protein
			Accession	Accession	Accession
		. *	No.	No.	No.
201444_s_at	1.26E-04	gb:NM_005765.1 /DEF=Homo	NM 005765		NP_005756
		sapiens ATPase, H+ transporting,	7	· .	<b>₹</b>
	• • •	lysosomal (vacuolar proton pump)			• • • •
		membrane sector associated	*		· ·
		protein M8-9 (APT6M8-9),			
		mRNA. /FEA=mRNA		. 0	
		/GEN=APT6M8-9	el e		
		/PROD=ATPase, H+ transporting,		*	
1 · · · ·		lysosomal (vacuolarproton pump)			
7 19 1		membrane sector associated			}
		protein M8-9			10
*		/DB_XREF=gi:5031590	. "		
		/UG=Hs.183434 ATPase, H+		A	
» i. , ·		transporting, lysosomal (vacuolar			·
		proton pump) membrane sector		,	
	• ,	1		ï.	
* (	:	associated protein M8-9		5	
		/FL=gb:AF248966.1			
		gb:NM_005765.1			
004450	E 00E 04	1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.	NIN 005044		ND COCOCE
201453_x_at	5.03E-04	_	NM_005614		NP_005605
		sapiens Ras homolog enriched in			
		brain 2 (RHEB2), mRNA.			
		/FEA=mRNA /GEN=RHEB2			
	•	/PROD=Ras homolog enriched in			/ " · .
		brain 2 /DB_XREF=gi:5032040			
		/UG=Hs.279903 Ras homolog	o .		
0.0	.,	enriched in brain 2		0	
- 1		/FL=gb:D78132.1	*		
* .	•	gb:NM_005614.1 gb:AF148645.1		1	
		8			-
201455_s_at	1.26E-04	Consensus includes	NM_006310	* 3	NP_006301
		gb:AJ132583.1:/DEF=Homo			
,		sapiens mRNA for puromycin	1.00	98	
V		sensitive aminopeptidase, partial.			
, · · · · · · · · · · · · · · · · · · ·	1	/FEA=mRNA /PROD=puromycin			1
*		sensitive aminopeptidase			
	ē	/DB_XREF=gi:4210725			1
		/UG=Hs.293007 aminopeptidase			
	. , *	puromycin sensitive			· ·
	,	/FL=gb:NM_006310.1			
201456_s_at	0.00161	BUB3 budding uninhibited by	AU160695	75	NP_004716
		benzimidazoles 3 homolog (yeast)		Hs.40323	

Gene Identifier	p-value	Description	Gene	Unigene	Protein
		* * * * * * * * * * * * * * * * * * * *	Accession	Accession	Acc ssion
			No.	No.	No.
201461_s_at	0.046906	gb:NM_004759.1 /DEF=Homo	NM_004759		NP_116584
		sapiens mitogen-activated protein			
		kinase-activated protein kinase 2			
		(MAPKAPK2), mRNA.	**	4	
		/FEA=mRNA /GEN=MAPKAPK2			
7 · 2 · 4	-	/PROD=mitogen-activated protein			
9	*	kinase-activatedprotein kinase 2	- 0		
		/DB_XREF=gi:10863900			
*	,	/UG=Hs.75074 mitogen-activated			
		protein kinase-activated protein		-	
	*	kinase 2 /FL=gb:NM_004759.1		1	
004400	0.005.04	gb:U12779.1	NI 000755		110 000740
201463_s_at	3.26E-04	gb:NM_006755.1 /DEF=Homo	NM_006755		NP_006746
W .	÷ .	sapiens transaldolase 1			
		(TALDO1), mRNA. /FEA=mRNA /GEN=TALDO1			,
	į.	/PROD=transaldolase 1			
	0	/DB XREF=gi:5803186		" ( °	
		/UG=Hs.77290 transaldolase 1		. "	
		/FL=gb:L19437.2 gb:NM_006755.1		0 *	
201470 at	2.05E-04	gb:NM_004832.1 /DEF=Homo	NM_004832		NP 004823
-		sapiens glutathione-S-transferase	*	-	<u></u>
		like; glutathione transferase			
		omega (GSTTLp28), mRNA.			ļ
		/FEA=mRNA /GEN=GSTTLp28			900
		/PROD=glutathione-S-transferase			
		like: /DB_XREF=gi:4758483			4
		/UG=Hs.11465 glutathione-S-			
	5	transferase like, glutathione		, 1	
	* * * * * * * * * * * * * * * * * * * *	transferase omega			i .
*		/FL=gb:BC000127.1 gb:U90313.1	1		
201170	5.005.04	gb:NM_004832.1 gb:AF212303.1			
201472_at	5.03E-04	gb:NM_003372.2 /DEF=Homo	NM_003372		NP_003363
		sapiens von Hippel-Lindau	]		
	-	binding protein 1 (VBP1), mRNA.	0).		
		/FEA=mRNA /GEN=VBP1		1	
		/PROD=von Hippel-Lindau binding protein 1 /DB_XREF=gi:9257253			]
		//UG=Hs.198307 von Hippel-			
		Lindau binding protein 1			194-
ì		/FL=gb:U96759.1			
-0.0					
*		gb:NM_003372.2			·

Gene Identifier	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201475_x_at	0.00228	gb:NM_004990.1 /DEF=Homo	NM_004990		NP_004981
	1	sapiens methionine-tRNA			
	1	synthetase (MARS), mRNA.			
		/FEA=mRNA /GEN=MARS			
C	1 .	/PROD=methionine-tRNA			
. *		synthetase /DB_XREF=gi:4826825		• 4	
		/UG=Hs.279946 methionine-tRNA	· .		
	1	synthetase /FL=gb:BC002384.1		*	
		gb:NM_004990.1 gb:D84224.1		,	0
					7
	1	Marine II	*		
201477_s_at	0.02145	gb:NM_001033.1 /DEF=Homo	NM_001033		NP_001024
6,		sapiens ribonucleotide reductase	;		
	* 1	M1 polypeptide (RRM1), mRNA.	• • •		
· *		/FEA=mRNA /GEN=RRM1	* * * * * * * * * * * * * * * * * * * *		
		/PROD=ribonucleotide_reductase			
* *		M1 polypeptide			
* (C		/DB_XREF=gi:4506748			
		/UG=Hs.2934 ribonucleotide			
		reductase M1 polypeptide			7
		/FL=gb:NM_001033.1			
201480_s_at	0.033381	gb:NM_003169.1 /DEF=Homo	NM_003169		NP_003160
		sapiens suppressor of Ty	*		
	Í	(S.cerevisiae) 5 homolog			·
		(SUPT5H), mRNA./FEA=mRNA			. (
: .		/GEN=SURT5H			
		/PROD=suppressor of Ty	8		ļ · · ·
	1 - ,	(S.cerevisiae) 5 homolog			
4.1	1	/DB_XREF=gi:4507312		;	
		/UG=Hs.70186 suppressor of Ty		į .	
		(S.cerevisiae) 5 homolog	=		
	1	/FL=gb:U56402.1 gb:AB000516.1	o •		
		gb:NM_003169.1			
201482_at	0.002536	gb:NM_002826.2 /DEF=Homo	NM_002826	-	NP_002817
1	1	sapiens quiescin Q6 (QSCN6),		*	
		mRNA. /FEA=mRNA			
	:	/GEN=QSCN6 /PROD=quiescin			
		Q6 /DB_XREF=gi:13325074			
		/UG=Hs.77266 quiescin Q6		1.	
\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		/FL=gb:L42379.1 gb:U97276.2			*
	1	gb:NM_002826.2			<u> </u>

G ne Identifier	p-value	Description	G ne	Unig ne	Protein
			Accession	Accession	Accession
			No.	No.	No.
201483_s_at	3.26E-04	gb:BC002802.1 /DEF=Homo	BC002802		NP_003159
		sapiens, suppressor of Ty			
		(S.cerevisiae) 4 homolog 1,		4.04	
		clone MGC:3864, mRNA,			
		complete cds. /FEA=mRNA	· · ·		
		/PROD=suppressor of Ty			
		(S.cerevisiae) 4 homolog 1		· ·	•
		/DB_XREF=gi:12803910			. ) **
360 T	-	/UG=Hs.79058 suppressor of Ty			
		(S.cerevisiae) 4 homolog 1			
		/FL=gb:BC002802.1 gb:U43923.1			·
		gb:U38818.1 gb:U38817.1			. /
		gb:NM_003168.1			
201487_at	3.26E-04		NM_001814		NP_680475
		sapiens cathepsin C (CTSC),			: 1
		mRNA /FEA=mRNA /GEN=CTSC			;
		/PROD=cathepsin C			·
		/DB_XREF=gi:4503140			X
*		/UG=Hs.10029 cathepsin C			
		/FL=gb:NM_001814.1	=	- 10	
201489_at	0.007779	10	BC005020	* 1	NP_005720
		sapiens, peptidylprolyl isomerase	1 + Y	1	
*		F (cyclophilin F), clone		1	
		MGC:11022, mRNA, complete			· · · · · ·
		cds. /FEA=mRNA			*
* "		/PROD=peptidylprolyl isomerase F	. 0		
i i		(cyclophilin F)	· .		. :
		/DB_XREF=gi:13477126			
		/UG=Hs.173125 peptidylprolyl	,		,
		isomerase F (cyclophilin F)	ļ		,
. ~		/FL=gb:BC005020:1 gb:M80254.1	1:		
201401	0.00404	gb:NM_005729.1	NINA (DADAAA		ND 000040
201491_at	0.00161	gb:NM_012111:1 /DEF=Homo	NM_012111		NP_036243
		sapiens chromosome 14 open			
	00	reading frame 3 (C14ORF3),		· -	
	·	mRNA. /FEA=mRNA /GEN=C14ORF3		100	
"					
		/PROD=chromosome 14 open reading frame 3			
*					
		/DB_XREF=gi:6912279 /UG=Hs.204041 chromosome 14			
<i>f</i>					
	)	open reading frame 3			
- H		/FL=gb:BC000321.1		*	
L	<u> </u>	gb:NM_012111.1 gb:AF164791.1			L

Gene Identifier	p-value	Description	Gene	Unigene	Protein
	,		Accession	Accession	Accession
	Ì		No.	No.	No.
201492 s_at	0.033381	gb:NM_021104.1 /DEF=Homo	NM 021104		NP_066927
201102 <u>-</u> 0_at	0.00000	sapiens ribosomal protein L41	021104	·	141 _000321
	1	(RPL41), mRNA. /FEA=mRNA	, ,		*
	1	/GEN=RPL41 /PROD=ribosomal		,	
•		protein L41			
	1.	/DB_XREF=gi:10863874			
	1.	I/UG=Hs.324406 ribosomal protein			*
×					
		L41 /FL=gb:NM_021104.1		*	
004400	2.005.04	7 O (O	DE330030	11 "0454	NO 050400
201493 <u>s</u> at		pumilio homolog 2 (Drosophila)	BE778078	Hs.6151	NP_056132
201494_at	1.26E-04	gb:NM_005040.1 /DEF=Homo	NM_005040		NP_005031
		sapiens prolylcarboxypeptidase		'	,.
Same Special Control		(angiotensinase C) (PRCP),			
		mRNA. /FEA=mRNA /GEN=PRCP			
	1	/PROD=prolylcarboxypeptidase			
		(angiotensinase C)	*		
* *		/DB_XREF=gi:4826939	. '		
()	*	/UG=Hs.75693		}	
*		prolylcarboxypeptidase			
		(angiotensinase C)		37	
		/FL=gb:L13977.1 gb:NM_005040.1			
	1 1 1		-:		
					*
201500_s_at	5.03E-04	gb:NM_021959.1 /DEF=Homo	NM_021959	1 a -	NP_740751
-:-		sapiens protein phosphatase 1,			
		regulatory (inhibitor) subunit 11	}		
		(PPP1R11), mRNA. /FEA=mRNA	in * or *		1.
		/GEN=PPP1R11 /PROD=protein			. '
		phosphatase 1, regulatory			
		(inhibitor)subunit 11			
	1	/DB_XREF=gi:11386174			
		/UG=Hs.82887 protein	, , , , , , , , , , , , , , , , , , ,		
		phosphatase 1, regulatory			
		(inhibitor) subunit 11			
-					
201507 -4	0.024490	/FL=gb:NM_021959.1	NA COCCO		ND 000040
201507_at	0.031189	gb:NM_002622.2 /DEF=Homo	NM_002622		NP_002613
		sapiens prefoldin 1 (PFDN1),			. '
		mRNA. /FEA=mRNA			
	111	/GEN=PFDN1 /PROD=prefoldin 1	*		
		/DB_XREF=gi:12408673			
*		/UG=Hs.132881 prefoldin 1			
"	1	/FL=gb:NM_002622.2		100	

Gene Identifier	p-value	Description	Gene	Unigene	Protein
, e			Acc ssion	Accession	Accession
			No.	No.	No.
201511_at	0.012818	gb:NM_001087.1 /DEF=Homo	NM_001087		NP_001078
-		sapiens angio-associated,			
		migratory cell protein (AAMP),	3(3)	*	
		mRNA. /FEA=mRNA			
		/GEN=AAMP /PROD=angio-			
		associated, migratory cell protein			
		/DB_XREF=gi:4557228			
		/UG=Hs.83347 angio-associated,		* : :	
	1.	migratory cell protein			
		/FL=gb:NM_001087.1	*		
		gb:M95627.1			
201515_s_at	0.02145	gb:NM_004622.1 /DEF=Homo	NM_004622		NP_004613
		sapiens translin (TSN), mRNA		,	
		/FEA=mRNA /GEN=TSN 😘			
		/PROD=translin			* * * * * * * * * * * * * * * * * * * *
		/DB_XREF=gi:4759269			1. S. 11.
	s = )	/UG=Hs.75066 translin		. 6	
- 1		/FL=gb:NM_004622.1			
201518_at	0.00161		NM_006807		NP_006798
		sapiens chromobox homolog 1 ·			
		(Drosophila HP1 beta) (CBX1),	* * * *		,
		mRNA. /FEA=mRNA /GEN=CBX1			
* 0.	1	/PROD=chromobox homolog 1	,		
		(Drosophila HP1 beta)			
		/DB_XREF=gi:5803075			
		/UG=Hs.77254 chromobox	. 0		
78 . A .		homolog 1 (Drosophila HP1	4.4	÷ .	
		beta) /FL=gb:U35451.1	1((a :		
		gb:BC002609.1 gb:NM_006807.1			
201527_at	0.00161	gb:NM_004231.1 /DEF=Homo	NM_004231		NP_004222
	1.5	sapiens ATPase, vacuolar, 14 kD		,	
	1-0	(ATP6S14), mRNA: /FEA=mRNA			* 11 / 1
* .		/GEN=ATP6S14 /PROD=ATPase,		*	
, • ,		vacuolar, 14 kD		. ·	
	] ; · · .	/DB_XREF=gi:4757819			
* * * *		/UG=Hs.78089 ATPase, vacuolar,		<b>\</b>	-20
		14 kD /FL=gb:D49400.1			
*	10	gb:NM_004231.1		1.	
			× ×		L .

G ne Identifier	p-value	Description	Gene	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201533_at	0.013223	gb:NM_001904.1 /DEF=Homo	NM_001904		NP_001895
		sapiens catenin (cadherin-			<del></del>
		associated protein), beta 1	·		
		(88kD) (CTNNB1), mRNA.	T e E		
-		/FEA=mRNA /GEN=CTNNB1	. ".	*	
* .		/PROD=catenin (cadherin-			*
		associated protein), beta 1(88kD)			
1		/DB XREF=gi:4503130	l e		
		/UG=Hs.171271 catenin (cadherin-			
		associated protein), beta 1	l the gi		. 1
		(88kD) /FL=gb:NM_001904.1			
				100	
201535_at	0.001116	gb:NM 007106.1 /DEF=Homo	NM 007106		NP 009037
		sapiens ubiquitin-like 3 (UBL3),	· · · ·		
*		mRNA. /FEA=mRNA /GEN=UBL3		\$* )	
		/PROD=ubiquitin-like 3			
0,		/DB_XREF=gi:6005927			-
*		/UG=Hs.173091 ubiquitin-like 3			
		/FL=gb:AF044221.1		** ** **	
(b		gb:AL080177.1 gb:NM_007106.1			
201539 s_at	0.023827	gb:U29538.1 /DEF=Human heart	U29538		NP 001440
	3.0202	protein with four and a half LIM		* * *	
		domains (FHL-1) mRNA,		9	
		complete cds. /FEA=mRNA			
		/GEN=FHL-1		· .	٠.
		/DB_XREF=gi:2078479			)
1.0		/UG=Hs.239069 four and a half			ĺ .
	-7-	LIM domains 1 /FL=gb:U29538.1		*	
		gb:U60115.1 gb:NM_001449.1			
		gs.000110.1 gs.11111_001443.1			
201541_s_at	0.001054	gb:NM 006349.1 /DEF=Homo	NM 006349	2 1	NP 006340
1201041_5_ut	0.001007	sapiens putative cyclin G1	11111_000010		-000010
		interacting protein (CG1I), mRNA.	1	. =	
*		/FEA=mRNA /GEN=CG1I	14. P		
	-	/PROD=putative cyclin G1			*
		interacting protein	•		-
	\	/DB XREF=gi:5453616			
	ľ	/UG=Hs.10028 putative cyclin G1			
		interacting protein			. ,
		/FL=gb:U61837.1		1	· .
		gb:NM 006349.1			
201543_s_at	0.016405	gb:NM_020150.1 /DEF=Homo	NM 020150	-	
201045_5_at	0.010493	1 · . —	14141_020130		31 ·
· · · · · · · · · · · · · · · · · · ·		sapiens SAR1 protein (SAR1), mRNA. /FEA=mRNA /GEN=SAR1		-	
		/PROD=SAR1 protein			0
		· · · · · · · · · · · · · · · · · · ·			e
		//DB_XREF=gi:9910541			*
*	1	/UG=Hs.110796 SAR1 protein			}
	-	/FL=gb:AY008268.1			1
8		gb:AL136724.1 gb:AF261717.1			
L	1	gb:NM_020150.1	<u> </u>	<u> </u>	<u> </u>

G n Identifier	p-value	D scription	Gene	Unigene	Prot in
			Accession	Accession	Accession
			No.	No.	No.
201546_at	1.26E-04	gb:NM 004238.1 /DEF=Homo	NM_004238		NP 004229
a.	1.232 0	sapiens thyroid hormone receptor	55 ,255	- ·	
		interactor 12 (TRIP12), mRNA.			
1 1		/FEA=mRNA /GEN=TRIP12		· ¥	
		/PROD=thyroid hormone receptor			
* *		interactor 12			
		/DB_XREF=gi:10863902	e * .	*	
•		/UG=Hs.138617 thyroid hormone		- i j	
		receptor interactor 12			
		/FL=gb:NM_004238.1			
		gb:D28476.1		·	
201548_s_at	0.016034	putative DNA/chromatin binding	AA729218		NP 006609
201340_S_at	0.010934	Imotif	AA123210	Hs.143323	145_000009
201549_x_at	0.00228	gb:NM 006618.1 /DEF=Homo	NM 006618	113.143323	NP_006609
(20 1349_X_at	0.00228	sapiens putative DNAchromatin	14141-000010		144-000009
		binding motif (PLU-1), mRNA.			
		/FEA=mRNA /GEN=PLU-1			
e .		/PROD=putative DNAchromatin			4.0
	-				7
		binding motif. As a second			
	. 4 14 1	/DB_XREF=gi:5729977	(3)		
		/UG=Hs.143323 putative	1		
		DNAchromatin binding motif			
004550	1 005 64	/FL=gb:NM_006618.1	NIM COFFOA		ND 005550
201552_at	1.26E-04	gb:NM_005561.2 /DEF=Homo	NM_005561		NP_005552
aye	,	sapiens lysosomal-associated		-	
1	1	membrane protein 1 (LAMP1),		*	
		mRNA. /FEA=mRNA	1-4		
	*	/GEN=LAMP1 /PROD=lysosomal-		-11-	
		associated membrane protein 1			
	ا مناسب	/DB_XREF=gi:7669500		c **C	1 44
		/UG=Hs.150101 lysosomal-		:	
		associated membrane protein 1			l
	-	/FL=gb:J04182.1 gb:J03263.1			
		gb:NM_005561.2			
004550	0.0005		NIA 205501		ND OCESES
201553_s_at	0.00228	gb:NM_005561.2 /DEF=Homo	NM_005561	,	NP_005552
		sapiens lysosomal-associated		-	
		membrane protein 1 (LAMP1),	*		"
· · · · · · · · · · · · · · · · · · ·		mRNA. /FEA=mRNA			
	1	/GEN=LAMP1 /PROD=lysosomal-	-3		,
		associated membrane protein 1			Q. v. (
1		/DB_XREF=gi:7669500			
		/UG=Hs.150101 lysosomal-			· ·
1 .		associated membrane protein 1			
		/FL=gb:J04182.1 gb;J03263.1			
		gb:NM_005561.2			
					L

Gene Identifier	p-value	Description	G ne	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201554_x_at	1.26E-04	gb:NM_004130.1 /DEF=Homo	NM_004130		NP_004121
J*	1	sapiens glycogenin (GYG),			
		mRNA. /FEA=mRNA /GEN=GYG			* 1 mg
,		/PROD=glycogenin			
· · ·		/DB_XREF=gi:4758491		:	
		/UG=Hs.174071 glycogenin	:		
,		/FL=gb:U44131.1 gb:BC000033.1			
		gb:NM_004130.1 gb:U31525.1.	•		
201558_at	1.26E-04	gb:NM_003610.1 /DEF=Homo	NM_003610		NP_003601
	-	sapiens RAE1 (RNA export 1,			
		S.pombe) homolog (RAE1),	<b>&gt;</b> ****		
		mRNA. /FEA=mRNA /GEN=RAE1			·
		/PROD=RAE1 (RNA export 1,			
		S.pombe) homolog			
		/DB_XREF=gi:4506398	*		
		/UG=Hs.196209 RAE1 (RNA			
		export 1, S.pombe) homolog	•	*	
		/FL=gb:U84720:1	]		
		gb:NM_003610.1		1	
201561_s_at	0.002418	gb:NM_014944.1:/DEF=Homo	NM_014944		NP_055759
		sapiens KIAA0911 protein		,	
		(KIAA0911), mRNA /FEA=mRNA		į.	
		/GEN=KIAA0911			
		/PROD=KIAA0911 protein		W : :	
		/DB_XREF=gi:7662373		1	
		/UG=Hs.29665 KIAA0911 protein	(8)	,	
*		/FL=gb:AB020718.1			
	3. 1	gb:NM_014944.1		,	
201563_at	0.007779	10	L29008		NP_003095
*		2 dehydrogenase mRNA,			
*		complete cds/FEA=mRNA	•)(s	Y	
*	. •	/PROD=L-iditol-2 dehydrogenase	i i		, '
		/DB_XREF=gi:496077 /UG=Hs.878		-	-
•	1	sorbitol dehydrôgenase			1.7
		/FL=gb:NM_003104.1 gb:L29008.1			
1. 1.		gb:U07361.1		* *	
			,		
201566_x_at	0.010205	gb:D13891.1 /DEF=Human mRNA	D13891		NP_002157
		for Id-2H, complete cds.	0.0		
. ``		/FEA=mRNA /GEN=Id-2H	*		
	.0	/PROD=Id-2H			
		/DB_XREF=gi:464183			
) · ·		/UG=Hs.180919 inhibitor of DNA			<u>,</u>
		binding 2, dominant negative		-	]
		helix-loop-helix protein			
4		/FL=gb:M97796.1	2		
		gb:NM_002166.1 gb:D13891.1		<u> </u>	<u> </u>

Gene Identifier	p-value	Description	Gen	Unigene	Protein
			Accession	Accession	Accession
			No.	No.	No.
201573_s_at	2.76E-04	gb:M75715.1 /DEF=Human TB3-1			NP_004721
7.7		mRNA, complete cds.			_
		/FEA=mRNA /PROD=TB3-1			
		/DB XREF=gi:338686			
		/UG=Hs.77324 eukaryotic	*		
`		translation termination factor 1.	8	* *	*
		/FL=gb:U90176.1 gb:M75715.1		· ,	
		gb:NM 004730.1	, , , , ,		
201574_at		gb:NM 004730.1 /DEF=Homo	NM 004730	7 7	NP 004721
		sapiens eukaryotic translation			
		termination factor 1 (ETF1),	,		
	*	mRNA. /FEA=mRNA /GEN=ETF1	1 / V	*	\ -
. * * *		/PROD=eukaryotic translation			
0.85		termination factor 1			
		/DB_XREF=gi:4759033		: *	
	3.00	/UG=Hs.77324 eukaryotic			
		translation termination factor 1			
		/FL=gb:U90176.1 gb:M75715.1			
		gb:NM 004730.1			
201575 at	0.013223	gb:NM_012245.1 /DEF=Homo	NM 012245		NP_036377
		sapiens SKI-INTERACTING	-		· -
		PROTEIN (SNW1), mRNA.	:		
		/FEA=mRNA /GEN=SNW1			
*		/PROD=SKI-INTERACTING			
		PROTEIN /DB_XREF=gi:6912675			
		/UG=Hs.79008 SKI-		4.0	
: //	* 0	INTERACTING PROTEIN			
		/FL=gb:U51432.1 gb:AF045184.1			9
		gb:NM_012245.1		3	
201576_s at	1.26E-04	gb:NM_000404.1 /DEF=Homo	NM 000404		NP_000395
		sapiens galactosidase, beta 1	· · ·		
	0	(GLB1), mRNA. /FEA=mRNA			
		/GEN=GLB1	**		
		/PROD=galactosidase, beta 1		:	) y
		/DB_XREF=gi:10834965	3.0	1	
	.0	/UG=Hs 79222 galactosidase,		·	-
		beta 1 /FL=gb:NM_000404.1			
		gb:M27507.1 gb:M22590.1	*	* .	
		gb:M34423.1	- 30		
201581 at	0.005852	hypothetical protein DJ971N18.2	AL544094	Hs.169358	NP 066979

Gene Identifier	p-value	Description	G ne	Unigene	Protein
4			Acc ssion	Accession	Accession
	4		No.	No.	No.
201582_at	0.001911	Consensus includes gb:AL121900	AL121900		
	1	/DEF=Human DNA sequence			
		from clone RP11-379J5 on			
		chromosome 20 Contains the			
4	1	last exon of the SEC23B gene			
		for Sec23 (S. cerevisiae)			
	1.	homolog B, a putative novel			
		gene, the 5 end of the gene for			
·#		a novel protein similar to	( )()		
		bacterial histidyl-tRNA synthetas			
		/FEA=mRNA			
		/DB_XREF=gi:11121203			
	- 4	/UG=Hs.173497 Sec23 (S.			
		cerevisiae) homolog B		. :	٠.
		/FL=gb:BC005404.1			. "
· ·		gb.NM_006363.1	· ·	- 00	3
201583_s_at	1 26F-04	gb:NM 006363.1 /DEF=Homo	NM 006363	= ()	NP 11678
	1.202.07	sapiens Sec23 (S. cerevisiae)	1000000		1.11 _ 1.107.0
		homolog B (SEC23B), mRNA.	l'		3.
The second second second		/FEA=mRNA /GEN=SEC23B			
1		/PROD=Sec23 (S. cerevisiae)			
		homolog B			
		/DB_XREF=gi:5454043			
		/UG=Hs.173497 Sec23 (S.			
	4	cerevisiae) homolog B			
		/FL=gb:BC005404.1			
	1,	, , ,			
204500 - 04	0.004446	gb:NM_006363.1	NINA COECCC	The second section is a second section of the second section is a second section of the second section is a second section of the second section is a second section of the second section is a second section of the second section is a second section of the second section is a second section of the section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the second section of the section of the second section of the section of	ND 00505
201586_s_at	0.001116	gb:NM_005066.1 /DEF=Homo	NM_005066		NP_00505
		sapiens splicing factor			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		prolineglutamine rich			
		(polypyrimidine tract-binding			1
		protein-associated) (SFPQ),			
	1 2	mRNA. /FÉA=mRNA /GEN=SFPQ		* : *	100
	• 6	/PROD=splicing factor			
		prolineglutamine			
_ *		rich(polypyrimidine tract-binding	1		}
		protein-associated)	:		
		/DB_XREF=gi:4826997	*		
•'		/UG=Hs.180610 splicing factor		1	,
		prolineglutamine rich		1	*
*		(polypyrimidine tract-binding			]
		protein-associated)		*	
		/FL=gb:NM_005066.1			

Gen Identifier	p-value	Description	Gene	Unigene	Prot in
			Accession	Accession	Accession
-	· ·		No.	No.	No.
201587_s_at	0.007779	gb:NM_001569.2 /DEF=Homo	NM_001569		NP_001560
		sapiens interleukin-1 receptor-	* 1		
*	o <b>:</b>	associated kinase 1 (IRAK1),	. 8		
		mRNA /FEA=mRNA /GEN=IRAK1 /PROD=interleukin-1			
		receptor-associated kinase 1			
		/DB_XREF=gi:4755143			
		/UG=Hs.182018 interleukin-1			
	1	receptor-associated kinase 1	* ***		*
*		/FL=gb:L76191:1 gb:NM_001569.2			
					* * * * * * * * * * * * * * * * * * * *
201588_at	0.00161	gb:NM_004786.1 /DEF=Homo	NM_004786		NP_004777
		sapiens thioredoxin-like, 32kD			
		(TXNL), mRNA. /FEA=mRNA	. 50		
		/GEN=TXNL /PROD=thioredoxin- like, 32kD /DB_XREF=gi:4759273			
	S. 1. 1. 1.	/UG=Hs.18792 thioredoxin-like,	" with the same of the same	. 3	
		32kD /FL=gb:BC001156.1			
		gb:AF003938.1 gb:AF051896.1			
		gb:AF052659.1 gb:NM_004786.1		·	
		7			
201589_at	5.03E-04		D80000		NP_006297
		/DEF=Human mRNA for			
		KIAA0178 gene, partial cds.		4	
		/FEA=mRNA /GEN=KIAA0178		· · · · · · · · · · · ·	
	6.	/DB_XREF=gi:1136415			
		/UG=Hs.211602 SMC1 (structural maintenance of chromosomes 1,	70.		
		yeast)-like 1 /FL=gb:NM 006306.1		•	
(m) 1		yeast, ii.e. 1 71 2. gb.1111_000000.1			
201593_s_at	3.26E-04	uncharacterized hypothalamus	AV716798		NP_060941
		protein HT010		Hs.6375	
201594_s_at	0.00161	10 -	NM_005134		NP_005125
		sapiens protein phosphatase 4,			
- 1		regulatory subunit 1 (PPP4R1),			
	1	mRNA. /FEA=mRNA			
		/GEN=PPP4R1 /PROD=protein			
		phosphatase 4, regulatory subunit 1 /DB_XREF=gi:4826933	*		
		/UG=Hs.3382 protein	2.34	*	
		phosphatase 4, regulatory subunit			
1	*	1 /FL=gb:AF111106.1			
		gb:NM_005134.1 gb:AF100744.1	-		

Gene Identifier	p-value	Description	Gene	Unigene	Protein
(a) (b) (c) (c) (d)		* * *	Accession	Accession	Accession
			No.	No.	No.
201595_s_at	0.016934	gb:NM_018471.1 /DEF=Homo	NM_018471		NP_060941
1.	1	sapiens uncharacterized			
	- i	hypothalamus protein HT010			<b>)</b> .
a a		(HT010), mRNA. /FEA=mRNA			
	,	/GEN=HT010			
	1	/PROD=uncharacterized			
		hypothalamus protein HT010	, i :		, '
		/DB_XREF=gi:8923807			1.00
		/UG=Hs.6375 uncharacterized			
		hypothalamus protein HT010			
		/FL=gb:AF220184.1		-	
		gb:NM_018471.1		#1	
201597_at	0.007779	gb:NM_001865.1 /DEF=Homo	NM 001865		NP 001856
	1,5.55,7,7	sapiens cytochrome c oxidase	551555		
		subunit VIIa polypeptide 2 (liver)	. 12		
		(COX7A2), nuclear gene			
	,	encoding mitochondrial protein,	10.00		
		mRNA. /FEA=mRNA	**		
		/GEN=COX7A2			
		/PROD=cytochrome c oxidase			
	0.5				
	4	subunit VIIa polypeptide 2(liver)		- ' : '	
		/DB_XREF=gi:4502988			
		/UG=Hs.70312 cytochrome c			
		oxidase subunit VIIa polypeptide			·.
		2 (liver) /FL=gb:NM_001865.1			
					3
201599_at	1.26E-04	gb:NM_000274.1 /DEF=Homo	NM_000274		NP_000265
		sapiens ornithine	8		
* *		aminotransferase (gyrate atrophy)			50
		(OAT), nuclear gene encoding			
		mitochondrial protein, mRNA.	i i		
	1 1	/FEA=mRNA /GEN=OAT			
		/PROD=ornithine aminotransferase			
	C-	precursor /DB_XREF=gi:4557808	9		*
*		/UG=Hs.75485 ornithine	. ,		
		aminotransferase (gyrate atrophy)	*		
	* * * * * * * * * * * * * * * * * * * *	/FL=gb:BC000964.1 gb:M12267.1	1,5		3.
ľ		gb:M23204.1 gb:M14963.1			(1)
		gb:NM_000274.1			1
	, '	2		h	
201602_s_at	6.68E-04	Consensus includes gb.BE737620	NM_002480	•	NP_002471
		/FEA=EST	_		<u> </u>
(		/DB_XREF=gi:10151612			
* *		/DB_XREF=est:601572895F1	. ,	- 3	
· ·		/CLONE=IMAGE:3839831		· ·	0
		/UG=Hs.16533 myosin		· ·	
1,		phosphatase, target subunit 1			
	70	/FL=gb:NM 002480.1		2	
	l'	17. E GD.14141_00Z-700.1	I	<u> </u>	L.:

Gene Identifier	p-value	D scription	Gene	Unigene	Prot in
		*	Accession	Accession	Acc ssion
			No.	No.	No.
201603_at	7.58E-04	Consensus includes gb:Al817061	NM_002480		NP_002471
- · . · .		/FEA=EST /DB_XREF=gi:5436140	. *		- ·
		/DB_XREF=est:wj76e05.x1			
r · · · · · · ·		/CLONE=IMAGE:2408768		1 100	
7 - 14		/UG=Hs.16533 myosin			
		phosphatase, target subunit 1	-1-		
	,	/FL=gb:NM_002480.1		. )	
			3		
201604_s_at	0.016934	gb:NM_002480.1 /DEF=Homo	NM_002480		NP_002471
, 1		sapiens myosin phosphatase,			j
• •		target subunit 1 (MYPT1),		• •	
	0	mRNA.:/FEA=mRNA		- 1 1	
		/GEN=MYPT1 /PROD=myosin			
		phosphatase target subunit 1			
		/DB_XREF=gi:4505316		}	
		/UG=Hs.16533 myosin			٠
1		phosphatase, target subunit 1			
	* - 3-2-5	/FL=gb:NM_002480.1			
201605_x_at	0.026891	gb:NM_004368.1 /DEF=Homo	NM_004368		NP_004359
		sapiens calponin 2 (CNN2),			
		mRNA. /FEA=mRNA /GEN=CNN2			
		/PROD=calponin 2			
\ .		/DB_XREF=gi:4758017		× .	•
* :	•	/UG=Hs.169718 calponin 2			
/ '		/FL=gb:D83735.1			
2046264	0.004440	gb:NM_004368.1	DE-200004		ND 000000
201606_s_at	0.001116	nuclear phosphoprotein similar to	BE796924	Un 170500	NP_008993
201609 x at	0.00545	S. cerevisiae PWP1 isoprenylcysteine carboxyl	AL578502	Hs.172589	NP 733806
201609_x_at	0.00545		AL3/0302	Hs.183212	NF_/33606
201619_at	1 265 04	methyltransferase gb:NM_006793.1 /DEF=Homo	NM 006793	ITIS. 103212	NP_006784
201019_at	1.205-04	sapiens peroxiredoxin- 3	14M_000193	*	147_000704
is .		(PRDX3), nuclear gene encoding		0 .	ė.
:		mitochondrial protein, mRNA.	9.1		
		/FEA=mRNA /GEN=PRDX3			
• •		/PROD=peroxiredoxin 3		;	
· · · · · · · · · · · · · · · · · · ·		/DB XREF=gi:5802973			
• *		/UG=Hs.75454 peroxiredoxin 3			·
·		/FL=gb:BC002685.1	* '.	[ ;	
÷ i	i	gb:NM_006793.1 gb:D49396.1			
		[32 <u>000.00</u> 90.0-10000	1	ı	